Chapter 11
DNA in the Courtroom

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I. INTRODUCTION[1]

§ 11:1 Overview

English geneticist Alec Jeffreys first described a method for "typing" human DNA in 1985. Since that time, DNA typing technology has advanced rapidly and the new DNA tests have been embraced eagerly by the criminal justice system. DNA tests are now routinely used to help identify the source of blood, semen, hair and other biological materials found at crime scenes and to establish family relationships in cases of disputed parentage. DNA tests have helped prosecutors obtain convictions in thousands of cases and have helped establish the innocence of thousands of individuals who might otherwise have become suspects.

Though it has been invaluable to the justice system, DNA evidence has the potential to be tremendously misleading in some cases. DNA tests can be botched, misinterpreted,

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[1]William C. Thompson, J.D., Ph.D. and Dan E. Krane, Ph.D., are the authors of sections 11:1 through 11:43. William Thompson is a professor in the Department of Criminology, Law & Society at the University of California, Irvine and a member of the California Bar. A frequent speaker on DNA and other matters, he has also written extensively about forensic DNA evidence and has represented a number of defendants in cases that turned on DNA evidence. He also serves Head Librarian for the NLADA on-line forensics library at www.nlada.org/Defender/forensics.

Dan E. Krane is an Associate Professor in the Department of Biological Sciences at Wright State University where he has been a faculty member since 1993. His research interests are primarily in the areas of molecular evolution and the way that gene frequencies change over the course of time in populations of organisms. He has published widely on the subject of forensic DNA testing and has testified in over 40 criminal cases since 1991 as an expert for both the prosecution and defense in the areas of population genetics, molecular biology and bioinformatics. He is also the president and founder of Forensic Bioinformatic Services, Inc (bioforensics.com) where he has overseen the development and implementation of software designed to automatically and objectively review STR DNA testing results.

mischaracterized and misunderstood. Cases have come to light in which innocent people were convicted based on bad DNA evidence. Controversy continues over how to assure the reliability of DNA tests and how to describe the statistical significance of test results. The issues lawyers face when dealing with DNA evidence can be extraordinarily complex and confusing.

This chapter is designed to help lawyers make sense of DNA evidence. It aims to be comprehensible even to the science-phobic while providing enough detail to allow understanding of the real issues.

Section I (Introduction) begins with a broad overview of the different DNA tests that lawyers may encounter, describing in general terms the strengths and weaknesses of each test. This overview will be particularly helpful for those who are encountering DNA evidence for the first time and for those who find themselves losing track of the "big picture" while wading through technical details (a common experience among lawyers who litigate DNA cases). Section II (A Closer Look at the Science of DNA Testing) provides a more detailed and technical account of the various DNA typing methods and includes discussion of steps lawyers should take to evaluate evidence generated by each method. It offers extensive coverage of the automated STR tests that are currently the most widely used. Section III (How the Courts Have Approached DNA Testing) provides a review of key appellate decisions from around the country on the admissibility and presentation of DNA evidence. It discusses the history and evolution of DNA litigation, including the most recent decisions. [Note: Because the science and the case law on DNA testing changes rapidly, it is essential for any practitioner dealing with this issue to update every case before relying upon it.] Section IV (Some Critical Thoughts on DNA Evidence) addresses some remaining concerns about DNA evidence, and Section V provides guides and checklists for prosecutors and defense lawyers on dealing with DNA evidence.

When discussing DNA evidence it is difficult to find an appropriate middle ground between a highly technical explanation that overwhelms readers with details and a more readily understandable explanation that leaves out crucial points. Readers should be aware that the materials in this chapter are introductory and by no means comprehensive. Lawyers

handling a DNA case would be well advised to consult the original source materials referenced in this section for more complete information on points relevant to their case. Seeking the assistance of a more experienced lawyer to evaluate your case is also helpful. Ultimately, there is no acceptable substitute for having an independent scientific expert review the underlying laboratory work to check for problems and to help you understand the strengths and possible limitations of the evidence. Prosecutors and defense lawyers are both well advised to have test results reviewed by an expert other than the one who produced them. Independent experts and consulting services (such as www.bioforensics.com)[2] can help organize and distill the complicated results of DNA testing procedures in a way that facilitates discussing the most important issues and alternative interpretations for your case.

§ 11:2 An introduction to DNA and DNA testing

The following sections provide an overview of DNA testing methods and introduces basic terminology. They are designed to orient DNA novices to the basic issues. More detailed treatments of the various methods are found in subsequent sections.[1]

§ 11:3 An introduction to DNA and DNA testing—The Nature of DNA

Deoxyribonucleic acid, or DNA, is a long, double-stranded molecule configured like a twisted ladder or "double helix." The genetic information of all organisms is encoded in the sequence of four organic compounds (bases) that make up the rungs of the DNA ladder. Most DNA is tightly packed into structures called chromosomes in the nuclei of cells. In

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[Section 11:1]

[2]Both Professors Thompson and Krane have a financial interest in Bioforensics.

[Section 11:2]

[1]For more detailed discussions, see National Research Counsel Report I ("NRCI"); National Research Counsel Report II ("NRCII"); John M. Butler, Forensic DNA Typing (Academic Press, 2001). Much of sections 11:2 through 11:10 is also found in W.C. Thompson, DNA Testing, Encyclopedia of Crime and Punishment (David Levinson, ed., (Sage, 2002)).

humans there are 23 pairs of chromosomes; half of each pair is inherited from the individual's mother, half from the father. The total complement of DNA is called the *genome*.

By some estimates, 99.9 percent of the genetic code is the same in all humans. To identify individuals, DNA tests focus on a few *loci* (plural of *locus*-a specific location on the human genome) where there is variation among individuals. These *loci* are called *polymorphisms* because the genetic code can take different forms in different individuals. Each possible form is called an *allele*.

Forensic DNA tests have examined two types of polymorphisms. *Sequence polymorphisms* vary only in the sequence of the genetic code. *Length polymorphisms* contain repeating sequences of genetic code; the number of repetitions may vary from person to person, making the section longer in some people and shorter in others.

Analysts begin the testing process by extracting DNA from cells and purifying it. They use test tubes, chemical reagents, and other standard procedures of laboratory chemistry.

In sexual assault cases, spermatozoa (containing male DNA) may be mixed with epithelial (skin) cells from the victim. Analyst generally try to separate the male and female components into separate *extracts* (samples) using a process called *differential lysis,* which employs weak detergents to liberate DNA from the epithelial cells followed by stronger detergents to liberate DNA from the tougher spermatozoa.

After the DNA is extracted, it can be "typed" using several different methods.

§ 11:4 An introduction to DNA and DNA testing—Overview of RFLP Analysis

When DNA tests were first introduced in the late 1980's, most laboratories employed a method called *RFLP analysis (restriction fragment length polymorphism analysis)*, which uses enzymes to break the long strands of DNA into shorter fragments *(restriction fragments)* and separates these by length (using a process called *electrophoresis*). A pattern of dark bands on an x-ray or photographic plate reveals the position (and hence the length) of target fragments that contain *length polymorphisms*.

Figure 1: RFLP Autorad in a Rape Case

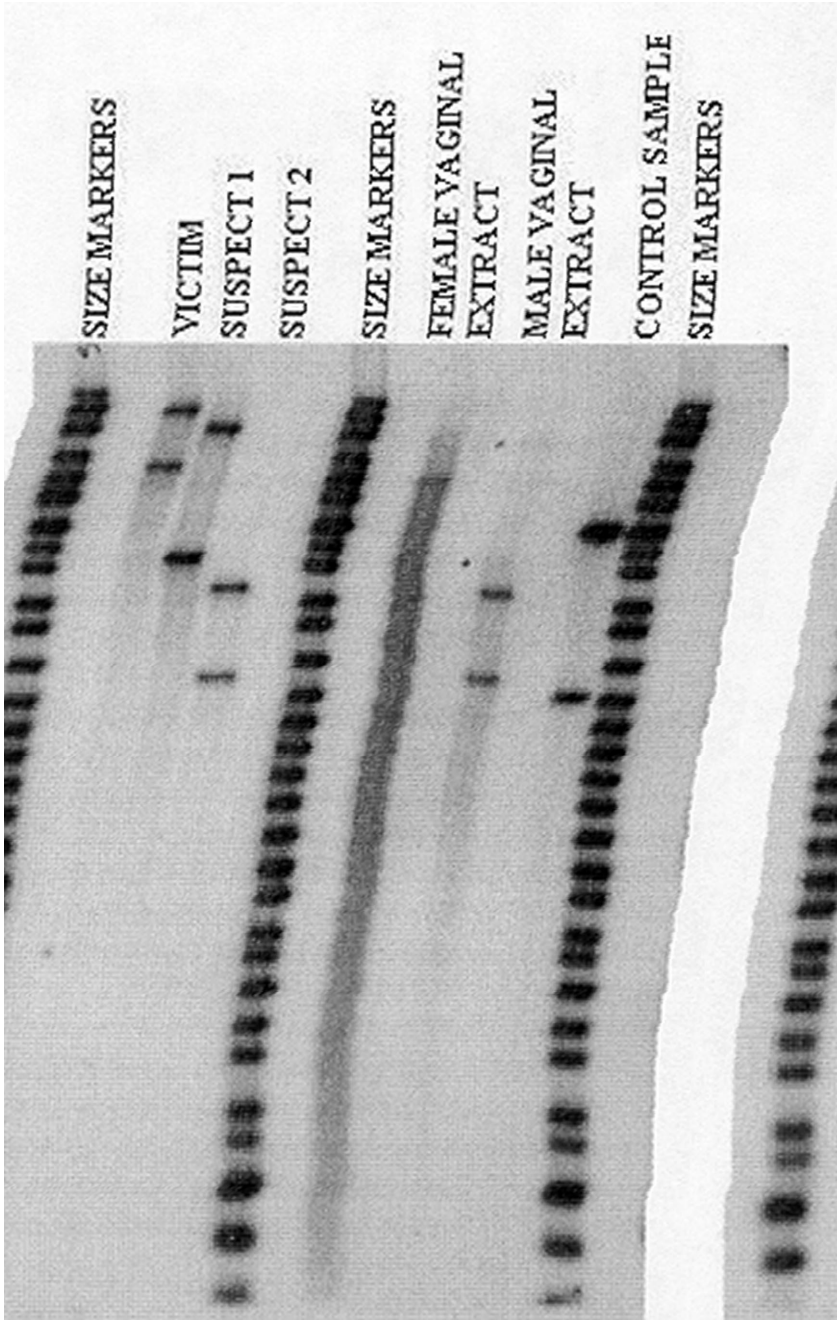
SIZE MARKERS
VICTIM
SUSPECT 1
SUSPECT 2
SIZE MARKERS
FEMALE VAGINAL EXTRACT
MALE VAGINAL EXTRACT
CONTROL SAMPLE
SIZE MARKERS

Figure 1 shows RFLP analysis of a single *locus* (containing a *length polymorphism*) in a case in which a woman was raped by two men. Each "lane" contains DNA from a different sample. The lanes labeled "size markers" contain DNA fragment of known size from bacteria and are used for calibration. Lanes on the left side show the band patterns produced by reference samples from the victim and two suspects. There are two bands in each lane because each individual has two copies of the relevant locus, one from the paternal half of the chromosome, the other from the maternal half.

Lanes on the right side of Figure 1 show the band patterns of evidence samples. The lane labeled "female vaginal extract" contains DNA from the female component (epithelial cells) of a vaginal sample taken from the victim. The DNA in this sample was too degraded to produce a distinct band pattern. The lane labeled "male vaginal extract" shows the band pattern of DNA from the male component (spermatozoa) of the same vaginal sample. This lane contains a band pattern similar to that of suspect 2, which indicates that the spermatozoa could have come from suspect 2.

In a typical case, four to six different loci (each containing a different length polymorphism) are examined in this manner. The full set of alleles identified in a sample is called its *DNA profile*. Because the probability of a "matching" pattern at any locus is on the order of one in hundreds to one in thousands, and the probabilities of a match at the various loci are assumed to be statistically independent, the probability of a match at four or more loci is generally put at one in many millions or even billions.

Although RFLP analysis is generally reliable, it sometimes entails subjective judgment. Whether the lane labeled "male vaginal extract" also contains bands corresponding to those of suspect 1 is a matter of judgment on which experts in this case disagreed. Dots to the left of the lane are felt-tip pen marks placed by a forensic analysis to indicate where he thought he saw bands matching those of suspect 1.[1]

RFLP analysis requires samples that are relatively large

[Section 11:4]

[1]Suspect 1 was charged with rape, but rape charges were later dropped when the defense was able to show that the laboratory could not reliably detect bands matching Suspect 1 using objective methods. For a useful

(blood or semen stains about the size of a quarter) and well-preserved. It is also slow. A typical case takes four to six weeks.

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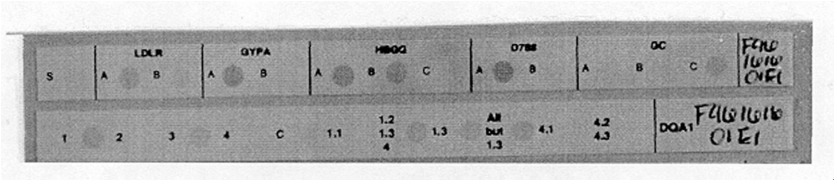
discussion of the scientific and legal issues in this case, see W. Thompson, Challenging the Forensic DNA Evidence in People v. Marshall, http://www.scientific.org/case-in-point/cases.html. (includes copies of motions filed in the case).

§ 11:5 An introduction to DNA and DNA testing—DQ-Alpha and Polymarker Tests

In the early 1990s, newer methods of DNA testing were introduced that are faster (producing results in a day or two) and more sensitive (i.e., capable of typing smaller, more degraded samples). The new methods use a procedure called *polymerase chain reaction (PCR)*, which can produce billions of copies of target fragments of DNA from one or more loci. These "amplified" DNA fragments (called *amplicons*) can then be typed using several methods.

In 1991, Perkin-Elmer (PE), a biotechnology firm, developed a test kit for amplifying and typing a *sequence polymorphism* known as the DQ-alpha gene. Six distinct *alleles* (variants) of this gene can be identified by exposing the amplified DNA to paper test strips containing *allele-specific probes* (see Figure 2). The dots on the strip signal the presence of particular alleles. This test has the advantage of great sensitivity (DNA from just a few human cells is sufficient to produce a result) and allows more rapid analysis (1-2 days), but it is not as discriminating as RFLP analysis.

Figure 2: Test Strip Showing Polymarker (top) and DQ-Alpha (bottom) Test Results



In 1993, PE introduced an improved kit that typed DQ-alpha and five additional genes simultaneously, thereby improving the specificity of this method (See Figure 2). With this new kit, known as the Polymarker/DQ-alpha test, individual profile frequencies are on the order of one in tens of thousands, however it still is not as discriminating as RFLP analysis. As with RFLP analysis, interpretation of the test strips may require subjective judgments. For example, experts disagreed on whether the dot labeled 1.3 in the lower strip shown in Figure 2 is dark enough to reliably indicate the presence of the allele designated 1.3.

§ 11:6 An introduction to DNA and DNA testing—STR Tests

The late 1990s saw the advent of *STR (short tandem repeat)* DNA testing. STR tests combine the sensitivity of a PCR-based test with great specificity (profile frequencies potentially as low as one in trillions) and therefore have quickly supplanted both RFLP analysis and the Polymarker/DQ-alpha test in forensic laboratories.

An *STR* is a DNA locus that contains a length polymorphism. At each STR locus, people have two alleles (one from each parent) that vary in length depending on the number of repetitions of a short core sequence of genetic code. A person with *genotype* 14, 15 at an *STR locus* has one allele with 14 repeating units, and another with 15 repeating units.

Figure 3: STR Test Results

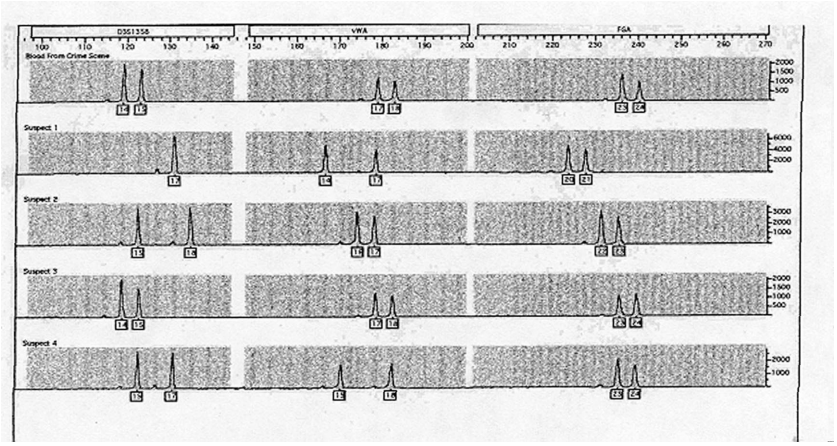


Figure 3 shows the results of STR analysis of five samples: blood from a crime scene and reference samples of four suspects. This analysis includes three loci, labeled "D3S1358," "vWA," and "FGA." Each person has two alleles (peaks) at each locus, one from the maternal portion and the other from the paternal portion of the chromosome. The position of the "peaks" on each graph (known as an electropherogram) indicates the length (and hence the number of core sequence repeats) of each STR. As can be seen, the profile of suspect 3 corresponds to that of the crime scene

sample, indicating he is a possible source. Suspects 1, 2 and 4 are eliminated as possible sources.

In 1997, the FBI identified 13 STR loci that it deemed appropriate for forensic testing. Commercial firms quickly developed test kits and automated equipment for typing these STRs. The most popular test procedure, developed by Applied Biosciences International (ABI), a PE subsidiary, includes a PCR kit known as *ProfilerPlus* that simultaneously "amplifies" DNA from up to nine STR loci and labels the loci with colored dyes. An automated test instrument called the ABI 310 Genetic Analyzer then separates the resulting amplicons by length (using electrophoresis) and uses a laser to cause fluorescence of the dye-labeled fragments. A computer-controlled electronic camera detects the size and relative position of the fragments, identifies alleles, and displays the results as shown in Figure 3.

STR tests have greatly improved the capabilities of forensic laboratories, allowing highly specific DNA profiles to be derived from tiny quantities of cellular material. Test results often allow a clear-cut determination of whether a particular individual could be the source of an evidentiary sample, although experts have differed over interpretation of results in some cases, particularly those involving mixed samples (DNA from more than one person) and low quantities of DNA.

§ 11:7 An introduction to DNA and DNA testing—Y-STR Tests

Several laboratories have recently developed tests to examine polymorphic areas of the Y-chromosome, which is possessed only by males. These tests may be useful in sexual assault cases where the DNA of a male contributor is mixed with DNA of a female victim. If there is too much DNA from the victim, relative to the male contributor, the male component is difficult to type using standard STR's. Because the Y-STR tests focus on DNA of males only, the male component is easier to detect and type with these tests.

The method for typing Y-STR markers is similar to that used for standard STR tests. Genetic probes identify and label relevant sections of the Y-chromosome, which are amplified using PCR and then run through an automated instrument such as the ABI 310 Genetic Analyzer, which

separates the fragments by length through electrophoresis and uses laser light and a computer-controlled camera system to detect the florescent dye-labeled fragments. The results are displayed on electropherograms that are similar in appearance to Figure 3, except that each person has a single peak at each locus (because the Y-markers are inherited only from the father).

The major disadvantage of Y-STR tests is that they are far less discriminating than standard STR tests. Moreover, they have not been as carefully validated or as widely used as standard STR tests, so they may be more vulnerable to admissibility challenges. Finally, because the Y-STR markers are inherited paternally, they will generally be the same for all men in the same paternal line. Hence, these tests cannot distinguish father from son, sons of the same father, or even paternal cousins.

§ 11:8 An introduction to DNA and DNA testing—Mitochondrial DNA Tests

The tests described thus far examine DNA from cell nuclei (*nuclear DNA*). DNA is also found in *cell mitochondria*, which are *organelles* (structures) in which the process of cellular respiration occurs. Mitochondrial DNA (often designated *mtDNA*) contains *sequence polymorphisms*. In the late 1990s, forensic scientists began testing mtDNA by using a procedure known as *genetic sequencing* to produce a read-out of the genetic code from two polymorphic areas of the *mitochondrial genome*. Forensic scientists describe an mtDNA profile by stating how its sequence differs from that of a reference standard called the *Anderson sequence*.

Mitochondrial DNA tests are highly sensitive and can produce results on samples that are not suitable for other DNA tests, such as hair shafts, bone, and teeth. Because mtDNA is present in hundreds or thousands of copies per cell, it often survives much longer than nuclear DNA in old, degraded cellular samples. DNA tests on very old samples, such as the bones of Czar Nicholas II of Russia, have detected and typed mtDNA.

Mitochondrial DNA tests are far less discriminating than STR tests. The frequency of mtDNA profiles is generally put at one in hundreds. Additionally, because mtDNA is inherited maternally, mtDNA tests generally cannot distinguish

between individuals in the same maternal line. Hence, sons of the same mother would be expected to have the same mtDNA profile, and this profile would also be found in daughters of the mother's sister and all of their children.

Minor variations are sometimes found in mtDNA profiles of different cells from the same person due to mutations. This phenomenon, known as *heteroplasmy*, complicates the process of determining whether two mtDNA profiles match. The appropriate standards for declaring an mtDNA match, and for estimating the rarity of matching profiles, are issues that have been debated in the courtroom.

Mitochondrial DNA tests are expensive and require special laboratory facilities and techniques. At this time only a few forensic laboratories perform these tests and they are used only where other types of DNA testing fail or cannot work. However, future technical improvements may lead to wider use of mtDNA tests.

§ 11:9 Reliability and Quality Assurance

Although current DNA technology is capable of producing highly reliable results, questions are sometimes raised about the quality of laboratory work. Key issues include the potential for biased or mistaken interpretation of laboratory results and the possibility for error due to mishandling of samples. Acknowledging problems with the quality of early DNA testing procedures, a 1992 report of the National Research Council called for broader scrutiny of forensic DNA testing by a scientific body from outside the law enforcement community.

In response, the U.S. Federal Bureau of Investigation (FBI) created its own advisory body that was initially called the Technical Working Group for DNA Analysis Methods (TWGDAM) and more recently called the Scientific Working Group for DNA Analysis Methods (SWGDAM). The FBI director appoints its members. Although it has not satisfied all critics of forensic laboratory practices, this body has been credited with issuing guidelines that have improved the quality of forensic DNA work. For example, SWGDAM guidelines call for each analyst to take two proficiency tests each year.

Another quality assurance mechanism is laboratory accreditation. The American Society of Crime Laboratory

Directors Laboratory Accreditation Board (ASCLAD-LAB) is a non-profit organization that reviews the protocols and procedures of forensic DNA laboratories and issues a certificate of accreditation to those meeting its standards. To help assure the competence of laboratory workers, a professional organization called the American Board of Criminology, has developed a certification program for DNA analysts.

Despite these efforts, problems occasionally come to light. Errors have occurred in proficiency tests and occasional errors arising from accidental switching and mislabeling of samples or misinterpretation of results have come to light in court cases. There are two known cases in which misinterpretation of DNA tests contributed to the wrongful rape convictions of a men who later were exonerated by more comprehensive DNA testing.

A 1996 report of the National Research Council suggested that retesting of samples is the best way to address remaining concerns about the quality of laboratory work. The great sensitivity of PCR-based DNA tests makes it possible to split samples for duplicate analysis in most cases.

§ 11:10 Dragnets, Databanks and Cold Hits

The United Kingdom and all fifty American states now have government-operated *databanks* containing the DNA profiles of known offenders. Many crimes have been solved when a databank search revealed a match between the DNA profile of a blood or semen sample left by the perpetrator at a crime scene and the profile of a known individual in the databank. A databank match is called a *cold hit*.

The FBI maintains a national databank of DNA profiles known as *CODIS (Combined DNA Indexing System*), which includes a Convicted Offender Index (containing profiles of offenders submitted by states) and a Forensic Index (containing DNA profiles of evidence related to unsolved crimes). CODIS allows government crime laboratories at a state and local level to conduct national searches which might reveal, for example, that semen deposited during an unsolved rape in Florida could have come from a known offender from Virginia.

Government databanks were initially limited to convicted violent or sex offenders. However, there has been serious discussion of expanding databanks to include arrestees, or

even to make them universal (perhaps by sampling DNA from all citizens at birth), in the interest of better crime control.

Civil libertarians have expressed concern that government agencies could use the genetic information they collect in an intrusive or inappropriate manner. The information included in CODIS is limited to numerical data that designate RFLP and STR profiles. These profiles are useful for identifying individuals but are linked to no known medical or behavioral characteristics. However, most states have retained blood samples from those included in state databanks. State and federal statutes limit the disclosure of information contained in government databanks and generally specify that it be used solely for law enforcement purposes.

When police have the DNA profile of a perpetrator but cannot establish his or her identity, they sometimes conduct what has become known as a *DNA dragnet*, in which large numbers of individuals in the relevant community are asked to submit samples voluntarily for DNA testing. Police generally collect samples by rubbing inside the individual's cheek with a cotton swab. Even if the guilty party does not submit a sample, the DNA dragnet may help police by narrowing the number of possible suspects. The first DNA dragnet, which was chronicled in Joseph Wambaugh's book "The Blooding," helped police solve two murders in Leicester, England, in 1987. The guilty man was identified when, in an effort to avoid suspicion, he asked a friend to submit a sample in his place. DNA dragnets have since been used repeatedly in Britain and are becoming more common in the U.S.

Prosecutors in some jurisdictions have developed a procedural innovation called a *DNA warrant* as a means of avoiding the statute of limitations in cases where they have DNA from the perpetrator but have not yet identified a suspect. Before the statute of limitations runs out, charges are formally filed in the case, but the "defendant" is identified by DNA profile rather than by name. The legality and constitutionality of this practice is still subject to debate.

§ 11:11 The rapidly evolving science of DNA testing

Continuing developments in molecular biology are sure to spawn further changes in DNA testing in the future. New

innovations often have a honeymoon period in which they are rapidly embraced by the courts, followed by a period of more critical scrutiny. When RFLP tests were first introduced in 1988, for example, they were virtually unchallenged. By 1991, however, serious questions were being raised about quality control and about the assumptions underlying statistical estimates. Lawyers should bear this history in mind when evaluating new DNA testing methods. It often takes time for problems to be identified and for scientific dissent to emerge.

At the time of this writing, STR testing is widely used. Although there is still some controversy about interpretation in some cases, particularly those involving mixtures and low quantities of DNA, the technology per se appears to be well established. Much of the current controversy, however, still centers around the flexibility associated with laboratory protocols and the possibility of errors and contamination occuring in the laboratory. Emerging issues appear to be questions regarding the appropriate statistics to apply in increasingly common cases where suspects are initially identified by DNA testing results ("cold hits" or "database trawls") and concerns over the lack of independence of most DNA testing labs from law enforcement agencies. Y-STRs and mtDNA are less widely used and may still be vulnerable to admissibility challenges as well as to attacks on the quality of results in specific cases.

Although this book will be updated on a regular fashion, there is no replacement for scanning through Westlaw and the Internet to find the most recent developments in the law. For example, in any three-month period, there may be dramatic changes in the DNA landscape of research that you will need to be aware of if you have a case with these issues.

In the event you work with the government, you can obtain access to the FBI's most recent data as well as their experts.[1] If you are a defense lawyer, you might want to contact the lawyers involved with the NACDL[2] DNA Task Force who

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[Section 11:11]

[1]A more recent FBI publication is IA US Dep't of Justice FBI Report, VNTR Population Data; A Worldwide Study (1993).

[2]National Association of Crime Defense Lawyers (NACDL).

specialize in DNA litigation[3] or utilize web based resources like www.bioforensics.com.

II. A CLOSER LOOK AT THE SCIENCE OF DNA TESTING

§ 11:12 What is DNA?

To biologists, DNA is *the* genetic material. That is a powerful statement in that it means that DNA is the molecule that is responsible for passing information from one generation to the next. As a result, DNA is often called the blueprint of life. A genome is the sum total of an organism's genetic material and is essentially contained entirely within the DNA molecules that make up its chromosomes. Information is stored in DNA in the sequence in which one of four different chemical building blocks (called nucleotides) are arranged in much the same way that information is stored in a written document by the specific sequence of letters that are used to spell out words. Current estimates are that the 3.2 billion nucleotides of the human genome spell out approximately 30,000 genes. Each of those genes is responsible for making at least one different protein. Failure to make one of those proteins at the appropriate place, time or level generally results in: death; a disease state (like cancer, cystic fibrosis or muscular dystrophy); or the normal differences we see between people (such as those associated with intelligence or height and hair, eye and skin coloration). People are remarkably similar to other organisms at the level of the nucleotide sequence of their DNA (on average, we are 98 percent identical to chimpanzees) as well as to each other (even the most distantly related people are 99.5 percent identical). However, only identical twins are absolutely identical at the level of their DNA and the small percent difference translates into an enormous number of differences given the overall size of the human genome.

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[3]The NACDL DNA Task Force has regional members. For further information, you can contact NACDL, 1110 Vermont Avenue, NW, Suite 1150, Washington 20005, tel. 202-872-8688; fax. 202-331-8269.

A perfect copy of an individual's DNA is found in all the nucleated cells of their body (of which there are trillions[1]) and is stored in forty-six pairs of chromosomes; twenty-three chromosomes are inherited from the mother and a roughly equivalent set of twenty-three are inherited from the father.[2] At a finer scale, DNA (an abbreviation for "deoxyribonucleic acid") has the shape of a double-helix, as first described in 1953 by scientists James Watson and Francis Crick, who won the Nobel Prize for the discovery of the structure of DNA.

DNA's double helix has been described as resembling a spiral staircase. The nucleotide components of a DNA molecule can themselves be broken down in three parts: a phosphate group, a sugar (ribose), and a nitrogenous base (one of four known as guanine, adenine, thymine or cytosine and commonly referred to by just the first letter of their name).

The "handrails" of the staircase are composed of the phosphate group and its linkage to the sugar of each nucleotide. Between the two handrails are the "steps" of the DNA staircase where the nitrogenous bases specifically interact with each other through hydrogen bonds. Each of the four types of these nucleotides (G, A, T and C as described above): pairs up only as either A:T or G:C. In other words, guanine cannot pair with thymine, nor can cytosine pair up with adenine.[3] These "nitrogenous base pairs" (or simply "basepairs" or "bp") effectively represent a simple alphabet that stores information useful to cells. The 0.5% difference in the nucleotide sequence between two people are not evenly distributed across the human genome. Locations (or loci, the plural of locus) where there is a great deal of difference in the base pair pattern of the genes are said to be "polymorphic" sites, meaning "many forms." Many polymorphic genes are known to be functionally important: some are responsible

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[1]Because red blood cells of mammals are not nucleated, they contain no DNA.

[2]See David H. Kaye and George F. Sensabaugh, Jr., Reference Guide on DNA Evidence, at 485, 491 in Reference Manual on Scientific Evidence (2d Ed. West Group, 2000) (hereinafter referred to in this section as "Reference Guide on DNA Evidence.").

[3]See People v. Soto, 21 Cal. 4th 512, 88 Cal. Rptr. 2d 34, 981 P.2d 958, 963 (1999).

for the color of eyes or hair and the type of blood we each have. Most, however, polymorphic regions are free to differ substantially between people because they appear to have no function and are typically the ones used in DNA testing. These polymorphic sites are the ones that DNA testers use in determining whether DNA from an evidence sample is likely to be from the same person that contributed a reference sample for DNA testing. How this process is completed is explained below.

At some of the polymorphic sites, the differences are due to the number of times that short sequences of the base pairs repeat in tandem, over and over. These repeating units are called a Variable Number Tandem Repeat (VNTR) and each of the repeated sequences may contain a few or several dozen nucleotide bases.[4] One currently very popular subset of VNTR loci have just four nucleotides in each repeated unit and are commonly referred to as Short Tandem Repeats (STRs).

§ 11:13 The RFLP method of creating DNA profiles[1]

In the short while since its first use in U.S. courts beginning in 1988, four substantially different methods of DNA profiling have been used. The earliest methodology used in forensic application in the United States is the so-called Restriction Fragmentation Length Polymorphism Method, commonly known as the "RFLP" method. RFLP analyses are no longer performed by the vast majority of DNA typing laboratories. The newer, more commonly used methods of

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[4]Reference Guide on DNA Evidence at 963.

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[1]In 2000, the Federal Judicial Center published the Second Edition of the Reference Manual on Scientific Evidence (West Group,2000). The chapter on DNA evidence provides an overview of DNA science and testing procedures, as well as a discussion of appropriate protocol and guidelines for collection, testing and interpretation of results. See David H. Kaye and George F. Sensabaugh, Jr., Reference Guide on DNA Evidence, at 485 in Reference Manual on Scientific Evidence (2d Ed. West Group, 2000). An electronic version of the Manual is online at http://air.fjc.gov/public/fjcweb.nsf/pages/16. One of the most comprehensive books about DNA technology to be published recently is John M. Butler, Forensic DNA Typing (Academic Press, 2001). This book contains an in-depth discussion and analysis of DNA, methods of DNA typing, and the established and developing technologies used in forensic DNA.

DNA profiling are discussed below but RFLPs are still described here because the DNA profiles generated in this way do still occasionally appear in court (particularly for older cases or those under appeal) and because the underlying methodology is a good starting point for understanding the latest approaches to DNA typing.

Forensic RFLP tests examine loci that contain highly variable numbers of tandem repeats, or VNTRs. A *tandem repeat* is an end-to-end duplication of a short sequence of the genetic code. If the DNA strand were a phonograph record, this would be an area where the record skipped and repeated a number of times before playing the rest of the tune. The number of repetitions tends to vary from person to person. Consequently, when the DNA strands are broken into fragments, and the fragments containing VNTRs are measured, their length tends to vary from person to person. (See Figure 1). This variation is known as a *length polymorphism*.

The DNA is broken into fragments by cutting it with one of several *restriction enzymes*. These enzymes act as "molecular scissors," cutting the DNA strand at specific, known sites, and producing shorter fragments known as *restriction fragments*. For example, the restriction enzyme HaeI cuts only at the sequence "AGGCCA" (which occurs randomly about once every 4,000 base-pairs). The restriction enzymes chosen for forensic RFLP tests cut in areas that flank the VNTRs. The goal of the test is to measure the length of these VNTR-containing restriction fragments, hence the overall procedure is called *restriction fragment length polymorphism analysis*.

In order to create a RFLP profile of DNA, a sample of blood the size of a quarter was needed or a sample of semen with several hundred thousand sperm must be collected. It is from these samples that scientists are able to determine a genetic or DNA profile, identifying a person through his[2] genetic code. Unlike regular fingerprinting which simply requires an ink pad, a set of fingers and a piece of paper, the method of obtaining genetic profiling is comparatively

[2]Since the overwhelming percentage (98 percent, according to some studies) of violent crimes are committed by men, the vast majority of DNA cases involve males, rather than females. Thus, the use of the male pronoun in this section seems more appropriate than a female or gender neutral pronoun.

complicated, and requires expensive, sophisticated equipment and computers for analysis. Once start-up costs have been covered, it has, however, become an affordable process.[3]

Two drawbacks to using the RFLP method are that it requires a larger size sample than other methods of testing, and its vulnerability to problems associated with the sample being degraded by exposure to the environment prior to testing.[4] A third problem with the use of the RFLP method is the length of time required to generate results: typically several weeks to months.

The following six sections describe how the RFLP genetic print is completed. Essentially, a DNA profile is created through the isolation and comparison of the lengths of several (often six to eight) highly polymorphic loci.[5]

§ 11:14 The RFLP method of creating DNA profiles—Extraction of DNA

The first step in DNA profiling is to extract the DNA from nucleated cells of the evidence sample obtained during the course of an investigation as well as from a reference sample of tissue or blood from the person in question. In order to obtain the DNA sample from the evidence, there must be a blood sample, tissue, bone or commonly a semen sample. The DNA is extracted from the cell in a fairly simple series of steps and the sample is chemically purified for use.

In sexual assault cases, evidentiary samples (e.g., vaginal swabs) often contain mixtures of the perpetrator's semen with epithelial cells of the victim. Forensic laboratories typically perform two extractions on such samples, one designed to obtain DNA from the female epithelial cells, and a second designed to obtain DNA from the semen. This procedure, known as *differential extraction* (also called *differential lysis*), is designed to separate the mixed DNA sample into male

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[3]According to representatives of Cellmark, the cost for RFLP testing never exceded is $1,000 per test.

[4]Donald E. Riley, Ph.D., DNA Testing: An Introduction For Non-Scientists, An Illustrated Explanation, 3, at http://www.scientific.org/tutorials/articles/riley/riley.htm (hereinafter "Riley, DNA Testing"). Scientific Testimony (http://www.scientific.org) is an online journal discussing new and developing forensic DNA and other types of scientific evidence as well as links to new case law on scientific evidence.

[5]RFLP is explained simply in Riley, DNA testing, at 3-4.

and female components. Although the separation is often incomplete (some male DNA may remain in the female component and vice-versa), this procedure can help distinguish contributors to mixed samples.

After extraction, laboratories typically estimate the quantity of DNA in each sample. The amount of DNA required for typing varies for different procedures. RFLP analysis requires the most DNA, typically 50-100 ng. (nanograms)[1]. DNA tests that make use of polymerase chain reaction (PCR) can type much smaller quantities of DNA. In theory, PCR-based tests can type the DNA of a single cell, but the manufacturer of a commonly used PCR test kit suggests that the reliability of its test may suffer when the amount of starting DNA is too low. For the DQ-Alpha and Polymarker tests, the manufacturer recommends no less than 2 ng.[2] For STR testing 1 ng. may be sufficient. Some labs report obtaining results with as little as 100 pg.[3] Attempting to type extremely low quantities of DNA increases the danger that minute quantities of human DNA that inadvertently contaminate the samples will be detected, causing spurious results.[4] It also increases the likelihood that some alleles that are present in the sample will fail to be detected, which could cause the sample to be mistyped.

Laboratories may also check the "molecular weight" of the DNA. In samples that have aged or been exposed to adverse environmental conditions, the DNA becomes degraded, i.e., the long strands (which are said to have high molecular weight) break into shorter, lighter pieces. The extent of degradation determines which testing methods are likely to succeed. RFLP analysis requires DNA of high molecular weight. PCR-based tests can type samples that are some-

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[1]A nanogram (ng.) is one-billionth of a gram (10-9 g). A bloodstain of one square centimeter contains approximately 200 ng. of DNA; a bloodstain of one square millimeter contains approximately 2 ng. of DNA. NRC Report, p. 28.

[2]Cetus Corp. Amplitype User Guide, Version 2 (1990), 6.2.2.

[3]A picogram (pg.) is one one-thousandth of a nanogram. Hence, 100 pg. =0.1 ng.

[4]W. Nividi, N. Arnheim, & M.Waterman, A Multiple-Tubes Approach for Accurate Genotyping of Very Small DNA Samples by Using PCR: Statistical Considerations, 50 Am.J.Hum.Genet. 347 (1992).

what more degraded. If the DNA is too degraded, however, no test can type it.

§ 11:15 The RFLP method of creating DNA profiles—Fragmentation by restriction enzymes

Once DNA is extracted, proteins called "restriction enzymes" are use to break long DNA molecules into shorter fragments by cutting them at specific sequences of nucleotides. When a tandemly repeated sequence occurs between two restriction enzyme sites on a DNA molecule the length of the resulting fragment will be determined in part by the number of times that the sequence is tandemly repeated. If the number of repeats differs from one person to the next (is polymorphic) those differences in the length of the resulting fragments can be used as identifying features in the following steps of the procedure. Generally speaking, restriction enzymes either cut DNA to yield fragments of specific length (they generate a result) or they do not (they generate no result) - it is not possible for one DNA profile to be converted to another.

§ 11:16 The RFLP method of creating DNA profiles—Gel electrophoresis

Separating DNA fragments on the basis of their size was and remains to be a very common practice for molecular biologists. The basis of virtually all DNA size fractionation is gel electrophoresis. In this process, DNA fragments are loaded onto small indentations called "wells" at one end of a flat gelatin surface containing agarose gel, a jello-like substance derived from kelp. One end of the gel is attached to a positively charged electrode and at the other to a negatively charged electrode. Because DNA is an intrinsically negatively charged molecule, it moves away from the negative electrode and travels toward the positive electrode. Larger fragments of DNA have more difficulty traveling through the gel's "matrix" (essentially a long series of sieves at a molecular level) than smaller fragments which move more quickly. Fragment sizes for RFLP analyses were typically in the range of between 200 bp and 7,000 bp. One of the problems with agarose gel electrophoresis is its ability to resolve fragments that do not differ in size by at least 20 to 100 bp since such fragments (especially fragments at the

larger end of the typical size range) move so similarly and because of sometimes subtle differences in how quickly DNA moves in one lane of a gel relative to another. As a result, most sizing of fragments for forensic purposes was done by "binning" - essentially saying that a fragment could be said to fall within a certain size range and other fragments that fell within the same size range were said "to match." This "match" would be declared even though the fragments might actually have different numbers of tandem repeats and could not have come from the same individual.

§ 11:17 The RFLP method of creating DNA profiles—Southern hybridization and visualization[1]

After their trip through the gel, the double stranded DNA fragments are chemically split into two strands, separating their paired nitrogenous bases from each other (A from T and C from G). These fragments are then directly transferred from the gel (which, like gelatin desserts, is difficult to handle and preserve intact) onto a sheet of a paper-like substance (usually either made of nylon or nitrocellulose) called a "filter" or "membrane." The separated DNA fragments are then permanently attached to the filter either by exposure to ultraviolet light or cross-linking chemicals.

§ 11:18 The RFLP method of creating DNA profiles—Hybridization

A restriction enzyme that recognizes a four nucleotide long restriction site (like *Hae*III mentioned above) should find such a site once every 256 base pairs on average if each of the nucleotides are equally represented in a random sequence. For a 3.2 billion nucleotide sequence such as that of the human genome, cutting with such an enzyme results in literally millions of fragments of a very wide variety of sizes. As a result, the gel electrophoresis of a restriction enzyme digested human genome is best described as a smear of fragments that contains no distinct bands.

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[1]"Southern Hybridization" is named for Dr. Edward H. Southern, who first developed the process in 1975. See generally Southern, Detection of Specific Sequences Among DNA Fragments Separated by Gel Electropheresis, 98 J Molecular Biology (1975).

The particular bands of interest to forensic scientists are recognized through the use of "probes" that seek out and bond with a locus of interest and no other. The tendency for A's and T's to interact and for G's and C's to interact allows single stranded DNA molecules to be designed that stick more stably to complementary sequences of nucleotides attached to the membrane of the Southern blotting step described above. Probes that are 20 base pairs long or longer are generally specific enough in their binding to interact with just one locus from a genome (such as a polymorphic VNTR locus). Such probes can either be made through the use of recombinant technology,[1] or chemically synthesized. These probes were originally tagged with radioactive markers that made it possible to determine where they had attached to a membrane but safer and more convenient fluorescent markers are also now available. Probes that do not find a complementary sequence to which they can bind are simply washed away while those that do bind give rise to a bar code type of pattern that is characteristic of the VNTR DNA typing methodology.

§ 11:19 The RFLP method of creating DNA profiles—Autoradiography and visualization of profiles

Once a probe is bound to DNA fragments originating from a specific locus, the membrane is placed against a piece of X-ray film and exposed for several days. When the film is developed, black bands appear where the labeled probes stuck to the fragments and the result somewhat resembles the bar codes on products in the store that are put through scanners. (See Figure 1, above). This picture is termed an "autoradiograph" or "autorad."

Each probe identified two fragments (alleles) in each person's DNA, one inherited from the person's mother and the other from the father. A person's genotype, for a given locus, is indicated by the lengths of this pair of fragments. Genotypes vary from person to person because the underlying fragments originate in loci that are where there is considerable variation in the length of restriction fragments.

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[1]Recombinant DNA technology is the incorporation of all or part of the DNA from one organism into the DNA of another organism--for instance, fragments of DNA from two different species, such as a bacterium and a reptile, spliced into a single molecule.

To reduce the likelihood of a false inclusion (coincidental match) between two samples, forensic laboratories generally used three to five separate probes. They generally applied the probes one at a time. The first probe was applied to the membrane and an x-ray film (*autorad*) was developed showing the resulting patterns of bands, which revealed the length of the restriction fragments from a particular locus (for all the samples on the membrane). Then the first probe was "stripped" from the membrane and a second probe was applied, a second autorad was developed, and so on. In a typical case, three to five probes were used and the results of the analysis were revealed on three to five autorads. If each fragment in one sample had the same length as the corresponding fragment in another sample (within a specified tolerance), the two samples were said to match, which means they could have come from the same person. If one or more fragments in the first sample differed in length (by an amount greater than a specified tolerance) from the corresponding fragment in a second sample, the two samples were declared a non-match (or exclusion), which means they could not have come from the same person.

Bands of evidentiary samples are sized by comparing their position to the position of "marker" bands in adjacent lanes. (See Figure 1). The marker bands are produced by an array of DNA fragments (from bacteria) that vary incrementally in length to produce a "sizing ladder." Sizing may be accomplished by simply measuring with a ruler to determine the position of bands in the various lanes.[1] However, forensic laboratories typically used computer-assisted imaging devices, which can score autorads more rapidly and can automatically perform the calculations needed to estimate the band sizes (fragment lengths) of the samples through interpolation.[1] Once the bands were sized, the *DNA profile* of each sample could be represented by a set of numbers

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[1]A band in the same position as a 1000-base-pair "marker," for example, would be "scored" as a 1000-base pair band (meaning that the underlying DNA fragment is estimated to be 1000 base pairs in length). If a band is between two markers, its length is determined by interpolation. These length estimates are sometimes called "band sizes."

[1]The use of computer-assisted scoring devices does not necessarily mean that the scoring and sizing of bands is "objective." Analysts are able to override the scorings of computer-assisted devices in order to add or

indicating the estimated length (in base pairs) of the restriction fragments at each locus.

§ 11:20 "Amplification" of DNA Using PCR

The DNA tests currently being used in forensic laboratories all make use of a procedure known as polymerase chain reaction, or PCR. PCR is a procedure that allows a small amount of DNA (which by itself would not be enough to type) to be *amplified* into an amount large enough for typing. It does this by making millions of copies of DNA fragments from a polymorphic area (or areas) of the genome. PCR is not a genetic test itself, but merely a tool to increase the amount of genetic material to be tested.

The "amplification" of DNA takes place in a test tube. The DNA that is extracted from each sample is placed in a separate tube, along with a mixture of *primers, enzymes*, and other reagents. The tubes are then placed in a machine known as a thermal cycler, which can control their temperature precisely while going through a series of heating and cooling cycles.

Each cycle has three steps. First, the tubes are heated to approximately 94 degrees Celsius. At this temperature the DNA denatures--that is, the double-stranded molecule "unzips" to form two complementary single strands.

In the second step, the tubes are cooled to about 60 degrees Celsius. At this temperature the primers *annea*l (bond) to the single strands of DNA. The primers are similar to genetic probes. They are single strands of organic bases (nucleotides), synthesized in a laboratory, that are complementary to specific target areas on the single stands of human DNA. The primers are designed to anneal at positions that flank the polymorphic areas to be amplified, thereby marking those areas.

In the third step, the tubes are heated to about 72 degrees Celsius. At this temperature, an enzyme known as Taq DNA polymerase acts as a catalyst, causing single DNA strands in

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delete bands based on subjective criteria. Most forensic laboratories fail to document operator overrides of machine scoring determinations, making it impossible to tell whether any given band was scored by objective or subjective criteria. The author's analysis of case work at one laboratory that does document such operator overrides (Cellmark Diagnostics) indicates that they are occur frequently.

the areas marked by the primers to attract and bond with complementary bases that are floating in the solution. Each single strand of DNA from the marked areas thus becomes one side of a new double strand. When this process is completed, the number of identical double strands of DNA from the polymorphic areas is twice what it was at the beginning of the cycle.

This three step cycle is repeated 25-35 times, doubling the number of copies of the target DNA each time, and producing literally billions of copies. The target DNA (from a polymorphic area, or areas), which was initially like a needle in a haystack of other DNA, is amplified to the point that there are far more needles than hay, at which point the needles can be typed using a variety of methods.

As a result of its ability to generate usable amounts of material from as little DNA as that which comes from a single cell, PCR-based approaches are amazingly sensitive and have the additional advantage of being much faster than RFLP analysis and better able to generate interpretable results even when evidentiary samples are degraded by exposure to the environment.

It is important to remember that PCR is simply a procedure for replicating DNA. It is not a method for typing DNA, although some courts have used the term incorrectly as a description for the DQ-alpha and Polymarker tests (describbed below). In fact, PCR is a component of every current DNA typing method.

§ 11:21 "Amplification" of DNA Using PCR—DQ-Alpha and Polymarker Tests

The first method that was developed for typing amplified DNA involved detection of specific sequences of genetic code in the amplified product. Each distinct sequence constitutes an allele, and the alleles were detected by using *allele-specific probes*, which are synthesized strings of organic bases that are complementary to the sequence they are designed to detect.[1] For example, if the target allele contained the

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[1]Remember, an allele is one of several alternate forms of a gene concerned with the same trait or characteristic and occupying a given locus on a chromosome. At the loci responsible for determining hair color,

sequence ACCTCG, the probe would have the sequence TGGAGC. Attached to each probe is a molecule that changes color when the probe bonds to its complementary sequence.

The standard method for deploying the probes was to spot them on to nylon test strips, with each probe in a specified location, and then to immerse the test strip in a solution of amplified, denatured DNA.[2] When one of the probes changed color in the presence of a particular allele, it produced a detectable spot in its place on the strip.[3] (See Figure 2 above). By seeing which probes "light up" in this manner and which do not, an analyst can determine which alleles are present in the amplified DNA. The scoring is entirely subjective (and different experts sometimes differ about whether a faint dot is truly present), but analysts typically photographed the strips in order to have a record of their observations.[4]

In 1991, Perkin-Elmer (PE) introduced a test kit for amplifying and typing alleles of the HLA (Human Leukocyte Antigen) DQ-alpha gene.[5] Fragments of DNA from the ap-

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for example, there may be alleles whose combination results in blond or red hair. The alleles for blond hair would contain similar, but measurably different information content relative to those that give rise to red hair.

[2]The amplification process is stopped at a point when the DNA is denatured (in single strands) so that the probes will be able to bind with their target sequences.

[3]This approach is often aptly referred to as a "reverse dot blot" approach (DNA fragments of interest are washed over probes attached to a membrane) - unlike the more conventional VNTR approach that relies upon "direct blot hybridization" (where probes are washed over DNA fragments of interest that have been attached to a membrane).

[4]A photograph is an important form of documentation because the strips themselves fade over time, making it impossible, in the absence of a photograph, for an independent analyst to check the scoring.

[5]See Edward Blake, Jennifer Mihalovich, Russell Higuchi, P.S. Walsh & Henry Erlich, Polymerase Chain Reaction (PCR) Amplification and Human Leukocyte Antigen (HLA)-DQ Oligonucleotide Typing on Biological Evidence Samples: Casework Experience, 37 J.Forensic Sci. 700 (1992); George Sensabaugh and Cecilia Von Beroldingen, The Polymerase Chain Reaction: Application to the Analysis of Biological Evidence, in M. Farley & J. Harrington, Forensic DNA Technology, 1991. The HLA DQ-alpha gene is an area of DNA on chromosome 6 that controls leukocyte (white blood cell) antigens. These antigens are important in tissue typing for organ transplantation.

propriate area were amplified using PCR and then exposed to test strips containing the probes.[6]

The DQ-alpha test was far less discriminating than RFLP tests: it could detect only seven different alleles of a single gene. Each person inherits two alleles, one from each parent, therefore the test could distinguish 28 different genotypes.[7] The frequency of the various genotypes in the population ranges from about one to fifteen percent, making the likelihood of a coincidental match between different samples much higher than with RFLP tests. But the DQ-alpha test was far more sensitive than RFLP procedures, allowing it to "type" samples that are much smaller and older.[8] For example, there is sometimes enough DNA in the dried saliva on a cigarette butt to be typed using the DQ-alpha test.

In 1993, PE introduced an improved kit that typed DQ-alpha and five additional genes, thereby improving the specificity of this method (See Figure 3).[9] With this new kit, known as the Polymarker/DQ-alpha test, individual profile frequencies were on the order of one in tens of thousands, however it still was not as discriminating as RFLP analysis.

The PE kits were widely used by forensic laboratories in the mid 1990s, but were gradually supplanted by STR tests beginning in about 1998. Commercial test kits for DQ-alpha and Polymarker testing have not been produced since 2002. However, a few labs still maintain stocks of the test strips to allow new samples to be compared to the results of these older tests. Because STR tests examine different loci, using a

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[6]The trade name for the test is the Amplitype HLA DQ alpha Forensic DNA Amplification and Typing Kit (Amplitype Kit, for short).

[7]The seven alleles are labeled 1.1, 1.2, 1.3, 2, 3, 4.1 and 4.2/4.3. One allele is inherited from each parent, therefore the 28 possible genotypes a person might have are 1.1,1.1; 1.2,1.2; 1.3,1.3; 2,2; 3,3; 4.1,4.1; 4.2/4.3,4.2/4.3; 1.1,1.2; 1.1,1.3; 1.1,2; 1.1,3; 1.1,4.1; 1.1,4.2/4.3; 1.2,1.3; 1.2,2; 1.2,3; 1.2,4.1; 1.2,4.2/4.3; 1.3,2; 1.3,3; 1.3,4.1; 1.3,4.2/4.3; 2,3; 2,4.1; 2,4.2/4.3; 3,4.1; 3,4.2/4.3; 4.1, 4.2/4.3. An early version of the test did not subtype the 4 allele, and therefore had only 21 genotypes.

[8]Russell Higuchi, Cecelia von Beroldingen, George Sensabaugh & Henry Erlich, DNA Typing from Single Hairs, Nature 332:543 (1988).

[9]See, B. Budowle, J. Lindsey, J. DeCou, B. Koons, A Giusti, & C. Comey, Validation and Population Studies of the Loci LDLR, GYPA, HBGG, D7S8, and Gc (PM loci), and HLA-DQ alpha Using a Multiplex Amplification and Typing Procedure, 40 J.Forensic Sci. 45 (1995).

different method, one cannot make comparisons among samples across methods.

§ 11:22 Short Tandem Repeats (STRs)[1]

In most forensic laboratories, STR testing has now supplanted both RFLP analysis and DQ-alpha/polymarker testing. STR tests offer the high sensitivity of PCR-based methods and have discriminating power as great as RFLP tests. And they can produce results in as little as one day. Most laboratories are using commercially available STR testing kits that permit simultaneous testing of STR markers at nine to fifteen loci (plus one, Amelogenin, that is useful for sex determination).

§ 11:23 Short Tandem Repeats (STRs)—Understanding the Lab Report in an STR Case

The first item a lawyer sees in a DNA case is typically the lab report. The report generally states what samples were tested, what type of DNA test was performed, and which samples could (and could not) have a common source. Reports generally also provide a "table of alleles" showing the *DNA profile* of each sample. The *DNA profile* is a list of the *alleles* (genetic markers) found at a number of loci (plural for "locus," a position) within the human genome. To understand DNA evidence, you must first understand the table of alleles.

Figure 4 shows a table of alleles, as represented in a typical lab report concerning STR testing. This table shows the DNA profiles of five samples-blood from a crime scene and reference samples from four suspects. These samples were tested with an automated instrument called the ABI Prism 310 Genetic Analyzer(tm) using a set of genetic probes called ProfilerPlus(tm). A company called Applied Biosystems, Inc. (ABI) developed this system for typing DNA. It is currently the most widely used method for forensic DNA typing in the

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[1]For more background information on STR testing, see John M. Butler, Forensic DNA Typing: Biology and Technology Behind STR Markers (2001).

United States, used by about 85% of laboratories that do forensic DNA testing.[1]

Across the top of the table are the names of the various loci examined by the test. The ProfilerPlus(tm) system examines ten loci. (Labs sometimes also run another set of genetic probes, called Cofiler(tm), which includes four additional loci). The alleles that the test detected at each locus are identified numbers. Thus, at locus D3S1358, the test detected alleles 15 and 16. At each locus, a person has two alleles, one inherited from each parent. In some cases, only one allele is detected, which is interpreted as meaning that by chance the person inherited the same allele from each parent. (See in Figure 4, e.g., Suspect 2's profile at locus D3S1358 and Suspect 4's profile at locus D8S1179). However, most samples will have two different alleles at each locus, as seen in Figure 4.

Figure 4: Table of Alleles. Which suspect is a possible source of the blood? Only one of the four suspects has a DNA profile that matches the DNA profile observed in the blood sample.

	D3S1358	VWA	FGA	Amel	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
Blood Stain	15, 16	15, 15	25, 26	XY	12, 13	27, 30	13, 14	10, 11	9, 12	10, 12
Suspect 1	16, 18	15, 16	21, 24	XY	12, 14	27, 28	13, 17	11, 12	8, 11	8, 12
Suspect 2	15, 15	18, 18	19, 23.2	XY	13, 15	29, 30	17, 17	11, 11	8, 9	9, 10
Suspect 3	15, 16	15, 15	25, 26	XY	12, 13	27, 30	13, 14	10, 11	9, 12	10, 12
Suspect 4	16, 16	16, 17	19, 24	XY	14, 14	30, 30	13, 16	9, 11	10, 11	9, 10

Each allele is a short fragment of DNA from a specific location on the human genome known as an STR (short tandem repeat). STRs are places in human DNA where a short section of the genetic code repeats itself. Everyone has

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[1]Bureau of Justice Statistics, Survey of DNA Crime Laboratories, 2001. National Institute of Justice, NCJ 191191, January 2002. http://www.ojp.usdoj.gov/bjs/pub/pdf/sdnacl01.pdf

these repeating segments, but the number of repetitions (and hence the length of these segments) varies among individuals. The numbers assigned to the alleles indicate the number of repetitions of the core sequence of genetic code. ProfilerPlus(tm) identifies and labels fragments of DNA that contain STRs. The Genetic Analyzer then measures their length and thereby determines which alleles are present.

By examining the DNA profiles, one can tell whether each suspect could or could not have been the source of the blood. Suspects 1, 2 and 4 are ruled out as possible sources because they have different alleles than the blood at one or more loci. However, Suspect 3 has exactly the same alleles at every locus, which indicates he could have been the source of the blood. In a case like this, the lab report will typically say that Suspects 1, 2 and 4 are "excluded" as possible sources of the blood, and that Suspect 3 "matches" or is "included" as a possible donor.

One of the loci analyzed is called amelogenin (Amel) and is used for typing the sex of a contributor to a sample. Males have X and Y versions of the alleles at that locus; females have only the X because they inherit two copies of the X chromosome. All of the profiles shown in Figure 4 appear to be of males.

Lab reports generally also contain estimates of the statistical frequency of the matching profiles in various reference populations (which are intended to represent major racial and ethnic groups). Crime labs compute these estimates by determining the frequency of each allele in a sample population, and then compounding the individual frequencies by multiplying them together. If 10 percent (1 in 10) of Caucasian Americans are known to exhibit the 14 allele at the first locus (D3S1358) and 20 percent (1 in 5) are known to have the 15 allele, then the frequency of the pair of alleles would be estimated as 2 x 0.10 x 0.20 = 0.04, or 4 percent among Caucasian Americans. The frequencies at each locus are simply multiplied together (sometimes with a minor modification meant to take into account the possibility of under-represented ethnic groups), producing frequency estimates for the overall profile that can be staggeringly small: often on the order of 1 in a billion to 1 in a quintillion, or even less. Needless to say, such evidence can be very impressive.

When the estimated frequency of the shared profile is very low, some labs will simply state "to a scientific certainty"

that the samples sharing that profile *are* from the same person. For example, the FBI laboratory will claim two samples *are* from the same person if the estimated frequency of the shared profile among unrelated individuals is below one in 260 billion. Other labs use different cut off values for making identity claims. All of the cut-off values are arbitrary: there is no scientific reason for setting the cut off at any particular level just as there is no formally recognized way of being "scientifically certain" about anything. Moreover, these identity claims can be misleading because they imply that there could be no alternative explanation for the "match," such as laboratory error, and they ignore the fact that close relatives are far more likely to have matching profiles than unrelated individuals. They can also be misleading in that the DNA tests themselves are powerless to provide any insight into the circumstances under which the sample was deposited and are generally unable to determine the type of tissue that was involved.

§ 11:24 Short Tandem Repeats (STRs)—The Role of Subjective Judgment in STR Testing

Many lawyers simply accept lab reports at face value without looking behind them to see whether the actual test results fully support the laboratory's conclusions. This can be a serious mistake. Examination of the underlying laboratory data sometimes reveals limitations or problems that would not be apparent from the laboratory report, such as inconsistencies between purportedly "matching" profiles, evidence of additional unreported contributors to evidentiary samples, errors in statistical computations and unreported problems with experimental controls that raise doubts about the validity of the results. Yet forensic DNA analysts report that they receive discovery requests from defense lawyers in only 10-15 percent of cases in which their tests incriminate a suspect.

Although STR tests rely heavily on computer-automated equipment, the interpretation of the results often requires subjective judgment. When faced with an ambiguous situation, where the call could go either way, crime lab analysts

frequently slant their interpretations in ways that support prosecution theories.[1]

Part of the problem is that forensic scientists refuse to take appropriate steps to "blind" themselves to the government's expected (or desired) outcome when interpreting test results. We often see indications, in the laboratory notes themselves, that the analysts are familiar with facts of their cases, including information that has nothing to do with genetic testing, and that they are acutely aware of which results will help or hurt the prosecution team. A DNA analyst in one case wrote:

> Suspect-known crip gang member--keeps 'skating' on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. [Detective] Miller wants to connect this guy to scene w/DNA . . .

In another case, where the defense lawyer had suggested that another individual besides the defendant had been involved in the crime, and might have left DNA, the DNA laboratory notes include the notation: "Death penalty case. Need to eliminate [other individual] as a possible suspect."

It is well known that people tend to see what they expect (and desire) to see when they evaluate ambiguous data.[2] This tendency can cause analysts to unintentionally slant their interpretations in a manner consistent with prosecution theories of the case. Furthermore, some analysts appear to rely on non-genetic evidence to help them interpret DNA test results. When an analyst's interpretation of a problematic case was questioned, the analyst defended her position by saying: "I know I am right-they found the victim's purse in [the defendant's] apartment." Backwards reasoning of this type (i.e., "we know the defendant is guilty, so the DNA evi-

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[Section 11:24]

[1]See, William C. Thompson, Subjective Interpretation, Laboratory Error and the Value of DNA Evidence: Three Case Studies, 96 Genetica 153 (1995); William C. Thompson, Accepting Lower Standards: The National Research Council's Second Report on Forensic DNA Evidence, 37 Jurimetrics 405 (1997); William C. Thompson, Examiner Bias in Forensic RFLP Analysis, Scientific Testimony: An Online Journal: www.scientific.org.

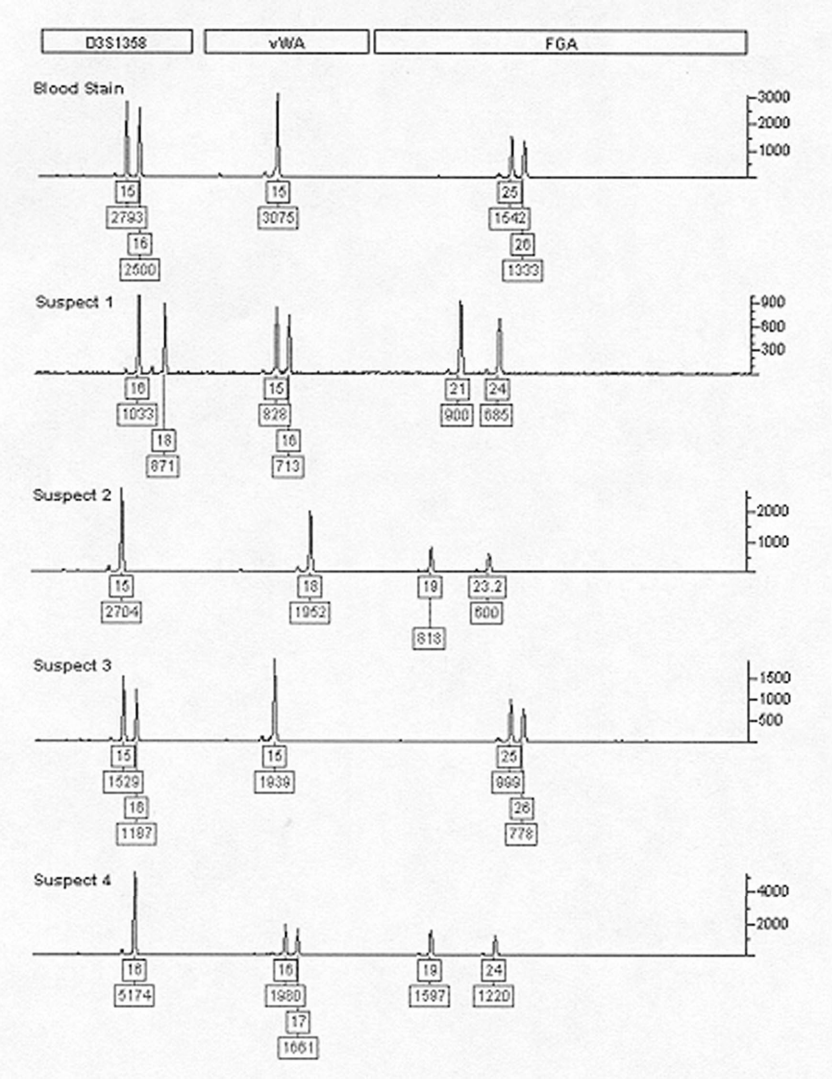
[2]See D. Michael Risinger, Michael J. Saks, William C. Thompson, & Robert Rosenthal, The Daubert/Kumho Implications of Observer Effects in Forensic Science: Hidden Problems of Expectation and Suggestion, 90 Cal.L.Rev. 1 (2002).

dence must be incriminating") is another factor that can cause analysts to slant their reports in a manner that supports police theories of the case. Hence, it is vital that defense counsel look behind the laboratory report to determine whether the lab's conclusions are well supported, and whether there is more to the story than the report tells.

§ 11:25 STR Electropherograms

Behind the Table of Alleles (Figure 4) is a set of computer-generated graphs called *electropherograms* that display the test results. When evaluating STR evidence, a lawyer should always examine the electropherograms because they sometimes reveal unreported ambiguities and, fairly frequently, evidence of additional, unknown contributors. The electropherograms shown in Figure 5 display the results for the crime scene blood and four suspects discussed above at three of the ten loci summarized in Figure 4.

Figure 5: Electropherograms Showing the Results of ProfilerPlus(tm) Analysis of Five Samples at Three Loci (D3S1358, vWa and FGA). Which suspect is a possible source of the blood? Boxes immediately below the peaks label the name of the alleles seen while boxes below indicate their heights in RFUs.



The "peaks" in the electropherograms indicate the presence of human DNA. The peaks on the left side of the graphs represent alleles at locus D3S1358; those in the center represent alleles at locus vWA; and those on the right represent alleles at locus FGA. The numbers under each peak are computer-generated labels that indicate which allele each peak represents and how high the peak is relative to the baseline.

By examining the electropherograms in Figure 5, one can readily see that the computerized system detected two alleles in the blood from the crime scene at locus D3S1358. These are alleles 15 and 16, which are reported in the Table of Alleles (Figure 4). The other alleles reported in the allele chart (Figure 4) can also be seen. Our initial examination of these electropherograms reveals no obvious problems of interpretation in this case.

ProfilerPlus(tm) uses "primers" to identify the relevant STR-DNA segments and then "amplifies" (replicates) these segments using a process called polymerase chain reaction (PCR). Each locus is "labeled" with a colored dye (either blue, yellow or green). The Genetic Analyzer measures the length of the DNA segments by using an electrical current to impel them through a narrow capillary tube, wherein the shorter fragments move more quickly than the longer fragments.[1] Under laser light, the colored dyes produce florescent light, signaling the presence of DNA. A computer-operated camera detects the light as the fragments reach the end of the capillary. The "peaks" on the electropherogram record these flashes of light. Based on the color of the light, and the time it took the DNA to pass through the capillary, a series of computer programs determines which alleles are present at each locus.

Figure 5 show the results for three loci that were labeled with blue dye. The position of the peaks on the graph (how far left or right) indicates how long it took the allele to pass through the capillary, which indicates the length of the underlying DNA fragment. From this, the computer program infers which allele is represented and generates the appropriate label.

The height of the peaks corresponds to the quantity of

[Section 11:25]

[1]The most commonly used capillary electrophoresis instruments are produced by a company called Applied Biosystems, Inc. and include the ABI 310 and ABI 3100 Genetic Analyzer machines. While its start up costs are much greater (costing many tens of thousands of dollars vs. several hundred dollars), capillary electrophoresis has several advantages over agarose gel electrophoresis including: greater resolving power (the length of DNA fragments between 30 and 1,000 bp can be determined precisely); very small amounts of PCR amplification product are needed; the loading of capillaries is easily automated; and the relative amounts of different DNA fragments can be easily quantitated.

DNA present. The unit of measurement for peak heights is the RFU, or "relative fluorescent unit," which reflects the intensity of the fluorescent light detected by the computer-operated camera. Peaks representing alleles from the same person are expected to have roughly the same heights measured in RFUs throughout a given sample, although *peak height imbalances* occasionally occur.

§ 11:26 Short Tandem Repeats (STRs)—Sources of Ambiguity in STR Interpretation

A number of factors can introduce ambiguity into STR evidence, leaving the results open to alternative interpretations. To competently represent an individual incriminated by DNA evidence, defense counsel must uncover these ambiguities, when they exist, understand their implications, and explain them to the trier-of-fact.

A. Mixtures. One of the most common complications in the analysis of DNA evidence is the presence of DNA from multiple sources. A sample that contains DNA from two or more individuals is referred to as a *mixture*. A single person is expected to contribute at most two alleles for each locus. If more than two peaks are visible at any locus, there is strong reason to believe that the sample is a mixture.

By their very nature mixtures are difficult to interpret. The number of contributors is often unclear. Although the presence of three or more alleles at any locus signals the presence of more than one contributor, it often is difficult to tell whether the sample originated from two, three, or even more individuals because the various contributors may share many alleles. If alleles 14, 15 and 18 are observed at a locus, they could be from two individuals, A and B, where A contributed 15 and B contributed 14, 18. Alternatively, A could have contributed 14, 15 while B contributed 15, 18, and so on. There might also be three contributors. For example A could have contributed 14, 15, while B contributed 15, 18 and C contributed 15. Many other combinations are also consistent with the findings. A study of one database of 649 individuals found over 5 million three-way combinations of individuals that would have shown four or fewer alleles across all 12 commonly tested STR loci.[1]

Figure 6: Presence of more than two alleles at a locus indicates a mixture

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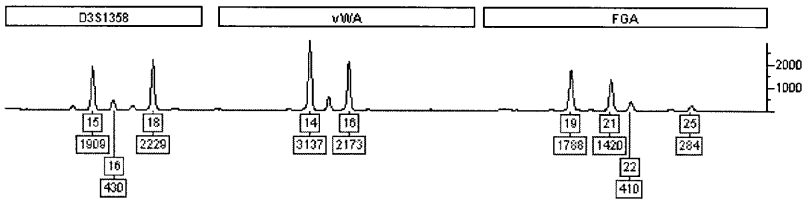
[Section 11:26]

[1]For more information about this study, contact Dan Krane.



Some laboratories try to determine which alleles go with which contributor based on peak heights. They assume that the taller peaks (which generally indicate larger quantities of DNA at the start of the analysis) are associated with a "primary" contributor and the shorter peaks with a "secondary" contributor. In Figure 6, for example, a laboratory analyst might conclude that a "primary contributor" is responsible for alleles 15 and 18 at locus D3S1358 and alleles 19 and 21 at locus FGA, while a "secondary contributor is responsible for allele 16 at D3S1358 and alleles 22 and 25 at locus FGA. But inferences of this kind are often problematic because a variety of factors, other than the quantity of DNA present, can affect peak height. Moreover, labs are often inconsistent in the way they make such inferences, treating peak heights as a reliable indicator of DNA quantity when doing so supports the government's case, and treating them as unreliable when it does not.

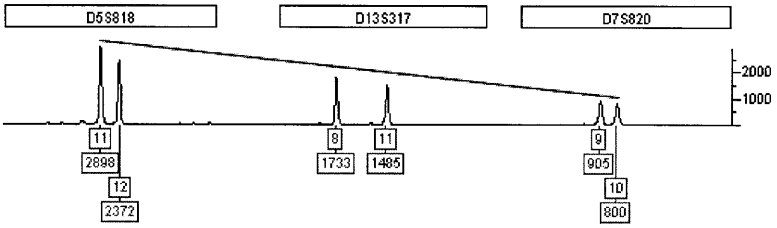
These interpretive ambiguities make it difficult, and sometimes impossible, to estimate the statistical likelihood that a randomly chosen individual will be "included" (or, could not be "excluded") as a possible contributor to a mixed sample. Lawyers should look carefully at the way in which laboratories compute statistical estimates in mixture cases because these estimates often are based on debatable assumptions that are unfavorable to the defendant.

B. Degradation. As samples age, DNA like any chemical begins to break down (or degrade). This process occurs slowly if the samples are carefully preserved but can occur rapidly when the samples are exposed for even a short time to unfavorable conditions, such as warmth, moisture or sunlight.

Degradation skews the relationship between peak heights and the quantity of DNA present. Generally, degradation produces a downward slope across the electropherograms in the height of peaks because degradation is more likely to

interfere with the detection of longer sequences of repeated DNA (the alleles on the right side of the electropherogram) than shorter sequences (alleles on the left side).

Figure 7: The progressively smaller peak heights in this sample from left to right are indicative of degradation

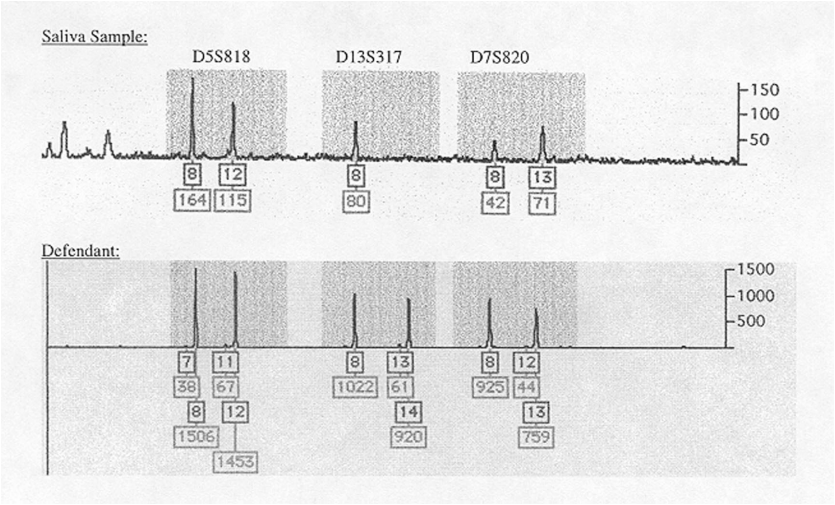


Degraded samples can be difficult to type. The process of degradation can reduce the height of some peaks, making them too low to be distinguished reliably from background "noise" in the data, or making them disappear entirely, while other peaks from the same sample can still be scored. In mixed samples, it may be impossible to determine whether the alleles of one or more contributors have become undetectable at some loci. Often analysts simply guess whether all alleles have been detected or not, which renders their conclusions speculative and leaves the results open to a variety of alternative interpretations. Further, the two or more biological samples that make up a mixture may show different levels of degradation, perhaps due to their having been deposited at different times or due to differences in the protection offered by different cell types. Such possibilities make the interpretation of degraded mixed sample particularly prone to subjective (unscientific) interpretation.

C. Allelic Dropout. In some instances, an STR test will detect only one of the two alleles from a particular contributor at a particular locus. Generally this occurs when the quantity of DNA is relatively low, either because the sample is limited or because the DNA it contains is degraded, and hence the test is near its threshold of sensitivity. The potential for allelic dropout complicates the process of interpretation because analysts must decide whether a mismatch between two profiles reflects a true genetic difference or simply the failure of the test to detect all of the alleles in one of the samples.

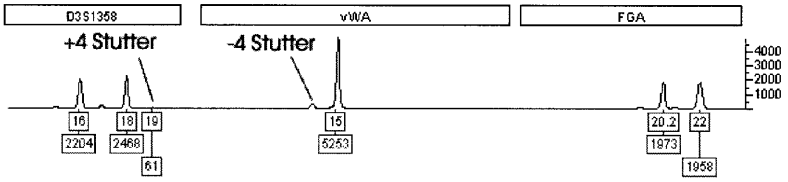
Figure 8 shows three loci from a case in which a defendant's profile was "matched" to the profile of a saliva sample from a woman's breast. The laboratory reported that the DNA profile of the saliva sample shown in Figure 8 was consistent with the defendant's profile, despite the absence of the defendant's 14 allele at locus D13S317 because the analyst assumed that the 14 allele had "dropped out." However, the occurrence of "allelic dropout" cannot be independently verified-the only evidence that this phenomenon occurred is the "inconsistency" that it purports to explain. Obviously, there is another possible interpretation that is more favorable for this defendant-i.e., that police arrested the wrong man.

Figure 8: Allelic Dropout or the Wrong Man?



D. Spurious Peaks. An additional complication in STR interpretation is that electropherograms often exhibit spurious peaks that do not indicate the presence of DNA. These extra peaks are referred to as "technical artifacts" and are produced by unavoidable imperfections of the DNA analysis process. The most common artifacts are *stutter peaks, noise* and *pull-up*.

Figure 9: This electropherogram contains technical artifacts called stutter that may mask the presence of true alleles present in an evidence sample.



Stutter peaks are small peaks that occur immediately before (and, less frequently, after) a real peak. Stutter occurs as a by-product of the process used to amplify DNA from evidence samples. In samples known to be from a single source, stutter is identifiable by its size and position. However, it is sometimes difficult to distinguish stutter bands from a secondary contributor in samples that contain (or might contain) DNA from more than one person.

Noise is the term used to describe small background peaks that occur along the baseline in all samples. A wide variety of factors (including air bubbles, urea crystals, and sample contamination) can create small random flashes that occasionally may be large enough to be confused with an actual peak or to mask actual peaks.

Pull-up (sometimes referred to as bleed-through) represents a failure of the analysis software to discriminate between the different dye colors used during the generation of the test results. A signal from a locus labeled with blue dye, for example, might mistakenly be interpreted as a yellow or green signal, thereby creating false peaks at the yellow or green loci. Pull-up can usually be identified through careful analysis of the position of peaks across the color spectrum, but there is a danger that pull-up will go unrecognized, particularly when the result it produces is consistent with what the analyst expected or wanted to find.

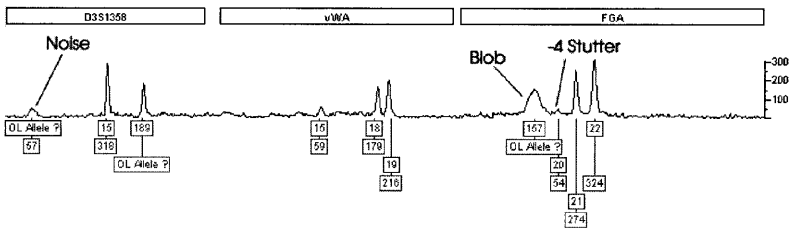
Although many technical artifacts are clearly identifiable, standards for determining whether a peak is a true peak or a technical artifact are often rather subjective, leaving room for disagreement among experts. Furthermore, analysts often appear inconsistent across cases in how they apply interpretive standards-accepting that a signal is a "true peak" more readily when it is consistent with the expected result than when it is not. Hence, these interpretations need to be examined carefully.

Spikes, blobs and other false peaks. A number of different

technical phenomena can affect genetic analyzers, causing spurious results called "artifacts" to appear in the electropherograms. *Spikes* are narrow peaks usually attributed to fluctuation in voltage or the presence of minute air bubbles in the capillary. Spikes are usually seen in the same position in all four colors. *Blobs* are false peaks thought to arise when some colored dye becomes detached from the DNA and gets picked up by the detector. Blobs are usually wider than real peaks and are typically only seen in one color. The "OL Allele" shown in Figure 10 below may be a blob.

Spikes and blobs are not reproducible, which means that if the sample is run through the genetic analyzer again these artifacts should not re-appear in the same place. Hence, the correct way to confirm that a questionable peak is an artifact is to rerun the sample. However analysts, to save time, often simply rely on their "professional experience" to decide which results are spurious and which are real. This practice can be problematic because no generally accepted objective criteria have yet been established to discriminate between artifacts and real peaks (other than retesting).

Figure 10: Blobs and other false peaks may hide the presence of true alleles.



Threshold Issues: Short Peaks, "Weak" Alleles. *When the quantity of DNA being analyzed is very low (as indicated by low peak-heights), the genetic analyzer may fail to detect the entire profile of a contributor. Furthermore, it may be difficult to distinguish true low-level peaks from technical artifacts. Consequently, most forensic laboratories have established peak-height thresholds for "scoring" alleles. Only if the peak-height (expressed in RFU) exceeds a standard value will it be counted.*

There are no generally accepted thresholds for how high

peaks must be to qualify as a "true allele." Applied Biosystems, Inc., which sells the most widely used system for STR typing (the ABI Prism 310 Genetic Analyzer(tm) with the ProfilerPlus(tm) system) recommends a peak-height threshold of 150 RFU, saying that peaks below this level must be interpreted with caution. However, many crime laboratories that use the ABI system have set lower thresholds (down to 40 RFU in some instances). And crime laboratories sometimes apply their standards in an inconsistent manner from case to case or even within a single case. Hence, a defendant may be convicted in one case based on "peaks" that would not be counted in another case, or by another lab. And in some cases there may be unreported peaks, just below the threshold, that would change the interpretation of the case if considered.

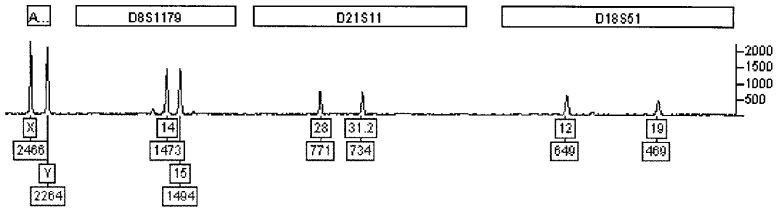
Finding and evaluating low-level peaks can be difficult because labs can set their analytic software to ignore peaks below a specified level and can print out electropherograms in a manner that fails to identify low-level alleles. The best way to assess low-level alleles is to obtain copies of the electronic data files produced by the genetic analyzer and have them re-analyzed by an expert who has access to the analytic software.

Figure 11 shows electropherograms from a rape/homicide case. The defendant admitted having intercourse with the victim, but contended another man had subsequently raped and killed her. The crime lab reported finding only the defendant's profile in vaginal samples from the victim; the lab report stated that the second man was "excluded" as a possible source of the semen collected from the victim's body. However, a review of the electronic data by a defense expert revealed low-level alleles (peaks) consistent with those of the second man, which significantly helped the defense case. Notice how these low-level alleles are obscured in the upper electropherogram (which the lab initially provided in response to a discovery request) due to the use of a large scale (0-2000 RFU) on the Y-axis. These low peaks are revealed in the lower electropherogram, where the defense expert set the software with a lower threshold of detection and produced an electropherogram with a lower scale (0-150 RFU).

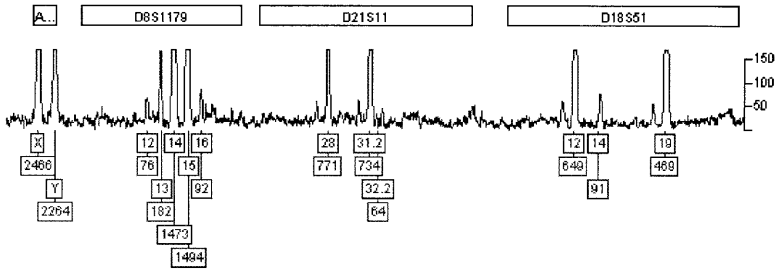
Figure 11: Defense Examination of Electronic Data Reveals Second Contributor to Vaginal Sample (After Crime Lab Reported the Second Man Had Been "Excluded")

	D8S1179	D21S11	D18S15
Defendant	14,15	28, 31.2	12,19
Second Man	13,16	28, 32.2	14,14

Vaginal Swab Profile (Showing Alleles Consistent with Defendant, but None Consistent with Second Man)



Vaginal Swab Profile After Defense Reanalysis of Electronic Data (Showing Additional Low-Level Alleles Consistent with "Excluded" Man)



§ 11:27 Short Tandem Repeats (STRs)—Reviewing Electronic Data in STR Cases

Reviewing the electronic files produced by the ABI Prism 310 Genetic Analyzer(tm) (or similar equipment) has a number of additional benefits beyond revealing unreported low-level peaks. The software that controls these devices creates a complete record of all operations the device performs while typing samples in a particular case and records the results for each sample.

These records can reveal a variety of problems in testing that a forensic laboratory may fail to notice or choose not to report, such as failure of experimental controls, multiple

testing of samples with inconsistent results, re-labeling of samples (which can flag potential sample mix-ups or uncertainty about which sample is which), and failure to follow proper procedures. In some cases review of electronic data has revealed that the laboratory failed to run all of the necessary control samples needed to verify the reliability of the test results, or that the laboratory ran the control samples under different conditions than the analytical samples (a major breach of good scientific practice).

The electronic files are also useful for producing trial exhibits. An expert with the right software can convert the files from their proprietary format into Adobe Acrobat files containing images that can easily be inserted into Powerpoint and Microsoft Word documents.

It is easy for crime laboratories to produce the electronic data that underlie their conclusions. All that is necessary is to copy the files produced in the case onto a CD-ROM, or other storage medium. CD-ROMs are generally preferred because they create an unalterable record of the data produced by the laboratory. Copying files to a CD-ROM is a simple point and click operation that can be accomplished in fifteen minutes or less in most cases. CD-ROM burners compatible with any laboratory computer are available commercially for under $200. There is no legitimate excuse for refusing to turn over electronic data for defense review. In a few instances laboratories have resisted producing electronic files, or have even destroyed the files, but the great majority of trial courts will not tolerate such obstructive behavior.

The electronic data produced by the ABI 310 Genetic Analyzer(tm) is in a proprietary format that can only be read and interpreted by ABI's Genescan(tm) and Genotyper(tm) software. Defense lawyers seeking a review of electronic data must find an expert who has access to this software. The review process typically takes a minimum of 3-4 hours, and may take much longer in an even moderately complicated case. The recent development of "expert system" software for analyzing Genescan(tm) and Genotyper(tm) data provides another option for analysis of electronic data.[1]

§ 11:28 [Reserved]

[Section 11:27]

[1]One option for review of electronic data is a service provided by Forensic Bioinformatics Services (FBS). FBS uses Genescan(tm) and

§ 11:29 [Reserved]

§ 11:30 Y chromosome STRs

The sex of an individual is determined by which pair of sex chromosomes they inherit - either an X and a Y (male) or two X's (female). A genetic marker associated with these two sex chromosomes, Amelogenin, is commonly examined to determine if the contributors to a sample include a male since a distinctive version of the locus is found on Y chromosomes. Very recently, a set of STR markers associated with just the Y chromosome have also been developed and their use has been validated by several laboratories. Like conventional STR markers, the loci are amplified in multiplex reactions where they are labeled with color dyes that allow the amplification products to be typed by a Genetic Analyzer. Since women do not have Y chromosomes as part of their genetic material, Y-STR typing has the promise of being useful in situations where it is necessary to unambiguously determine what a male has contributed to a mixed sample (i.e. those collected as part of most rape investigations). Unlike conventional STRs (sometimes called "autosomal STRs" to distinguish them from Y-STRs), where two alleles per locus is the norm, each version of a Y-STR is normally represented only once in each male. Further, these markers all travel from generation to generation as part of a single chromosome that never has an opportunity to ex-

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Genotyper(tm) to analyze electronic data according to a systematic protocol that was designed to detect ambiguities, problems, and evidence supporting alternative interpretations. FBS is able to do the work at relatively low cost by using an automated "expert system" called Genophiler(tm). Genophiler(tm) is a computer program that operates Genescan and Genotyper the way a highly sophisticated human operator would--but faster and more systematically. Genophiler(tm) extracts all necessary information, analyzes it, and produces various reports of its results.

Lawyers can use these reports to rapidly determine whether there are any significant issues or problems in a case. Defense experts can use these reports as a basis for their own analysis and assessment of the case. All of the electropherograms and other critical data are automatically converted to Adobe Acrobat format, so that the defense expert need not have access to Genescan(tm) and Genotyper(tm) software to review and evaluate the electronic files. An example of Genophiler's(tm) outputs and reports can be found at the FBS web site at www.bioforensics.com.

Dan Krane, one of the authors of this chapter, is president of FBS. William Thompson, another author, has a financial interest in this company.

change information with another Y chromosome. This associated pattern of inheritance undermines the logical foundation for using the product rule (described in § 11:21) to estimate the chance of coincidental matches with other possible male contributors. As a result, the rarity of Y-STR profiles must be determined by empirical studies (i.e. a particular combination of alleles was observed only three times in a sampling of 300 males, therefore it is expected to occur with a frequency of approximately one in 100) and the associated statistics are (and will remain) far less impressive than those generated with conventional STR testing.

§ 11:31 Mitochondrial DNA sequencing

When viewed with a microscope, mitochondria are among the most prominent organelles within human cells. They are primarily known for the central role that they play in the generation of metabolic energy. In humans (and most animals), mitochondria are exclusively inherited through the mother because eggs (and not sperm) are the major contributor of cytoplasm to zygotes. A typical human cell contains between 1,000 and 10,000 mitochondria to satisfy its energy-production needs. Each of these mitochondria contains a copy of the mitochondrial genome which is very small in comparison to the nuclear genome where STR loci are found (16,569 bp vs. 3.2 billion bp for the genome overall). Within that relatively small genome is a stretch of nucleotides called the "mitochondrial D-loop" that tends to differ in its particular sequence of nucleotides (but not its length) from one maternal lineage to another. Analyses of the mitochondrial D-loop sequences have been very useful to biologists studying the migration patterns of humans another mammals. From a forensic perspective, the presence of 1,000 to 10,000 more copies of mitochondrial DNA than nuclear DNA per cell gives analyses of it a distinct advantage in situations where a sample is not expected to have much DNA associated with it (i.e. a hair shaft or a fingerprint) or the DNA within a sample is badly degraded (i.e. after cremation). The utility of mitochondrial DNA sequencing in forensic casework, however has been limited due to: (1) the fact that a single cells fairly frequently contain more than one kind of mitochondria (a situation known as "heteroplasmy"); (2) differences between mitochondrial DNA are not easily detected differences in length like those for STRs and must be

determined by comparatively costly and subjective DNA sequencing; (3) like Y-STRs, the rarity of mitochondrial sequences must be determined by empirical studies and the associated statistics are (and will remain) far less impressive than those generated with STR testing; (4) all maternally related individuals are expected to have the same mitochondrial DNA sequence(s); and (5) the ease with which samples are contaminated and cross-contaminated with mitochondrial DNA.

§ 11:32 Forensic use versus paternity case use

Even though the typing kits are often used in forensic and paternity testing, DNA is used differently in forensic cases than in paternity cases. In criminal cases, the DNA is extracted from evidentiary samples without the knowledge of whose DNA it is. The laboratory then uses statistics to determine the probability that the DNA found on a sample matches the reference sample of the suspect's or victim's DNA. This is not what is done in paternity cases. Instead, the DNA from the child is compared to the parents' DNA to determine if it is possible for either or both parents to have contributed the particular alleles present in the child. For instance, assume that a child has a 10 and an 11 allele at a particular locus and the child's mother is known to possess a 10 and a 12 allele at the same locus. The mother must have contributed the 10 allele and the 11 allele must be paternal. In this example, any man who does not possess an 11 allele could not be the child's father (barring the possibility of mutation that converts one allele to another - something that is unlikely but can be taken into consideration if needed). In the event that a man is not excluded the likelihood that a randomly chosen man might also be able to provide the same paternal alleles in the child can be determined by examining their frequency of occurrence in a relevant reference population.

Sometimes courts will confuse the two types of DNA testing. It is important to clarify this issue for judges who may be misapprehending the issues. For purposes of this chapter, when DNA testing is discussed, reference is to the testing in a forensic setting and not the testing in a paternity case.

§ 11:33 [Reserved]

§ 11:34 [Reserved]

§ 11:35 DNA Statistics

Evidence of a DNA "match" between two samples is impossible to understand and interpret without knowing the probability that a match would be declared if the samples are from different individuals. A match based on the fact that both the suspect's blood and blood at the crime scene contain hemoglobin, for example, would be meaningless because all blood contains hemoglobin. A "match" provides useful evidence of identity only to the extent that different people are unlikely to match. Thus, the question for statisticians is to determine whether the match is as common as a Chevy or as rare as a still-running Edsel. Many commentators consider the ability to quantify the probability of a "match" between samples from different people to be crucial to the admissibility of DNA-derived evidence: "without being informed of such background statistics, the jury is left to its own speculations."[1]

When DNA evidence is offered in the courtroom, it is usu-

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[1]McCormick, Evidence, 655 (Cleary ed.). Appellate courts in most jurisdictions have required that DNA evidence be accompanied by appropriate statistics as a condition of admissibility, see, e.g., People v. Barney, 8 Cal. App. 4th 798, 10 Cal. Rptr. 2d 731, 742 (1st Dist. 1992) ("The statistical calculation step is the pivotal element of DNA analysis, for the evidence means nothing without a determination of the statistical significance of a match of DNA patterns."); People v. Axell, 235 Cal. App. 3d 836, 866, 1 Cal. Rptr. 2d 411, 430 (2d Dist. 1991) ("We find that...a match between two DNA samples means little without data on probability..."); People v. Wallace, 14 Cal. App. 4th 651, 17 Cal. Rptr. 2d 721, n. 3 (1st Dist. 1993) (without valid statistics DNA evidence is "meaningless"); Com. v. Curnin, 409 Mass. 218, 565 N.E.2d 440 (1991) ("It is apparent from the basis on which we decide the DNA testing issue that we would not permit the admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring"); Ex parte Perry, 586 So. 2d 242, 254 (Ala. 1991); State v. Cauthron, 120 Wash. 2d 879, 846 P.2d 502 (1993) ("[t]estimony of a match in DNA samples, without the statistical background or probability estimates, is neither based on a generally accepted scientific theory nor helpful to the trier of fact."); Nelson v. State, 628 A.2d 69, 76 (Del. 1993) (trial court's exclusion of match frequency "inherently inconsisitent" with its admission of testimony of a match, because "without the necessary statistical calculations, the evidence of the match was 'meaningless' to the jury."); State v. Brown, 470 N.W.2d 30 (Iowa 1991) ("Without statistical evidence, the ultimate results of DNA testing would become a

ally accompanied by an estimate of the *frequency* of the matching DNA profile in a reference population. The frequency is assumed to represent the probability of a *coincidental match* between a given individual and another member of the same population. Suppose, for example, that a "match" was declared between a suspect's DNA profile and the profile of a rapist's semen. If the matching profile is found in only one person in a million, then the probability that an innocent suspect would, by coincidence, happen to match the rapist was assumed to be one in a million. Courts in most jurisdictions refused to admit DNA evidence unless it was accompanied by frequency estimates, and much of the controversy surrounding the admissibility of DNA evidence has concerned the scientific validity of the methods used to estimate DNA profile frequencies.

Of course, frequency statistics do not tell the whole story. When assessing the value of DNA evidence for proving two samples have a common source, the trier-of-fact must consider the reliability of the test as well. A DNA "match" between different individuals can occur in two ways: there may be a *coincidental match* between two people who happen to have the same genotypes, or there may be a *false positive*--that is, a false match due to an error in collecting, handling, processing or typing the samples. The potential for false positives can greatly reduce the probative value of DNA evidence.[2] However, courts have not required forensic experts to present estimates of the false positive rate of laboratories-perhaps because these error rates are difficult to estimate.

If no match has been declared between a reference and evidentiary sample, then the inquiry ends there. Exclusions in DNA testing require no statistical probabilities. They are considered absolute.

§ 11:36 DNA Statistics—Calculating Frequency Statistics

Forensic laboratories generally provide estimates of the frequency of a matching DNA profiles among members of

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matter of speculation."); State v. Vandebogart, 136 N.H. 365, 616 A.2d 483, 494 (1992) ("A match is virtually meaningless without a statistical probability expressing the frequency with which a match would occur.").

[2]See, Thompson, Taroni & Aitken, How the Probability of a False Positive Affects the Value of DNA Evidence, 48 J. Forensic Sci. 47 (2003).

three broad racial groups in North America: Caucasians, African-Americans, and Hispanics.[1] The frequency estimates are derived from databases in which are recorded the DNA profiles of a large number of individuals (usually several hundred) from each racial group. The individuals profiled in the databases are usually "convenience samples" of blood donors or paternity case litigants.

To generate frequency estimates that may be as rare as one in a billion, or even one in a trillion, from a database of several hundred individuals, forensic laboratories typically follow a three-step procedure. First, they estimate the frequency of each allele in the DNA profile by simply counting to determine the proportion of people in the database who have it. If two percent of the alleles (of a particular locus) are type A and three percent are type B, their frequencies would be stated as.02 and.03 respectively.

Second, they estimate the frequency of each genotype by using the formula 2pq, where p and q are the frequencies of the two alleles in the genotype. Suppose, for example, that a genotype consisted of alleles A and B. The frequency of genotype AB would be estimated to be 2 x.02 x.03=.0012 (approximately 1 in 833).[2] This formula assumes that the frequencies of the two alleles in a genotype are statistically independent and may significantly underestimate the frequency of genotypes if the allele frequencies are not independent.[3]

Third, they estimate the frequency of the overall DNA profile by multiplying the frequencies of each genotype. For example, suppose that there is a three-locus match between

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[1]Some laboratories divide Hispanics into subcategories (Southwestern and Southeastern Hispanics) and some include additional groups (e.g., Orientals, American Indians).

[2]The product of the individual allele frequencies is multiplied by 2 because there are two ways a person can get a given genotype. A person may have genotype AB as a result of receiving A from his father and B from his mother, or vice versa. By analogy, there are two ways to roll number eleven with a pair of dice: a five on the first die and a six on the second, or vice-versa. Hence, the probability of rolling eleven is 2 x 1/6 x 1/6 =1/18

[3]When alleles at any genotype are statistically independent in a particular population, the population is said to be in Hardy-Weinberg equilibrium. See NRC Report, p. 78.

the suspect and the evidentiary sample. At the first locus, both have genotype AB, which has an estimated frequency of 0.0012; at the second locus, both have genotype CD, which has an estimated frequency of 0.005; at the third locus both have genotype EF, which has an estimated frequency of 0.01. An analyst would typically report that the frequency of the overall profile, across the three loci, is.0012 x.005 x.01 =.00000006, or one in 16.7 million. This formula, sometimes called the product rule, assumes that the frequencies of the genotypes are statistically independent and may significantly underestimate the frequency of the multi-locus genotype if the frequencies are not independent.[4]

§ 11:37 DNA Statistics—Concerns About Population Structure

The assumption that the alleles in DNA profiles are statistically independent has been a key point of contention. When DNA evidence was first introduced, a number of experts raised the concern that human populations might be structured, such that certain DNA profiles are particularly common in people of the same ethnic, religious or geographic subgroup. If there is a significant amount of structure in U.S. populations, then the standard method of calculating DNA profile frequencies, which assumes alleles are statistically independent, would be invalid and might greatly underestimate the frequency of a matching profile.

By analogy, suppose that a population survey showed that 10 percent (1 in 10) of Europeans have blond hair, 10 percent have blue eyes, and 10 percent have fair skin. Multiplying these frequencies yields a figure of.001 (1 in 1000) for the frequency of Europeans with all three traits. This estimate is invalid because these traits tend to occur together among Nordics. The estimate of .001 is obviously far too low for Scandinavia, where Nordics are concentrated. Moreover, because Nordics constitute a significant percentage of the

[4]When the genotypes at different loci are statistically independent in a given population, the population is said to be in linkage equilibrium. See NRC Report, p. 78-79.

European population, the estimate of.001 is also too low for Europe as a whole.[1]

Whether there is sufficient structure in human populations to invalidate forensic statistics was a hotly debated issue in the early 1990s,[2] although empirical research has since allayed much of the concern. In the early 1990s, this debate led courts in several jurisdictions to exclude DNA evidence under the *Frye* standard, on grounds that the method for statistical computation was not generally accepted.[3] A second National Research Council report in 1996 (commonly referred to as NRC II) indicated that the population substructure controversy had subsided and recommended that an alternative corrective factor often referred to as "theta" be applied in product rule calculations for only those loci where an individual possesses two copies of the same allele. "The abundance of data in different ethnic groups within the major races and the genetically and statistically sound methods recommended in this report imply that the ceiling principle and the interim ceiling principle are unnecessary."[4] Most laboratories today follow the NRC recommendations.

One of the most recent statements of acceptance of the

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[1]Any errors caused by population structure are exacerbated when the frequency of individual characteristics is estimated from an inappropriate database. For example, if one relied on a population of Sicilians to estimate the frequency of blond hair, blue eyes and fair skin, among Europeans, one might mistakenly assume each characteristic was found in one person in 100, rather than 1 in 10. Multiplication would then lead to an estimate that only 1 person in one million has blond hair, blue eyes, and fair skin.

[2]For reviews, see K. Roeder, DNA Fingerprinting: A Review of the Controversy, 9 Statis.Sci 222 (1994), and accompanying commentary by multiple authors; B. Weir, Population Genetics in the Forensic DNA Debate, 89 Proc.Natl.Acad.Sci. 11654 (1992); D. Kaye, DNA Evidence: Probability, Population Genetics, and the Courts, 7 Harv. J. L & Tech. 101 (1993); Thompson, 48 J. Forensic Sci. at 61-89.

[3]Com. v. Curnin, 409 Mass. 218, 565 N.E.2d 440 (1991); Com. v. Lanigan, 413 Mass. 154, 596 N.E.2d 311 (1992); People v. Barney, 8 Cal. App. 4th 798, 10 Cal. Rptr. 2d 731 (1st Dist. 1992); State v. Vandebogart, 136 N.H. 365, 616 A.2d 483 (1992); U.S. v. Porter, 618 A.2d 629 (D.C. 1992); People v. Wallace, 14 Cal. App. 4th 651, 17 Cal. Rptr. 2d 721 (1st Dist. 1993); State v. Bible, 175 Ariz. 549, 858 P.2d 1152 (1993).

[4]National Research Council, Committee on DNA Forensic Science: An Update, the Evaluation of Forensic DNA Evidence (1996).

unmodified product rule was made by the Supreme Court of California, a court that has rigorously examined DNA evidence.[5] In *People v. Soto*,[6] the court concluded that "the [courts below] correctly determined that the unmodified product rule, as applied in DNA forensic analysis, is generally accepted in the relevant scientific community of population geneticists, and that statistical calculations made utilizing that rule meet the *Kelly* standard of admissibility."[7]

§ 11:38 DNA Statistics—Error Rate Statistics

Although the validity of frequency statistics has been the primary focus of the debate over forensic DNA evidence, some commentators have argued that having valid estimates of the rate of laboratory error is at least as important as having valid frequency estimates. Frequency statistics speak to the probability of a *coincidental match*, which is only one of the ways a "match" might occur between samples from different individuals. Another way is a *false positive* due to error in the collection, handling, processing or typing of samples. For example, DNA from one sample may inadvertently be mixed with another sample, causing the same profile to appear in both, or a laboratory analyst might mistakenly declare a match by misinterpreting an ambiguous test result.[1] To evaluate DNA evidence, the trier-of-fact needs to know the overall probability of a false match (which includes the probability of a false positive), not just the probability of a coincidental match.[2]

When DNA evidence was first introduced, promoters of the

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[5]See, e.g., People v. Venegas, 18 Cal. 4th 47, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998) (recognizing the general scientific acceptance of RFLP).

[6]People v. Soto, 21 Cal. 4th 512, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999).

[7]981 P.2d at 960. For a more complete understanding of the contents and recommendations of the Report, a copy of the Executive Summary can be reviewed online at http://www.nap.edu/readingroom/books/DNA and can be ordered from the National Academy of Science.

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[1]See Thompson, 96 Genetica 153, for examples of the sort of ambiguous test results that might be misinterpreted, causing false positives, and a discussion of how subjectivity in interpreting DNA tests is conducive to such results.

[2]The probability that a match would be declared if the samples are from different people is approximately (although not precisely) the sum of

new tests often claimed that false positives are impossible.[3] Professor Jonathan Koehler has suggested that test promoters "engaged in a sinister semantic game" in which they were able to issue misleading denials of the possibility that a DNA *test* could make an "error" by excluding consideration of human error in *administering* or *interpreting* the test.[4] Needless to say, the effort to distinguish "human error" from "test error" is pointless and misleading when humans are necessarily involved in administration and interpretation of the test and it is necessary to know the overall rate of error (from whatever cause) to evaluate the test results. "For juries it is of little significance what causes an innocent person to match, what matters is how often such matches might be

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the probability of a false positive and the probability of a coincidental match. Let S designate that two samples have the same source and NS that they do not; M designates that two samples have matching DNA profiles and NM that they do not; and D designates that a match is declared by a DNA analyst following testing. The overall probability of a false match being called, p(D/NS), is not simply the sum of the probability of a coincidental match, p(M/NS), and the probability of a false positive, p(D/NM). Rather, p(D/NS) = p(D/M)p(M/NS) + p(D/NM)p(NM/NS). Because p(D/M) and p(NM/NS) will usually be close to one, however, the sum of the probability of a coincidental match and a false positive is a close approximation to the probability of a false match.

[3]See, People v. Shi Fu Huang, 145 Misc. 2d 513, 546 N.Y.S.2d 920 (County Ct. 1989) ("Dr. Baird testified that it is impossible to get a false positive"); People v. Wesley, 140 Misc. 2d 306, 533 N.Y.S.2d 643 (County Ct. 1988), aff'd, 183 A.D.2d 75, 589 N.Y.S.2d 197 (3d Dep't 1992), appeal granted, 81 N.Y.2d 978, 598 N.Y.S.2d 779, 615 N.E.2d 236 (1993) and order aff'd, 83 N.Y.2d 417, 611 N.Y.S.2d 97, 633 N.E.2d 451 (1994) ("[I]t is impossible under the scientific principles, technology and procedures of DNA Fingerprinting (outside of an identical twin), to get a 'false positive' -- i.e., to identify the wrong individual as the contributor of the DNA being tested.... Under the undisputed testimony received at the hearing, no 'wrong' person, within the established powers of identity for the test, can be identified...."); Hicks v. State, 860 S.W.2d 419 (Tex. Crim. App. 1993) ("According to Caskey, a false positive finding was impossible..."); Cobey v. State, 80 Md. App. 31, 559 A.2d 391, 392 (1989) ("[A]n incorrect match is an impossible result"); see also Jonathan J. Koehler, DNA Matches and Statistics: Important Questions, Surprising Answers, 76 Judicature 222 (1993); Jonathan Koehler, Error and Exaggeration in the Presentation of DNA Evidence at Trial, 34 Jurimetics 21 (1993) (quoting a number of similar statements from transcripts of expert testimony).

[4]Koehler, 34 Jurimetics at 24.

expected."[5]

The potential for false positives in DNA testing is now broadly recognized,[6] although the rate at which they occur is difficult to estimate due to the paucity of research on the issue. The limited research to date, however, suggests that false positives may be far more common than coincidental matches (at least for multi-locus RFLP tests).[7] Some commentators have argued that the probability of a false positive is so much greater than the probability of a coincidental match that frequency statistics have little bearing on the value of DNA evidence.[8] Indeed, several commentators have

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[5]Laurence Mueller, The Use of DNA Typing in Forensic Science, 3 Accountability in Research 55, 56 (1993); see also William C. Thompson, Evaluating the Admissibility of New Genetic Identification Tests: Lessons from the "DNA War", 84 J. Crim. L. & Criminology 22, 92 (1993).

[6]"Laboratory errors happen, even in the best laboratories and even when the analyst is certain that every precaution against error was taken." NRC Report, p. 88-89; Donald Berry, Comment, 9 Stat. Sci. 252, 253 (1994) ("Only the frequency and type of errors are at issue."); R.C. Lewontin, Comment: The Use of DNA Profiles in Forensic Contexts, 9 Stat. Sci. 259 (1994) (discussing sources of error); William C. Thompson, Comment, 9 Stat. Sci. 263, 265 (1994) (discussing data on laboratory error); cf. Dan L. Burk, DNA Identification: Possibilities and Pitfalls Revisited, 31 Jurimetics 53, 80 ("Bald statements or broad hints that DNA testing is infallible...are not only irresponsible, they border on scientific fraud").

[7]See Koehler, 76 Judicature at 229 ("[B]ased on the little evidence available to date, a reasonable estimate of the false positive error rate is 1-4 percent."); Koehler, 34 Jurimetics at 26 (proficiency testing shows error rate of 1-4 %).

[8]Paul J. Hagerman, DNA Typing in the Forensic Arena, 47 Am.J.Hum.Genet. 876 (high false positive rate makes probability of coincidental match irrelevant); Richard Lempert, Some Caveats Concerning DNA As Criminal Identification Evidence: With Thanks to the Reverend Bayes, 13 Cardozo L.Rev 303, 325 (the probability of a coincidental match between people who have the same DNA profile "is usually dwarfed by the probability of a false positive error"); Mueller, 3 Accountability in Research at 58 (exact probability of a coincidental match "should hardly matter" to jury given much greater likelihood of false positive).

For example, if the probability of a false match due to laboratory error were.01 (one chance in 100) and the frequency of the profile were.000000001 (one in one billion), then the overall probability of a match between samples from different people would be approximately.010000001, a number that rounds off to.01 (one in 100). If the frequency were instead.001 (one in 1000), then the overall probability

gone so far as to suggest that jurors be told only the false positive rate[9] to avoid the risk that they will be confused or unduly swayed by an impressive frequency (e.g., one in one million) that has little meaning or value relative to the false positive rate.[10]

In 1992 a report of the National Research Council (NRC I) called for more extensive proficiency testing, declaring that "laboratory error rates must be continually estimated in blind proficiency testing and must be disclosed to juries" (1). The NRC called for external, blind proficiency tests "that are truly representative of case materials (with respect to sample quality, accompanying description, etc.)". Thereafter, the Federal DNA Identification Act of 1994 required the director of the National Institute of Justice (NIJ) to report to Congress on the feasibility of establishing an external blind

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of a match would be approximately.011, a number that still rounds off to.01 (one in 100). In other words, when the false positive rate is one in 100, the value of the DNA evidence is about the same whether the frequency of the matching profile is one in a thousand or one in a billion.

This example shows that having accurate statistics on the probability of a false positive may be far more important than having accurate statistics on the probability of a coincidental match if, as some experts have suggested, false positives are more common than coincidental matches.

[9]"The rate of false positives defines a practical lower bound on the probability of a match, and probability estimates based on population data that are smaller than the false-positive rate should be disregarded." R.C. Lewontin & Daniel Hartl, Population Genetics in Forensic DNA Typing, 254 Science 1745, 1749 (1991).

Professor Paul Hagerman has suggested that the frequency and false positive rate be combined into a single number by adding them together. Hagerman, DNA Typing in the Forensic Arena, 47 Am.J. Hum. Genet. 876 (1990). Where the frequency is much smaller than the probability of a false positive, the effect of this suggestion is nearly the same as simply presenting the false positive.

[10]Professor Richard Lempert specifically cites the danger of confusion and prejudice as a reason for presenting only the error rate statistic in cases where the probability of a false positive greatly exceeds the probability of a coincidental match....jurors provided with a laboratory's false positive rate and with information about the likelihood, assuming no testing error, of a match if the evidence DNA was not the defendant's, are likely to be hopelessly confused about the weight to accord the testimony because ordinary people are not very good at working with conditional probabilities. Thus, jurors ordinarily should receive only the laboratory's false positive rate as an estimate of the likelihood that the evidence DNA did not come from the defendant. Lempert, 13 Cardozo L.Rev at 325.

proficiency testing program for DNA laboratories. But the move toward external blind proficiency testing lost momentum when the NIJ director raised a number of practical concerns. It was dealt another blow by the 1996 report of the National Research Council, which downplayed the need for proficiency testing. The 1996 NRC report suggested that the problem of laboratory error be addressed through a variety of means, and concluded that the best way to safeguard against error is to allow re-testing of samples.

§ 11:39 DNA Statistics—The "uniqueness" of DNA profiles

When the estimated frequency of the shared profile is very low, some labs will simply state "to a scientific certainty" that the samples sharing that profile *are* from the same person. For example, the FBI laboratory will claim two samples are from the same person if the estimated frequency of the shared profile among unrelated individuals is below one in 260 billion. Other labs use different cut off values for making identity claims. All of the cut-off values are arbitrary: there is no scientific reason for setting the cut off at any particular level just as scientists have not arrived at any formally recognized way of being "scientifically certain" about anything (in fact, many would argue that it is essential for scientists to be uncertain about essentially everything). Moreover, these identity claims can be misleading because they imply that there could be no alternative explanation for the "match," such as laboratory error, and they ignore the fact that close relatives are far more likely to have matching profiles than unrelated individuals. They can also be misleading in that the DNA tests themselves are powerless to provide any insight into the circumstances under which the sample was deposited and are generally unable to determine the type of tissue that was involved.

§ 11:40 DNA Statistics—Probabilities of exclusion from mixed samples

As described earlier, the interpretation of DNA profiles obtained from mixtures is difficult at best. One especially dangerous warning sign is that many testing laboratories decline to draw conclusions regarding mixed samples in the absence of knowledge regarding the DNA profiles of individu-

als that are expected by investigators to be a contributor to a sample. The relevant question for mixed samples is "What fraction of the general population would be definitively excluded as being a possible contributor to this evidentiary sample?" It is possible to objectively address the possibility that alleles are masked by the presence of either alleles from other contributors or by technical artifacts (such as stutter peaks). Such approaches typically generate fairly unimpressive numbers - particularly when the discretion to dismiss a small number of "anomalous" results are taken into account as well. As a result, it is common (though not generally acceptable to the scientific community) for analysts to report the answer to a very different question, namely "What is the rarity of the reference sample in the general population?"

§ 11:41 DNA Statistics—Cold hit statistics

Until recently, the DNA profiles that have been generated for forensic purposes have been almost exclusively those that could be characterized as "probable cause matches," in which DNA testing has been performed upon a reference sample taken from a suspect that has already been linked to a crime by direct or circumstantial evidence. A new category of DNA profile "matches" are becoming increasingly common however - those that are generated as a result of "cold hits" that result from the trawling of a large number of DNA profiles maintained in databases (usually those of previously convicted offenders). Since the primary difference between these kinds of matches is the manner in which a suspect is first identified, it is generally accepted that it is not possible to convert one type of case into the other (for instance, by simply retesting a reference sample once a "cold hit" has been identified). It is also generally accepted in the scientific community that the statistical significance of those two kinds of DNA profile matches should be determined differently. However, there are at least three different commonly held opinions on how the statistics associated with "cold hits" should be generated and presented.

The first group to address this issue was a body of experts appointed to the Committee on DNA Science by the National Research Council in 1992. The position of this group is that database searches should be used to identify potential suspects but not to calculate frequency estimates. When successful, suspects identified by these searches would then be

tested at a completely different group of independent genetic markers that would also be compared to the evidence. If these additional genetic loci also match between the suspect and evidence sample, they alone would be used to compute probabilities that reflect the significance of a match. With this methodology the genetic markers used in the original database search are specifically and deliberately excluded from any statistical calculation.

A second committee of prominent experts advocated a significantly different approach in 1996. They specifically recommended that, "When the suspect is found by a search of DNA databases, the random-match probability should be multiplied by N, the number of persons in the database."[1] Proponents of this approach feel that the first method is too conservative. Their alternative method differs in three ways: (1) no testing is performed at additional loci; (2) genetic markers used in the original database search are included in the statistical calculations; and (3) the size of the database being searched (N) is taken into consideration.

A third group is comprised of individual scientists who have published peer-reviewed manuscripts in which they argue that a "cold hit" should actually be given more weight than a match found in a "probable cause" case. Their position is based on the thinking that not only has the defendant been found to match the evidence, but many more individuals have been found to not match. In "probable cause" cases where only a single match is found during the course of DNA testing, there is at least still a formal possibility that one or more untested people may also match the evidence - that possibility becomes increasingly less likely as the database used for a cold hit becomes larger. Proponents of this approach also feel that the first method is too conservative. Their method differs from it in three ways: (1) no testing is performed at additional loci; (2) genetic markers used in the original database search are included in the statistical calculations; and (3) the size of the database being searched (*N*) is taken into consideration. It also differs from the second in one very important way: the effect of the database size on the significance of a match is precisely opposite - large

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[1]The Evaluation of Forensic DNA Evidence, National Research Council Press, p. 40, 161 (1996).

databases generate the most damning statistics for a defendant while, in the second approach, the larger the database the less damning the statistics become to a defendant. The second and third approaches are diametrically opposed with respect to implications of the size of the database that is searched.

The proponents of each of these three approaches include many eminent scholars in the field of genetics and statistics. For instance, the blue ribbon panel of experts that generated the first National Research Council on DNA typing report (which supports the first approach as described above) includes Drs. Mary-Claire King, Richard Lempert, Eric Lander, Ruth Macklin, Thomas Marr, Victor McKusick, Philip Reilly and Sandy Zabel. Members of the second National Research Council on DNA Typing (which recommends the second approach as described above) include prominent population geneticists and statisticians such as Drs. James Crow, Arno Motulsky, Thomas Nagylaki, Mashotoshi Nei, David Siegmond and Stephen Stigler. The third approach (described above) is one that has been principally advocated by very influential and often cited geneticists and statisticians such as Drs. David Balding, Peter Donnelly and Bruce Weir (as in publications such as: *Errors and Misunderstandings in the Second NRC Report*, D. J. Balding, Jurimetrics, Summer 1997, 37:469-476; *Evaluating DNA Profile Evidence When the Suspect Is Identified through a Database Search*, D. J. Balding and P. Donnelly, Journal of Forensic Science, 1996, 41:603-607; and *Interpreting DNA Evidence,* I. W. Evett and B. S. Weir, Sinauer Press, 1998, pp. 219-222). This appears to represent a genuine split between three fundamentally different approaches by experts who are significant both in number and in eminence within their fields.

§ 11:42 Laboratory Errors

Promoters of forensic DNA testing have done a good job selling the public, and even many criminal defense lawyers, on the idea that DNA tests provide a unique and infallible identification. DNA evidence has sent tens of thousands of people to prison and, in recent years, has played a vital role in exonerating men who were falsely convicted. Even former critics of DNA testing, like Barry Scheck, are widely quoted attesting to the reliability of the DNA evidence in their cases. It is easy to assume that any past problems with DNA evi-

dence have been worked out and that the tests are now unassailable.

The problem with this assumption is that it ignores case-to-case variations in the nature and quality of DNA evidence. Although DNA technology has dramatically improved since it was first used just 15 years ago, and the tests have the *potential* to produce powerful and convincing results, that potential is not realized in every case. Even when the reliability and admissibility of the underlying test is well established, there is no guarantee that a test will produce reliable results each time it is used. Case-specific issues and problems often greatly affect the quality and relevance of DNA test results. In those situations, DNA evidence is far less probative than it might initially appear.

When DNA evidence was first introduced, a number of experts testified that false positives are impossible in DNA testing.[1] This claim is now broadly recognized as wrong in principle[2] and it has repeatedly proven wrong in practice.[3] But it has been mentioned frequently, without skepticism, in appellate court opinions.[4]

Why did experts offer this questionable testimony? One commentator has suggested that avid proponents of DNA evidence sought to allay judicial concerns about the potential for error by engaging in "a sinister semantic game".[5] They were able to deny that a DNA test could produce an error by excluding consideration of human error in administering or interpreting the test. Sinister or not, it is misleading to exclude considerations of human error in DNA testing when

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[1]See, William C. Thompson, "Forensic DNA Evidence" in Expert Evidence: A Practitioner's Guide to Law, Science and the FJC Manual 195-266 (1997); Koehler, 34 Jurimetics at 21-39.

[2]See, National Research Council, DNA Technology in Forensic Science (1992); Kaye, 7 Harv. J. L & Tech at 101-72; Randolph N. Jonakait, Stories, Forensic Science and Improved Verdicts, 13 Cardozo L. Rev. 343 (1991); Koehler, 76 Judicature at 222-29; William C. Thompson, Comment on Roeder K., DNA Fingerprinting: A Review of the Controversy, 9 Stat. Sci. 263 (1994).

[3]See, Thompson, 96 Genetica at 153-68; Jonathan Koehler, The Random Match Probability in DNA Evidence: Irrelevant and Prejudicial?, 35 Jurimetrics 201 (1995); Thompson, 37 Jurimetrics at 405-24.

[4]See Kaye, 7 Harv. J.L & Tech 101; Thompson, 37 Jurimetrics 405.

[5]Koehler, 34 Jurimetics 21.

humans are necessarily involved in the administration and interpretation of DNA tests. For those who must evaluate DNA evidence, it makes little difference what causes a false match, what matters is how often false matches might be expected.

False positives have occurred in proficiency tests[6] and in actual cases.[7] For example, the Philadelphia City Crime Laboratory recently admitted that it had accidentally switched the reference samples of the defendant and victim in a rape case. The error led the laboratory to issue a report that mistakenly stated that the defendant was a potential contributor of what the analysts took to be "seminal stains" on the victim's clothing.[8] The report also stated that the defendant's profile was "included" in a mixed sample taken from vaginal swabs. After the sample switch came to light, the laboratory reassessed the evidence and concluded that the "seminal stains" were actually bloodstains that matched the victim's DNA profile and that the defendant was excluded as a potential contributor to the vaginal sample.[9]

In 1995, Cellmark Diagnostics made a similar error when it reported, incorrectly, that a rape defendant's DNA profile was found in what was characterized as a semen stain from a rape case. In fact, Cellmark had found the rape victim's own profile in the stain (which obviously was not semen), but had misinterpreted its own results by mixing up the defendant's and victim's profiles while recording the test results. This error was undetected when a second analyst at Cellmark reviewed the first analyst's work. It came to light only after a Cellmark witness had presented erroneous

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[6]See, William C. Thompson, Ford S., "The Meaning of a Match: Sources of Ambiguity in the Interpretation of DNA Prints" in Forensic DNA Technology (1991); Thompson, 96 Genetica 153; Koehler, 76 Judicature 222; Thompson, 9 Stat. Sci. 263; Koehler, 35 Jurimetrics 201; Thompson, 37 Jurimetrics 405; Mueller, 3 Accountability in Research 55; Roeder, 9 Stat. Sci. 222.

[7]Thompson, 37 Jurimetrics 405; Scheck B, Neufeld P, Dwyer F., Actual Innocence (2000).

[8]Brenner L, Pfleeger B., Investigation of the Sexual Assault of Danah H. Philadelphia (PA): Philadelphia Police Department DNA Identification Laboratory; 1999 Sept. 24. Lab No.: 97-70826.

[9]Brenner L, Pfleeger B., Amended Report: Investigation of the Sexual Assault of Danah H. Philadelphia (PA): Philadelphia Police Department DNA Identification Laboratory; 2000 Feb. 7. Lab No.: 97-70826.

testimony about the false match in a pretrial hearing in the case. Cellmark issued a revised report that stated that the evidentiary sample matched the victim's own DNA profile and that the defendant was excluded as a potential donor.[10]

False positives can also arise due to misinterpretation of test results. One such error led to the false conviction of Timothy Durham.[11] In 1993 a Tulsa Oklahoma jury convicted Durham of the rape of an 11-year-old girl. He was sentenced to 3,000 years in prison. The prosecution presented three pieces of evidence against him: the young victim's eyewitness identification, testimony that Durham's hair was similar (in microscopic examination) to hair found at the crime scene, and a DNA test (DQ-alpha) that reportedly showed that Durham's genotype matched that of the semen donor. Durham presented eleven witnesses who placed him in another state at the time of the crime, but the jury rejected his alibi defense. Fortunately for Durham, post-conviction DNA testing showed that he did not share the DQ-alpha genotype found in the semen. He was also excluded at several other genetic loci in multiple tests. The initial DNA test result that helped convict Durham was proven to have been a false positive. The error arose from misinterpretation. The laboratory had failed to completely separate male from female DNA during differential extraction of the semen stain. The victim's alleles, when combined with those of the true rapist, produced an apparent genotype that matched Durham's. The laboratory mistook this mixed profile for a single source result, and thereby falsely incriminated an innocent man. Durham was released from prison in 1997.

In 2003, another DNA false positive came to light. Josiah Sutton, a 16-year-old from Houston was falsely convicted of rape in 1996 and sentenced to 25 years in prison based on a misinterpreted DNA test. The error came to light when one of the authors of this chapter was reviewing casework from the Houston Police Department DNA/Serology laboratory at

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[10]Cotton RW, Word C., Amended Report of Laboratory Examination, Germantown (MD): Cellmark Diagnostics; 1995 Nov 20. Case No.: F951078. A transcript of testimony in this case, in which a Cellmark expert admits to the error, can be found at www.scientific.org.

[11]Thompson, 37 Jurimetrics 405; Scheck, Neufeld & Dwyer, Actual Innocence.

the request of a Houston television station. Retesting using STRs proved conclusively that Sutton was innocent.[12]

Although experience has shown that false positives can occur, the rate at which they occur is difficult to estimate on the basis of existing data. Most laboratories participate in periodic proficiency tests, which can cast some light on the potential for error. European forensic laboratories have carried out collaborative exercises involving analysis of stains from known sources. However, this work is designed more to test the uniformity of DNA test results among laboratories using the same protocol than to determine the rate of errors. In the United States, TWGDAM guidelines call for each analyst to take two proficiency tests each year[13] and proficiency testing is a requirement for laboratory certification under the program administered by ASCLAD-LAB.[14] However, these tests generally are not well designed for estimating the rate of false positives. The tests typically are not blind (i.e., the analysts know they are being tested), they involve limited numbers of samples, and the samples may be easier to analyze than those encountered in routine casework.

It is not always possible to tell from the laboratory records whether samples *actually* were mixed up or cross-contaminated. However, careful review of the laboratory records will usually provide important information about whether such errors *could have happened*. For example, evidence that a reference sample from the defendant was handled or processed in close proximity to samples from the crime scene can support the theory that a sample handling error explains incriminating results. In one case, review of a criminalist's notes showed that the defendant's trousers, collected at his home, were transported to the laboratory in the same box that contained a number of items from the crime scene that were saturated with the victim's blood. This fact cast important new light on a seemingly incriminating

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[12]Several articles about this case can be found at www.scientific.org

[13]Technical Working Group on DNA Analysis Methods (TWGDAM) established guidelines for a quality assurance program for DNA testing laboratories; including RFLP and PCR technologies. 18 Crime Lab Dig. 44 (1995).

[14]National Research Council, The Evaluation of Forensic DNA Evidence (1996).

result: blood from victim was detected on the defendant's trousers.

It is suggested that defense lawyers obtain and review complete copies of all records related to evidentiary samples collected in the case. It should be possible to document the complete history of every sample from the time it was initially collected through its ultimate disposition.

§ 11:43 Inadvertent Transfer of DNA

One of the most striking developments in forensic DNA testing in recent years is the testing of ever smaller biological samples. Whereas the original DNA tests required a fairly large amount (i.e. a blood stain the size of a dime) of biological material to get a result, current DNA tests are so sensitive that they can type the DNA found in samples containing only a few cells. There is likely to be enough of your DNA on the book you are reading right now for your DNA profile to be determined by a crime lab.

The increasing sensitivity of DNA tests has affected the nature of criminal investigations and has created a new class of DNA evidence. Analysts talk of detecting "trace DNA," such as the minute quantities of DNA transferred through skin contact. DNA typing is currently being applied, with varying degrees of success, to samples such as doorbells pressed in home invasion cases, eyeglasses found at a crime scene, handles of knives and other weapons, soda straws, and even single fingerprints.

These developments will bring more DNA evidence to court in a wider variety of cases and may well open new lines of defense. A key issue will be the potential for inadvertent transfer of small amounts of DNA from one item to another, a process that could easily incriminate an innocent person. Studies have documented the presence of typeable quantities of human DNA on doorknobs, coffee cups and other common items.[1] Studies have also documented the inadvertent

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[Section 11:43]

[1]See, R.A.H. van Oorschot, DNA Fingerprints from Fingerprints, Nature, June 19, 1997, at 767; Findlay, et al, DNA Fingerprinting from Single Cells, Nature, October 9, 1997, at 555-556; Ladd, et al, A Systematic Analysis of Secondary DNA Transfer, 44 J. Forensic Sci. 1270 (1999).

transfer of human DNA from one item to another.[2] *Primary transfer* occurs when DNA transferred from a person to an item. *Secondary transfer* is when the DNA deposited on one item is transferred to a second item. *Tertiary transfer* is when the DNA on the second item is, in turn, transferred to a third. There are published studies that document secondary transfer of DNA (in quantities that can be detected by STR tests) from items that people simply touched to other items.

A recent study commissioned by a wealthy defendant was used to show that tertiary transfer of DNA could have occurred in a manner that falsely incriminated the defendant. Dr. Dirk Greineder, a prominent physician and adjunct Harvard Professor, was accused of killing his wife.[3] A DNA profile similar to Greineder's was found, mixed with his wife's profile, on gloves and a knife found near the crime scene. Greineder denied touching these items, which appeared to have been used by the killer. But how did his DNA get on them?

Greineder offered a two-pronged defense. First, he challenged the conclusion that his DNA matched that on the gloves, noting inconsistencies between his profile and the profile on the gloves. The crime laboratory had shifted its threshold for scoring alleles in a manner that allowed it to count alleles that matched with Greineder, while ignoring some that did not. And the lab had to evoke the theory of "allelic drop out" to explain why some of Greineder's alleles were not found.

Greineder's second line of defense is our focus here. He argued that his DNA could have gotten onto the glove

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[2]R.A.H. van Oorschot, et al, HUMTH01 Validation Studies: Effect of Substrate Environment and Mixtures, 41 J. Forensic Sci. 142 (1996); van Oorschot, DNA Fingerprints from Fingerprints, Nature, June 19, 1997, at 767; Findlay, et al, DNA Fingerprinting from Single Cells, Nature, October 9, 1997, at 555-556; Van Hoofstat, et. al., DNA Typing of Fingerprints Using Capillary Electrophoresis: Effect of Dactyloscopic Powders, 20 Electrophoresis 2870 (1999); Szibor, et al, Efficiency of Forensic mt DNA Analysis: Case Examples Demonstrating the Identification of Traces, 113 Forensic Science International 71 (2000); A.E. Kisilevsky, et al, DNA PCR STR Profiling of Skin Cells Transferred through Handling, Abstract from the 46th Annual Meeting of the Canadian Society of Forensic Scientists (Edmonton, Alberta, November 16-21, 1999.

[3]Commonwealth v. Greineder (Norfolk County Superior Court, No. 108588, 2001).

through tertiary transfer. He and his wife had shared a towel the morning of the murder-perhaps his DNA was transferred from his face to the towel, and from the towel to his wife's face. His wife was later attacked by a glove-wearing stranger who struck her on the face, strangled her, and stabbed her, in the process transferring Greineder's DNA from his wife's face to the gloves and the knife. According to this theory, the tell-tale extra alleles on the gloves and knife that matched neither Greineder nor his wife were those of the killer.

To support the theory that his DNA could have been transferred innocently to the instruments of murder, Greineder commissioned a study. Forensic scientists Marc Taylor and Elizabeth Johnson, of Technical Associates (an independent laboratory in Ventura, California) simulated the sequence of events posited by the defense theory: a man wiped his face with a towel, then a woman wiped her face with the towel, then gloves and a knife like those used in the murder were rubbed against the woman's face. DNA tests on the gloves and knife revealed a mixture of DNA from the man and woman-exactly what was found in the Greineder case. Taylor was allowed to present his findings to the jury. Although the jury ultimately convicted Greineder (there was other incriminating evidence besides the DNA), the case is a good example of how the amazing sensitivity of contemporary DNA profiling methods facilitate a plausible explanation for what might at first seem to be a damning DNA test result.

III. HOW THE COURTS HAVE APPROACHED DNA TESTING

§ 11:44 Generally

By and large, the earliest cases regarding DNA testing were more accepting of the results of such testing and, before 1991, there were virtually no cases that seriously questioned either the validity of the testing or even the statistical odds that were admitted—including such astronomical odds as 30 billion to one!

There were a few reasons for the courts' early acceptance of DNA testing. First, until the critics of DNA testing became more vocal in their disapproval of the testing procedures, lay persons were unaware of the problems with the science and unable to challenge the science. Virtually no lawyers understood the science fully enough to challenge it and few, if any, knew who to contact for assistance.

Second, most defense lawyers were unaware of who the experts in the field of DNA testing were until such individuals began to publish their works. Third, the vast majority of forensic DNA work was done by private laboratories, which, citing proprietary reasons, did not make their preliminary studies and results available. The few laboratories that perform DNA testing—namely, Cellmark, Lifecodes and even the FBI—have been proprietary about their underlying data.[1] As such, it was difficult to challenge the underlying information when much of it was not being revealed to the public.

Once certain experts began to question aspects of the science, however, those experts began to testify in courts. With the publication of the populations substructure controversy in *Science* in 1991 and in the NRC study, many courts began to seriously question the validity of DNA testing as reliable forensic evidence.

The reaction in the courtroom to DNA testing has gone through a type of metamorphosis during the past few years. At first, there was widespread acceptance, which gave way to a decline in the admission of the evidence, followed by an admission of the testimony but in a more guarded fashion. Most recently, courts have once again begun to loosen the restrictions on admission of the evidence.

Not surprisingly, the way in which the jurisdictions initially considered DNA testing seems to have had a lot to do with the manner in which the state dealt with the issue of scientific admissibility. For those states that retained a more traditional *Frye* -type standard, the question of admissibility of the evidence proved to be more daunting than in those states that have supplanted the test with a newer, "relevancy" type standard. Accordingly, as part of the analysis of the various states' approaches, the test of admissibility will be addressed where relevant.[2]

§ 11:45 Jurisdictions admitting DNA evidence

By now, nearly all jurisdictions have admitted DNA

[Section 11:44]

[1]See generally Thompson, Lessons From the "DNA War," at 36 and 78-79.

[2]For a complete discussion of the admissibility of scientific evidence, see Chapter 10 supra, which devotes a substantial portion to the admission of novel scientific evidence.

evidence. By and large, the cases that admitted DNA evidence without much (or any) challenge were the earliest cases. As the science developed and the critics became more involved in the science, many of the courts began seriously questioning whether DNA evidence met the *Frye* standard of admissibility.

Since the publication of the 1992 NRC Report, a number of cases have questioned the appropriateness of DNA evidence in the courtroom and a number of courts have put the admission of the evidence on hold until certain problems have been satisfactorily resolved. Following the 1996 Prepublication Report of the NRC, finding the ceiling principle and modified ceiling principle no longer necessary, the case law has begun to change again, moving toward more complete acceptance of DNA evidence. Many jurisdictions have admitted DNA evidence, holding that the problems with DNA evidence go to the question of weight, not admissibility.

§ 11:46 Jurisdictions admitting DNA evidence—The early cases

An early case addressing DNA testimony in a forensic setting was a South Carolina case entitled *State v. Ford*.[1] In *Ford*, the victim was raped by a man wearing a Halloween mask and was subsequently unable to identify Ford as her assailant. From the sperm taken from a vaginal swab and the victim's clothing, the prosecution claimed that the sample matched the defendant's DNA.

At the time of trial, the defendant conceded that DNA extraction and the electrophoresis process had gained general scientific acceptance, but that "the process as a whole" had not. The Supreme Court of South Carolina remarked that while there were possible problems with the forensic use of DNA such as contamination of the samples, such concerns were individual concerns of individual cases and did not affect the general scientific reliability of the process. Thus, the court found that:

> DNA print testing and the process of RFLP analysis have been recognized as reliable and have gained general acceptance in

[Section 11:46]

[1]State v. Ford, 392 S.E.2d 781 (S.C. 1990).

> the scientific community. In addition, the evidence indicated that RFLP analysis involves scientifically and professionally established techniques rather than untested methods or unproven hypotheses. Thus, the RFLP analysis and test results would be admissible under . . . the Frye standard.[2]

Maryland addressed the issue of DNA in an early case entitled *Cobey v. State*.[3] In *Cobey*, the victim was raped and brutalized by a man who attacked her in a park and then stole her car. Upon his arrest, a DNA analysis comparing the defendant's blood to semen found on the victim's underclothing was undertaken and they were found to match.

The defense challenged primarily the methods used by the laboratory (Cellmark), but the court also addressed the admissibility of DNA analysis as a whole. Providing an encapsulated discussion of how a DNA profile is made, the court quoted a law review article for the proposition that "[c]ommercial laboratories marketing the tests say their research shows that DNA typing is as accurate as a fingerprint."[4]

In *Cobey*, the prosecution introduced five experts to vouch for the acceptability of DNA profiling in the scientific community, while the defense presented no evidence to the contrary. Determining that the evidence was admissible, the court found that that defense challenges to the procedures of the laboratory were not persuasive, remarking that it was significant that the defendant produced no expert testimony.

However, the court did question the future admissibility of DNA evidence, stating as follows:

> We make crystal clear that we are not, at this juncture, holding that DNA fingerprinting is now admissible willy-nilly in all criminal trials conducted between this date [and when the new statute takes effect]. . . We are merely holding that, based upon this record, Judge Ruben did not err in finding that DNA fingerprinting was generally acceptable in the scien-

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[2]Id. at 784.

[3]Cobey v. State, 559 A.2d 391 (Md. App. 1989), cert. denied, 565 A.2d 670 (Md. 1989).

[4]559 A.2d at 392, quoting Moss, DNA—The New Fingerprints, 74 ABA J 66 (1988).

tific community and in permitting its introduction into evidence, since there was no evidence to the contrary.[5]

Subsequently, Maryland enacted a statute governing the admissibility of DNA evidence.[6]

In 1991, in a lengthy opinion addressing the standards of admissibility of scientific evidence,[7] Arkansas determined in *Prater v. State*,[8] that DNA evidence met such a standard and should be admissible. The Arkansas Supreme Court adopted a three-part "relevancy approach" which required a judge to conduct a preliminary hearing to determine: " (1) the reliability of the novel process used to generate the evidence, (2) the possibility that admitting the evidence would overwhelm, confuse or mislead the jury, and (3) the connection between the novel process evidence to be offered and the disputed factual issues in the particular case."[9]

Under this new approach, the court first determines whether the proffered evidence is reliable, not misleading, and helpful. With DNA testing, the court found that all the prongs of the standard were met concerning the testing procedure itself. "In sum, we have no hesitancy in affirming the trial court's ruling that DNA testing is such a sufficiently reliable scientific procedure that it may be admitted in evidence."[10]

The Arkansas Supreme Court did remark, however, that challenges to the protocol used by laboratories were still available to defendants in individual cases, but that there was no error in the admission in the particular case.

Finally, the court addressed the issue of probabilities concerning the DNA match. Noting that there were concerns about the probabilities of population genetics, the court nonetheless concluded that under the relevancy standard, the probabilities should be admissible. Significant to its decision was the failure of the defense to adequately challenge the

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[5]Id. at 398.

[6]See § 11:44 infra.

[7]For a discussion of this and other cases addressing the standards of novel scientific evidence, see Chapter 10, supra.

[8]Prater v. State, 820 S.W.2d 429 (Ark. 1991).

[9]Id. at 431, citing Weinstein & Berger, Weinstein's Evidence ¶ 702[03] at 702-18 to 702-20 (1991).

[10]Id. at 436.

issue. The court left the door open on the issue, stating that "just because there was no meaningful attack upon the population genetics in this case does not mean that there can not be a successful attack in future cases."[11]

In New Jersey, the Superior Court (the intermediate appellate court) found that DNA testing of the PCR type (rather than the RFLP type) was admissible in the case of *State v. Williams*.[12] In New Jersey, the courts use a hybrid of the *Frye* admissibility test which requires as proof that a science has met the threshold of scientific acceptability in the community and that the moving party introduce sufficient evidence in the form of expert opinions, authoritative scientific and legal writings and/or judicial opinions.

The experts in the case at bar were impressive, having testified numerous times as experts and having published over 100 times each in peer review journals. The defense, the court noted "did not offer a single witness in opposition."[13] Thus, the court found that the prosecution had met its burden of the standard of admissibility of PCR testing of DNA. It stated:

> The record contains an abundance of evidence offered by the State supporting its contention that PCR testing has gained general acceptance in the particular field in which it belongs. Its reliability has been proven pursuant to the standard [required] . . ., by the testimony of experts, by evidence of hundreds of authoritative scientific articles and other literature supporting this testing technique, and by the overwhelming acceptance of PCR testing in dozens of judicial decisions in other states throughout the nation.[14]

Thus, based upon the evidence presented in that case, the court ruled that the standard of admissibility for novel scientific evidence was met in this case to permit into evidence PCR testing.

The Supreme Court of Missouri in *State v. Davis*,[15] determined that evidence of DNA testing was admissible, although it noted that some jurisdictions had criticized the

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[11]Id. at 439.

[12]State v. Williams, 599 A.2d 960 (N.J. Super. 1991).

[13]Id. at 967.

[14]Id.

[15]State v. Davis, 814 S.W.2d 593 (Mo. 1991), cert. denied, 502 U.S. 1047 (1992).

testing and statistical procedure employed by some of the laboratories at the time. Despite the *Davis* court's recognition of the shortcomings of certain laboratory procedures, it was convinced that DNA testing met the standard required for admissibility and that any problems with the manner of testing went to the weight of the evidence and not its admissibility. Based on that rationale, the court concluded that "[i]t is within the trial court's sound discretion to admit or exclude an expert's testi mony . . . and no abuse of discretion has been demonstrated."[16]

The Ohio Court of Appeals determined that DNA evidence was admissible in *State v. Thomas*,[17] although it did so with virtually no meaningful discussion of the challenges raised to the evidence. In this rape case, the defendant challenged the evidence on the grounds that: (1) there was no evidence that the person who testified about the DNA match was an expert qualified to render an opinion, and (2) there was no evidence to establish that DNA testing was based on a reasonable degree of scientific certainty.

The court disagreed with both allegations and found that the scientific evidence complies with the state rules of evidence governing the admission of such evidence. Quoting *State v. Williams*,[18] the court stated:

> [W]e refuse to engage in scientific nosecounting for the purpose of deciding whether evidence based on newly ascertained or applied scientific principles is admissible. We believe the Rules of Evidence establish adequate preconditions for admissibility of expert testimony, and we leave to the discretion of this state's judiciary, on a case by case basis, to decide whether the questioned testimony is relevant and will assist the trier of fact to understand the evidence or to determine a fact in issue.[19]

Ohio, a state that abandoned the *Frye* test in favor of a relevancy test, uses the catch-phrase "scientific nosecounting" as a shorthand expression for what it perceives to be wrong with the *Frye* test. Other jurisdictions, including the

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[16]Id. at 603 (citations omitted).

[17]State v. Thomas, 579 N.E.2d 290 (Ohio App. 1991).

[18]State v. Williams, 446 N.E.2d 444 (Ohio 1983).

[19]579 N.E.2d at 448.

Third Circuit,[20] Colorado,[21] Maine,[22] and New Jersey,[23] have also referred to the *Frye* test as "nosecounting"—a concept that does not seem to be a fair interpretation of the *Frye* test.

In early 1992, the NRC issued its position on DNA testing, challenging some of the concepts that certain scientists claimed were settled principles. Despite the publication of that document, certain courts chose to ignore the dispute and continued admitting DNA evidence in a liberal fashion, generally claiming that the disputes went to the weight of the evidence, not to its admissibility.[24]

§ 11:47 Jurisdictions admitting DNA evidence—Cases in the early to mid-1990s

In a very brief decision, the Court of Criminal Appeals of Texas upheld the admission of DNA testing in which the expert testified that the odds of DNA belonging to someone other than the defendant were one in 18 billion.[1]

In a slightly more detailed opinion, that same court determined that: (1) Texas no longer used a *Frye* standard, and (2) the RFLP technique of DNA testing, along with the population frequency studies, was also valid and admissible.[2] In *Kelly*, the court concluded that the *Frye* general acceptance test was no longer the law in Texas, stating that there was no "textual basis in Rule 702 for a special admissibility

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[20]Deluca v. Merrell Dow Pharms., Inc., 911 F.2d 941, 955 (3d Cir. 1990), overruled on other grounds, Merrell Dow Pharms., Inc. v. Havner, 953 S.W.2d 706 (Tex. 1997), citing Daubert v. Merrell Dow Pharms., Inc., 509 U.S. 579 (1993).

[21]Lindsey v. People, 892 P.2d 281, 289 (Colo. 1988).

[22]State v. Williams, 388 A.2d 500 (Me. 1978).

[23]State v. Williams, 599 A.2d 960, 964 (N.J. Sup. Ct. 1991).

[24]Other decisions in the late 1980s and early 1990s also admitted DNA without much challenge: Smith v. Deppish, 807 P.2d 144 (Kan. 1991); State v. Ford, 392 S.E.2d 781 (S.C. 1990); Glover v. State, 787 S.W.2d 544 (Tex. App. 1990), aff'd, 825 S.W.2d 127 (Tex. App. 1992); and State v. Woodall, 385 S.E.2d 253 (W. Va. 1989).

[Section 11:47]

[1]Glover v. State, 825 S.W.2d 127 (Tex. App. 1992).

[2]Kelly v. State, 824 S.W.2d 568 (Tex. App. 1992).

standard for novel scientific evidence."[3] Second, "as should be fairly obvious, scientific evidence may be shown reliable even though not yet generally accepted in the relevant scientific community."[4]

The *Kelly* court also determined that the trial court did not abuse its discretion in admitting the DNA evidence. It stated:

> We conclude that it was demonstrated by clear and convincing evidence that the scientific principle underlying the RFLP technique was valid, that the RFLP technique itself was valid, that the technique was properly applied in this case, and that the related population frequency studies were also valid and reliable.[5]

The Supreme Court of Ohio, in *State v. Pierce*,[6] reaffirmed its earlier case law admitting DNA evidence. Repeatedly, the court remarked that the standard of admissibility was the relevancy test, not the *Frye* test and, therefore, a discussion of whether the science was generally accepted in the scientific community was irrelevant.

In the *Pierce* case, there were three victims who were alleged to have been raped by the defendant. At trial, the prosecutor introduced evidence that the defendant's DNA matched specimens from the crime scene. During that trial, the prosecution's experts claimed that the chances were "one in forty billion" that the DNA came from someone other than the defendant, over the defense's strong challenges to such evidence.

The defense in *Pierce* informed the court about the dispute recognized in the NRC Report over statistical models, to which the court acknowledged that "[a] number of scientists and other commentators have criticized the soundness of [the statistical assumptions supporting DNA comparisons]."

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[3]Id. at 572.

[4]Id. The court also suggested that the courts use the seven-factor Weinstein & Berger test to determine whether the evidence was "reliable." A complete discussion of this test is contained in Chapter 10.

[5]Id. at 574.

[6]State v. Pierce, 597 N.E.2d 107 (Ohio 1992). But see State v. Nemeth, 694 N.E.2d 1332 (Ohio 1998) (remarking that Pierce predates the amendment to Rule 702, which now explicitly requires "that information forming the basis of the expert testimony by 'reliable.' " Thus, the Pierce case can no longer be considered good law).

Nevertheless, the court was unswayed by the criticisms of the various scientists to whose work the report referred. "The jury was free to reject the DNA evidence if it is concluded that the trial court did not abuse its discretion in admitting the calculations as to the frequency probability, and it was for the jury to determine what weight, if any to give such evidence."[7]

The Supreme Court of Virginia completely avoided the issues raised in the 1992 NRC Report in the case of *Satcher v. Commonwealth*.[8] In that case, the defendant was accused of the attempted rape and robbery of one woman and the rape and the murder of another. Semen found at the scene of murder matched the DNA taken from the defendant.

The Virginia court skirted the problems outlined in the 1992 NRC Report by claiming that DNA testing had been found to be a reliable scientific technique in the earlier 1989 *Spencer* case[9] —despite the fact that in the earlier case no challenge had been made to the evidence and that in the interim the NRC Report had been issued.[10] Rather, the court stated: "We reiterate our adherence to the *Spencer* rule that DNA testing is a reliable scientific technique."[11] The court then found that the trial judge was correct in ruling that DNA evidence was appropriately given to the jury to consider.

The Michigan Supreme Court held in *People v. Adams*[12] that, "given the overall acceptance of the technique in other jurisdictions, we hold that trial courts may take judicial notice of the reliability of DNA identification testing."[13] Although the Michigan court did address the fact that the

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[7]Id. at 115.

[8]Satcher v. Commonwealth, 421 S.E.2d 821 (Va. 1992), cert. denied, 507 U.S. 733 (1993), rev'd in part on other grounds, Satcher v. Pruett, 126 F.3d 561 (4th Cir. 1997).

[9]Spencer v. Commonwealth, 385 S.E.2d 850 (Va. 1989), cert. denied, 110 493 U.S. 1093 (1990).

[10]An earlier reference in the *Satcher* case concerning how DNA profiles are made cites the NRC Report, thus indicating the court's awareness of the study.

[11]Id. at 834.

[12]People v. Adams, 489 N.W.2d 192 (Mich. App. 1992), judgment modified, 441 Mich. 916 (1993).

[13]Id. at 197.

defense raised the Hardy-Weinberg equilibrium problem, it found that those contentions were inconsistent with the testimony presented in the lower court.

Additionally, the court dismissed the contentions of the defense that the admission of DNA statistical evidence would lead to "trial by mathematics," as in the instant case, where an expert claimed that the chances of the DNA in question belonging to someone other than the defendant were one in 400 million. Noting that the statistical evidence introduced in DNA testing is independently proved, the court found that without statistics the evidence is speculative. Here, however, the jury is "free to disregard or discredit the evidence."[14]

In *Polk v. State*,[15] the Mississippi Court adopted a "three prong" approach similar to those suggested by a New York court[16] and an Alabama court.[17] The three prongs identified by the *Polk* case were:

1. Is there a theory, generally accepted in the scientific community, that supports the conclusion that DNA forensic testing can produce reliable results?
2. Are there current techniques that are capable of producing reliable results in DNA identification and that are generally accepted in the scientific community?
3. In this particular case, did the testing laboratory perform generally accepted scientific techniques without error in the performance or interpretation of the tests?

The court's answer to each of the questions was in the affirmative. First, the court determined that there was ample evidence that the DNA testing does produce reliable results and that the trial judge's decision in that regard was supported by ample evidence. Second, the court also found that the results of DNA testing were reliable and were generally accepted in the scientific community. Third, the court reviewed the techniques used by the laboratory in question and determined that they were acceptable. The defendant's

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[14]Id. at 198.

[15]Polk v. State, 612 So. 2d 381 (Miss. 1992).

[16]People v. Castro, 545 N.Y.S.2d 985 (Sup. Ct. 1989). But see People v. Mohit, 579 N.Y.S.2d 990 (N.Y. Ct. 1992).

[17]Ex parte Perry v. State, 586 So. 2d 242 (Ala. 1991).

challenge to such technique was that their own expert was unable to duplicate the measurements. The court, however, found that such a challenge was no more than an attack on the credibility of the evidence, not its competency as a matter of law.

Significantly, the court in this case issued guidelines to be followed when a case involved DNA evidence. Those guidelines, set forth as the appendix to the case, provide that the laboratory must follow strict quality control guidelines throughout the entire procedure. The court focused on the areas where the DNA testing could be contaminated and emphasized that the procedures must be documented. In the event you have a case in Mississippi, make sure to be familiar not only with the case, but with the guidelines as well.

In 1993, Oregon, North Carolina and Wyoming all jumped on the bandwagon admitting DNA evidence. Oregon, unlike most jurisdictions, has addressed both RFLP DNA evidence as well as PCR evidence. In *State v. Futch*,[18] the Oregon Court of Appeals, citing the *Daubert* case, found RFLP evidence admissible. *Futch* is a classic example of where a *Frye*-type analysis would preclude the admission of the evidence, a less stringent analysis would permit such admission.[19] In *Futch*, the defense experts claimed both that the match between the crime scene and the known sample was in error and that the database used by the laboratory was scientifically unacceptable. The court described the scientific debate in the following terms:

> The record is a classic example of a "battle of the experts," a phenomena not uncommon to all trials in which scientific evidence is admitted into evidence. There was expert testimony presented in both the state's and defendant's cases-in-chief, as well as on rebuttal and surrebuttal, on the validity of the testing process used in this case. Each point made was the subject of a counterpoint explaining why the point was not valid, which in turn was countered by more scientific opinion.[20]

These problems, nevertheless, were rather glossed over by

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[18]State v. Futch, 860 P.2d 264 (Or. App. 1993), aff'd, 924 P.2d 832 (Or. 1996).

[19]Oregon employs a multifactor test that has also been held to be "consistent with" the *Daubert* approach. See 860 P.2d at 268-70; State v. Brown, 687 P.2d 751 (Or. 1984).

[20]860 P. 2d at 271.

the courts, who permitted the evidence to come in and let the jury sort it out. The conclusion of the court after addressing the facts of the specific allegations was as follows:

> In the light of this record, we cannot say that the state's evidence, concerning the testing procedures used in this case, was so lacking that it had no weight whatsoever. Although reasonable factfinders might differ as to whether the tests performed were accurate, it would be improper for us to preempt the jury's determination of the issue on this record.[21]

The court likewise dismissed the contentions of the defense concerning the statistical analysis problems, stating "[e]ven if the defendant's experts are correct in their assessment of the statistical probability involved, that probability is sufficient to make the question of a 'match' a jury issue."[22]

In *State v. Lyons*,[23] the Court of Appeals of Oregon also determined that PCR evidence met the requirements for admissibility. *Lyons* involved a particularly gruesome rape and murder of a woman. According to the expert for the prosecution, the gene type taken from specimens at the crime scene (and which were not from the victim) were the same gene type as those of the defendant and were found in two to three percent of the Caucasian population.

After a detailed discussion of the PCR method of analysis as well as the seven-factor relevancy test for admissibility,[24] the court con cluded that the evidence should be admissible. It held that the PCR method was relevant and helpful to the jury. In addition, the probative evidence outweighed any possible prejudice. The court stated:

> [W]e find nothing about the PCR method that would undeniably cause jurors to misuse, misinterpret or overvalue the results. Unlike the RFLP method at issue in Futch the results of the PCR method are not expressed in terms of statistical probabilities capable of creating the aura of absolute identification. Instead, the results are expressed as a conclusion that the identified gene type common to the sample and the defendant is one found in a certain percentage of a population group. We conclude that the probative value of PCR

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[21]Id. at 272.

[22]Id. at 273.

[23]State v. Lyons, 863 P.2d 1303 (1993),aff'd, 324 Or. 256, 924 P.2d 802 (1996).

[24]Oregon's seven-factor relevancy test is addressed in Chapter 10.

> method DNA evidence is not outweighed by [unfair prejudice and other dangers] . . .[25]

The Court of Appeals of North Carolina held that the RFLP type of DNA testimony was admissible in the case of *State v. Futrell*.[26] In *Futrell*, the defendant introduced expert evidence that was critical of the FBI's statistical methodology, specifically challenging the size of the database that the FBI used. Additionally, the defense raised the Hardy-Weinberg Equilibrium problem.

The court dismissed these claims, citing to an early 1990 case, *State v. Pennington*,[27] where the Supreme Court of North Carolina had admitted DNA evidence, albeit stating that issues pertaining to relevancy or prejudice could still be raised. For example, if the defendant in another case was able to establish contamination or other problems, the issues could be introduced relevant to the issue of the weight of the evidence. In the event the defendant could establish that the evidence was so tainted as to be totally unreliable, then it could be excluded.

However, citing a later case than *Pennington*,[28] the court of appeals in *Futrell* found that any challenges that did not pertain to relevancy or prejudice were matters for the jury and not the court. Quoting *Bruno*, the court in *Futrell* stated:

> [W]here unfair prejudice is not clear and where there is merely conflicting evidence or where two experts have reached differing results based on independent analyses of the DNA, the issue becomes one of credibility of the experts. In that situation the jury is obligated to determine what weight each expert's testimony should receive.[29]

In the *Futrell* case, the court found that while the evidence was conflicting on the technical matters raised, it was for the jury to determine what weight to give the evidence and the allegation of "unfair prejudice"[30] was not established by the defendant.

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[25]863 P.2d at 1311.

[26]State v. Futrell, 436 S.E.2d 884 (N.C. App. 1993).

[27]State v. Pennington, 393 S.E.2d 847 (N.C. 1990).

[28]State v. Bruno, 424 S.E.2d 440 (N.C. App. 1993), appeal dismissed, 428 S.E.2d 185 (N.C. 1993).

[29]436 S.E.2d at 889.

[30]Establishing "unfair prejudice" would take the issue from the jury ac-

The Supreme Court of Wyoming upheld the admission of RFLP analysis in DNA testing in the very interesting case of *Springfield v. State*.[31] *Springfield* presents a unique circumstance which brings into focus the exact nature of the population substructure problem. In this case, the defendant was three-fourths Crow Native American and one-fourth Black. The DNA profile was compared to databases of Black, Caucasian, Hispanic and Native American profiles, and the probabilities of a match ranged from a low of one in 250,000 (Native American) to a high of one in 250 million (Caucasian). Curiously, however, the 200-person Native American database was composed of 100 Sioux plus Navajo, Cherokee, and Cheyenne tribes, but no Crow.

The defense aggressively challenged the findings of the prosecution concerning the statistical probabilities of a match. Specifically, the defense expert claimed that because the Native American tribes were each a subgroup of a subgroup of a racial classification, the possibility of error was substantial. The court described the testimony as follows:

> According to [the defense expert], Indian tribes are a "subgroup of a subgroup of a racial classification." In looking at the same allele segments used by the FBI in their analysis, Dr. Shields cited major differences that exist between Native American groups in Canada, which constituted a "monstrous allele frequency difference." In another example, [the expert] discussed . . . findings . . . concerning "statistically significant allele frequency differences" among two South American tribes living 300 miles apart and a tribe in Mexico. The underlying theory that supports the frequency differences is called endogamous breeding, or a tendency for individuals to mate "with individuals that they grew up with; in essence, individuals from the same geographic locale, the same ethnic group, the same religion, the same socioeconomic status." In sum, . . . "If you use the appropriate database, you may actually find lots of matches. If you used the wrong database, you may have none. . ."[32]

The court remarked that the defendant did not put in any evidence that the Crow tribe was endogamous and held that "any questions concerning the size of the database or the

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cording to the law in *Pennington*.

[31]Springfield v. State, 860 P.2d 435 (Wyo. 1993).

[32]Id. at 446.

Hardy-Weinberg equilibrium goes to the weight of the evidence and is properly left to the jury."[33] Rather, the court determined that the potential impact of substructure on the accuracy of the estimates is a matter of weight, not admissibility. The court in *Springfield* relied on an earlier case, *Rivera v. State*,[34] which had determined that the proper approach to the admission of DNA (and other scientific) testimony was an analysis of relevancy, rather than a *Frye*-type approach. "Relevancy is the 'linchpin of admissibility' and is preferable to the 'general acceptance' approach of *Frye* which is predicated on a 'nose counting'. . ."[35]

Rather, the approach of the Wyoming court is to throw the matter to the jury once the court is satisfied that there is a "requisite foundation" for the evidence. The Wyoming Supreme Court stated:

> We agree that the "focus of the court must be on 'the admissibility or non-admissibility of a particular type of scientific evidence,' not 'the truth or falsity of an alleged scientific "fact" or "truth."'
>
> In other words, the court need not make the initial determination that the expert testimony or the evidence proffered is true before submitting the information to the jury. The court must allow the jury to discharge its duties of weighing the evidence, making credibility determinations, and ultimately deciding the facts.[36]

Additionally, in this case, the court was satisfied that the introduction into evidence of the ceiling principle, recommended by the NRC Report, provided the most conservative—and acceptable—estimate for the courts.

One of the most recent state courts to admit DNA evidence is New Mexico, in *State v. Anderson*.[37] The Supreme Court of New Mexico reversed the Court of Appeals of New Mexico in this case, determining that under the newly adopted standard of admissibility, the DNA evidence should be admitted.

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[33]Id. at 447.

[34]Rivera v. State, 840 P.2d 933 (Wyo. 1992).

[35]860 P.2d at 442.

[36]Id. at 443.

[37]State v. Anderson, 881 P.2d 29 (N.M. 1994). State v. Duran, 881 P.2d 48 (N.M. 1994), was also decided that same day and is in accordance with the holding of *Anderson*.

Between the court of appeals decision in *Anderson* and the supreme court decision, the court changed the standard of admissibility of novel scientific evidence. In *State v. Alberico*,[38] New Mexico abandoned the *Frye* test and decided to admit novel scientific evidence pursuant to a three-part standard. "The first requirement is that the expert be qualified."[39] "The second consideration for the admissibility of scientific evidence in the form of expert testimony is whether it will assist the trier of fact."[40] The third requirement is that "an expert may testify only as to 'scientific, technical or other specialized knowledge'" with a reliable basis.[41]

To determine whether the evidence was "reliable," the *Alberico* court followed the four factors cited by the *Daubert v. Merrell Dow Pharmaceuticals*[42] decision.[43] Using these tests, the supreme court in *Anderson* cited a number of other jurisdictions with relevancy standards that admitted DNA evidence.[44] Additionally, the court followed the holding in *United States v. Bonds*[45] where the Sixth Circuit determined that the DNA evidence had met the *Daubert* standard for admissibility.

Unlike the *Bonds* court, however, the *Anderson* court did examine the NRC Report and found the report to be supportive of admitting DNA evidence. "We find the report persuasive and would like to see DNA typing in this state performed with the report's guidelines in mind, specifically

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[38]State v. Alberico, 861 P.2d 192 (N.M. 1993).

[39]Id. at 202.

[40]Id.

[41]Id.

[42]Daubert v. Merrell Dow Pharms., Inc., 509 U.S. 579 (1993).

[43]The four-part test suggested by *Daubert* is: (1) whether the theory or technique can and has been tested; (2) whether the theory or technique has been subjected to peer review and publication; (3) the known or potential rate of error in using a particular scientific technique and the existence and maintenance of standards controlling the technique's operation; and (4) whether the theory or technique has been generally accepted in the particular scientific field. 509 U.S. at 591-593.

[44]See cases collected at 881 P.2d 40.

[45]United States v. Bonds, 12 F.3d 540 (6th Cir. 1993). *Bonds* is discussed at length at § 11:36-11:39.

the 'ceiling principle' approach."[46] Further, the court determined that the "modified ceiling principle" could be used immediately in the courts.[47]

Thus, with that provision and with the determination that the effect of population substructure went to the weight of the evidence, not the admissibility, the court held:

> In conclusion, we hold that the trial court did not abuse its discretion in concluding that the DNA typing evidence and the accompanying statistical calculations in this case were admissible. Any controversy over the results of the testing and the statistical calculations goes to the weight of the evidence and is properly left to the trier of fact.[48]

In 1995, a number of states approved the admission of DNA evidence, finding that many of the previously voiced concerns were no longer relevant.[49] Significant to some courts was the 1994 article by Lander and Budowle, entitled *DNA Fingerprinting Dispute Laid to Rest,*[50] which stated: "Most of all, the public needs to understand the DNA fingerprinting controversy has been resolved. There is no scientific reason to doubt the accuracy of forensic DNA typing results, provided that the testing laboratory and the specific tests

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[46]881 P.2d at 47.

[47]In this case, after a hearing in which the prosecution's experts testified that the likelihood of a match was "1 in 30.5 million," the trial court indicated it would admit the DNA evidence. The defendant entered a conditional plea and the issue of DNA's admissibility was preserved for the appeal. On appeal, the court of appeals reversed the trial court's decision, finding that the *Frye* standard was not met. The *Alberico* decision did away with the *Frye* test and this decision followed, which upheld the modified ceiling principle's use in DNA cases. Thus, the anticipated result is that the defendant's guilty plea would still be viable, but the "1 in 30.5 million" number would be substantially reduced.

[48]881 P.2d at 47-48.

[49]See, e.g., Lindsey v. People, 892 P.2d 281 (Colo. 1995); Hayes v. State, 660 So. 2d 257 (Fla. 1995)(admissible upon retrial); State v. Haddock, 897 P.2d 152 (Kan. 1995)(holding both PCR and RFLP evidence admissible); People v. Lee, 537 N.W.2d 233 (Mich. App. 1995), appeal denied, 554 N.W.2d 12 (Mich. 1996) (PCR evidence admissible of prosecutor establishes generally accepted laboratory procedures were followed); State v. Streich, 658 A.2d 38 (Vt. 1995)(adopting *Daubert* and limiting admissibility to ceiling principle results); and Taylor v. State, 889 P.2d 319 (Okla Crim. App. 1995) (adopting *Daubert*and admitting DNA evidence without limitation of ceiling principle).

[50]Lander & Budowle, DNA Fingerprinting Dispute Laid to Rest, Nature, Oct 27, 1994, at 735.

are on par with currently practiced standards in the field."[51]

§ 11:48 Jurisdictions admitting DNA evidence—*United States v. Bonds*: a key decision admitting DNA

An early and influential case upholding the admission of DNA evidence was *United States v. Bonds*.[1] In *Bonds*, the Court of Appeals for the Sixth Circuit approved of the admission of the RFLP type DNA test results, specifically declining to remand the case to consider the effect, if any, of the NRC Report. The court stated:

> There is no dispute that the NRC Report exists, but there is considerable dispute over the significance of its contents. We acknowledge that several appellate courts have considered the NRC Report retroactively, asked the parties to brief the significance of the report, or remanded for consideration of it [citations omitted]. However, we do not agree with those courts that have considered the NRC Report retroactively or remanded for consideration of it, and we decline to take judicial notice of an article published a year after defendant's convictions were handed down.[2]

The court in *Bonds* went on to say that the "key is whether the testimony met the requirements of Federal Rule of Evidence 702 at the time of the district court's admissibility determination, not whether subsequent events provide evidence that contradicts or calls into question the district court's view at the time of its admissibility ruling."[3]

The *Bonds* court, although it did not consider the NRC

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[51]Id. at 738.

[Section 11:48]

[1]United States v. Bonds, 12 F.3d 540 (6th Cir. 1993), reh'g denied, 1994 U.S. App. LEXIS 3679, aff'g United States v. Yee, 134 F.R.D. 161 (N.D. Ohio 1991).

[2]Id. at 553.

[3]Id. Taken at face value, this statement is nothing short of remarkable. In essence, the court is proclaiming that it is irrelevant if the science was wrong at the time of conviction as the court of appeals' role is only to review whether the trial court erred—given what they knew at the time of trial. Taken to its extreme, that would mean that in a case in which scientific proof of innocence discovered post-conviction that wholly contradicted the trial evidence would be irrelevant to the reviewing court. While in the case at bar the result may not have been different, the precedent it created is on shakier grounds.

Report, provided a thorough review of the science as it was presented in the trial court and employed the four-part test of *Daubert v. Merrell Dow Pharmaceuticals, Inc.*[4] in its analysis.[5]

As recommended by the *Daubert* court, the Sixth Circuit in *Bonds* focused on whether the "principles and methodology" underlying the testimony are valid and not on "the reliability of the conclusions."[6] Using this analysis, the *Bonds* court concluded that the evidence met the "liberal Rule 702 test adopted by the Supreme Court."[7] The following is a summary of the opinion of the Sixth Circuit Court of Appeals.[8]

Using the "relevant-reliable" approach suggested by *Daubert*, the court went through each of the four *Daubert* prongs, and found the test satisfied.

§ 11:49 Jurisdictions admitting DNA evidence—*United States v. Bonds*: a key decision admitting DNA—Testing of theory or technique

First, the court held that the technique of DNA testing could be tested, stating that "the particular technique employed by the FBI lab, can in fact be tested by comparing the results generated from one set of samples with the results reached after repeating the matching and probability estimate process on control samples."[1]

The court found that the FBI's testing methods were subject to internal proficiency standards and were found to

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[4]Daubert v. Merrell Dow Pharms., Inc., 509 U.S. 579 (1993).

[5]The four-part test suggested by *Daubert* is: (1) whether the theory or technique can and has been tested; (2) whether the theory or technique has been subjected to peer review and publication; (3) the known or potential rate of error in using a particular scientific technique and the existence and maintenance of standards controlling the technique's operation; and (4) whether the theory or technique has been generally accepted in the particular scientific field. 509 U.S. at 591-593.

[6]12 F.3d at 556.

[7]Id. at 557.

[8]The *Bonds* decision is given more extensive analysis, due to the highly influential nature of the case and the fact that most—if not all—of the prominent DNA experts on both sides testified in the case.

[Section 11:49]

[1]Id. at 558.

be reliable and further that their theories, principles, methods, and techniques could be tested and have in fact been tested. The court did note that while the FBI's proficiency testing program had "serious deficiencies," such deficiencies did not affect the reliability of the testing procedures.

§ 11:50 Jurisdictions admitting DNA evidence—*United States v. Bonds*: a key decision admitting DNA—Peer review

Normally, results of a science in its developing stages will be published in a peer-review journal once enough scientists have decided that the results are worthy of publication. Thus, such publication is considered an important measure of whether a scientific theory or technique has attained a threshhold of reliability.

Although very few articles were actually "peer-reviewed journal" articles, the court found that there were enough articles published about the FBI's procedures to enable it to meet this prong of the analysis. The court also stated that "[i]n addition, the magistrate in this case anticipated Daubert by concluding that expert testimony from experts outside the proponents' lab and acceptance of the proponent's writings in professional journals—in essence peer evaluation or review—were factors to consider in determining general acceptance and thus admissibility."[1]

§ 11:51 Jurisdictions admitting DNA evidence—*United States v. Bonds*: a key decision admitting DNA—Rate of error

The court remarked that it was troubled by the "serious deficiencies" in the internal proficiency tests that were conducted to perform a rate of error analysis. Despite this concern, the court nonetheless concluded that "the error rate is only one in a list of nonexclusive factors . . . that bear on . . . admissibility."[1] Thus, the court seemed to be content to pass on this issue, despite the fact that this issue should be

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[Section 11:50]

[1]Id. at 560.

[Section 11:51]

[1]Id. at 560.

much more troubling to the court, since it may suggest that the test itself is flawed.

§ 11:52 Jurisdictions admitting DNA evidence—*United States v. Bonds*: a key decision admitting DNA—General acceptance

The final category of reliability, general acceptance, was changed by the *Daubert* decision to be one of the inquiries for the court, rather than the only inquiry.[1] In this rather lengthy discussion, the court stated:

> In examining "general acceptance" and in addressing the parties' arguments, we are confronted in this case with the question of what exactly must be generally accepted: whether only the theory of DNA profiling needs to be accepted or whether the FBI's methodology for conducting DNA testing need also to be generally accepted. . . We find that general acceptance encompasses both.[2]

What is surprising about this decision is that the court did not merely re-focus the factors to be considered by a court concerning novel scientific evidence, but in fact it changed its own interpretation of the phrase "general acceptance." The *Bonds* court remarked that pre- *Daubert* cases had interpreted "general acceptance" to mean that "a substantial portion of the pertinent scientific community accepts the theory, principles, and methodology underlying scientific testimony because they are grounded in valid scientific theory."[3]

The new interpretation of "general acceptance," however, does not require unanimity, or even consensus, within the scientific community. Rather, the test is one of exclusion, rather than inclusion. "Only when a theory or procedure does not have the acceptance of most of the pertinent scientific community, and in fact a substantial part of the scien-

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[Section 11:52]

[1]Likewise, the importance of the "general acceptance" test became reduced with the adoption of the *Daubert* standard. Now, it is merely one factor and need not be actually met to provide acceptance of the science. For further discussion of this subject see Scheck, DNA and Daubert, 15 Cardozo L Rev 1959 (1993).

[2]12 F.3d at 562.

[3]Id. at 561.

tific community disfavors the principle or procedure, will it not be generally accepted."[4]

The court's holding in *Bonds* on what constitutes "general acceptance" is at odds with prior case law in its circuit as well as with other cases around the country.[5] Nonetheless, the court used this standard in the instant case and held that "the defendants' experts did not in fact show that the procedures were not generally accepted; they only showed a substantial controversy over whether the results produced were reliable and accurate."[6] Since the focus—according to *Daubert*—was on "principles and methodology" and not on conclusions, however, the court had little trouble finding that the general acceptance was met.

The court then moved on to the substance of the defendant's contentions—namely, whether the statistical probability estimates were not generally accepted in the scientific community. The *Bonds* court held that the issue of the viability of population substructure was a dispute over the accuracy of the probability results that went to the weight of the evidence, not to the admissibility of such evidence. It stated:

> The evidence and testimony presented . . . demonstrate that the DNA evidence was not based on untested or unacceptable theories or procedures. Because the DNA results were based on scientifically valid principles and derived from scientifically valid procedures, it is not dispositive that there are scientists who vigorously argue that the probability estimates are not accurate or reliable because of the possibility of ethnic substructure. The potential of ethnic substructure does not mean that the theory and procedure used by the FBI are not

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[4]Id. at 562.

[5]Some courts require a "consensus," or the absence of public opposition by "scientists significant either in number or expertise," as a prerequisite for "general acceptance." See People v. Reilly, 196 Cal. App. 3d 1127, 1134-45 (1987); State v. Cauthron, 846 P.2d 502, 505 (Wash. 1993),abrogated on other grounds, State v. Copeland, 922 P.2d 1304 (Wash. 1995).

Scheck, DNA and Daubert, 13 Cardozo L Rev 1959, 1960, n.4 (1993). The *Cauthron* court went so far as to state that a "trial court's determination cannot be sustained, for example, on a mere finding that the record contains 'sufficient evidence' of the reliability of the challenged method." 846 P.2d at 506.

A more complete discussion of these tests is contained in Chapter 10, supra.

[6]12 F.3d at 562.

> generally accepted; it means only that there is a dispute over whether the results are as accurate as they might be and what, if any, weight the jury should give those results.[7]

The *Bonds* decision has been cited and followed by a number of courts since it was published. The wisdom of the decision has been questioned by those who believe that the court's rush to admit DNA evidence has adversely affected the quality of the court's analysis.[8]

§ 11:53 [Reserved]

§ 11:54 Jurisdictions disallowing or limiting DNA evidence

Although most jurisdictions have allowed—at least on a limited basis—forensic DNA results to be admitted at trial, some courts have expressly disallowed such testimony until such time as either the court is convinced that the science meets the *Frye* standard of acceptability or there is more uniformity in the opinions of those in the field.

The first court to really question DNA evidence before the existence of the NRC Report was Massachusetts. Other states subsequently followed, but primarily after the NRC Report.

§ 11:55 Jurisdictions disallowing or limiting DNA evidence—The early cases

One of the first cases to disallow DNA testing using the RFLP analysis was *State v. Schwartz*.[1] In *Schwartz*, the Supreme Court of Minnesota first rejected a move to change the *Frye* standard to a relevancy standard, stating that "without this safeguard [of general acceptance], we believe an undesired element of subjectivity is possible in evidentiary rulings under the relevancy approach. The *Frye* standard, on the other hand, facilitates more objective and

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[7]Id. at 564-65.

[8]See, e.g., State v. Moore, 885 P.2d 457 (Mont. 1994), overruled on other grounds, State v. Gollehon, 906 P.2d 697 (Mont. 1995).

[Section 11:55]

[1]State v. Schwartz, 447 N.W.2d 422 (Minn. 1989).

uniform rulings."[2]

In *Schwartz*, Minnesota determined, on the basis of the *Frye* hearing in which numerous experts testified, that although DNA typing was generally reliable, Cellmark's admissions of errors in a proficiency test cast grave doubts upon the reliability of the laboratory's testing procedures. Thus, the court held that:

> While we agree with the trial court that forensic DNA typing has gained general acceptance in the scientific community, we hold that admissibility of specific test results in a particular case hinges on the laboratory's compliance with appropriate standards and controls, and the availability of their testing data and results . . . Because the laboratory in this case did not comport with these guidelines, the test results lack foundational adequacy and, without more, are thus inadmissible.[3]

The *Schwartz* court made an additional limitation on the use of population frequency statistics, requiring that "a limitation on the use of [such evidence] is necessary because of the danger that such evidence will have a 'potentially exaggerated impact on the trier of fact.'"[4]

Minnesota has an interesting rule concerning the admissibility of statistical evidence, termed the "Carlson-Boyd-Kim" trilogy, which precludes experts from expressing an opinion in terms of statistical probabilities. The reason for this rule is that "[t]estimony expressing opinions or conclusions in terms of statistical probabilities can make the uncertain seem all but proven, and suggest, by quantification, satisfaction of the requirement that guilt be established 'beyond a reasonable doubt.'"[5]

In the case of *State v. Alt*,[6] the Minnesota Supreme Court followed the "Carlson-Boyd-Kim" trilogy and remanded the

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[2]Id. at 424.

[3]Id. at 428.

[4]Id. at 428, quoting State v. Joon Kyu Kim, 398 N.W.2d 544 (Minn. 1987). Subsequent to *Schwartz*, the Minnesota legislature enacted a statute allowing DNA evidence to be admitted, 1989 Minn Stat § 634. Additionally, the holding in State v. Alt, 504 N.W.2d 38 (Minn. App. 1993) appeared to adopt the "ceiling principle" recommended by the NRC Report and thus, affected the holding of *Schwartz*.

[5]State v. Bloom, 516 N.W.2d 159, 164 (Minn. 1994), citing Tribe, Trial by Mathematics, 84 Harv L Rev 1329.

[6]State v. Alt, 505 N.W.2d 72 (Minn. 1993).

lower court decision, finding that the only DNA frequency evidence to be admitted at trial is the population frequency evidence of the individual bands.

In the *Bloom* case, however, the Minnesota Supreme Court, in a lengthy and well-researched opinion detailing the objections to DNA evidence, held that DNA evidence could be admissible and additionally determined that the prior limitations on statistical evidence were not necessarily appropriate for DNA cases. The high court held:

> [F]irst, that the National Research Council's recent adoption of the conservative, "interim ceiling method" for computation of the probability that a randomly selected person would have the same DNA profile as that of a sample of bodily fluids found at a crime scene justifies the creation of a DNA exception to the rule against the admission of statistical probability evidence in criminal prosecutions to prove identity; second, that if the evidentiary foundation provided by the proponent of the evidence is sufficient, a properly qualified expert may express the opinion that, to a reasonable degree of scientific certainty, the defendant is (or is not) the source of the bodily evidence found at the crime scene.[7]

Thus, under the *Bloom* exception, the expert, if the foundation is sufficient, may "give an opinion as to random match probability using the NRC's approach to computing that statistic."[8]

The Supreme Judicial Court of Massachusetts, in *Commonwealth v. Curnin*,[9] also disallowed the admission of DNA evidence, where the court held that "evidence of DNA testing was inadmissible because the methods used by Cellmark to calculate the statistical probability of a random match were not generally accepted by the relevant scientific

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[7]516 N.W.2d at 160. Given the court's focus in this case on the numerous possible error as well as the difficulty of accurate statistical probability in DNA testing, the abrupt conclusion the court reaches is difficult to understand. Nevertheless, the case is replete with discussions of errors in DNA testing which makes it a helpful primer for those needing to know where DNA testing can fail.

[8]Id. at 167.

[9]Commonwealth v. Curnin, 565 N.E.2d 440 (Mass. 1991). *Curnin* was substantially overruled by Commonwealth v. Lanigan, 641 N.E.2d 1342 (Mass. 1994)(Lanigan II), where the court held that DNA evidence was reliable and should be admitted.

community."[10]

§ 11:56 Jurisdictions disallowing or limiting DNA evidence—Post-1992 NRC Report cases

Following the publication of the 1992 NRC Report, several courts were concerned enough about DNA testing to preclude or limit such evidence. One of the first courts to question the appropriateness of DNA evidence was the California Court in *People v. Barney*.[1] In *Barney*, the trial court conducted a "Kelly-Frye" hearing[2] and determined that "the statistical significance of a match between a defendant's DNA and the DNA in bodily material found at the crime scene . . . does not satisfy the Kelly-Frye test."[3] The *Barney* court took notice of the appellate court's decision in *People v. Axell*[4] holding that DNA testing and statistical interpretation met the *Kelly- Frye* standard. However, the court in *Barney* determined that the new debate ongoing in the scientific field concerning the value of statistical interpretation needed further review.

According to the Kelly-Frye standard, the admissibility of novel scientific evidence is predicated on the following:

> (1) the reliability of the method must be established, usually by expert testimony, and (2) the witness furnishing such testimony must be properly qualified as an expert to give an opinion on the subject. . . Additionally, the proponent of the

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[10]Id.

[Section 11:56]

[1]People v. Barney, 10 Cal. Rptr. 2d 731 (Cal. App. 1992). In 1998, the Supreme Court of California clarified much of the confusion that has surrounded DNA evidence and held that: (1) the RFLP method of DNA analysis was generally accepted; and (2) use of the modified ceiling statistical analysis method was also generally accepted. See People v. Venegas, 954 P.2d 525 (Cal. 1998).

[2]This refers to the California test combining the *Frye* test with the test enunciated in People v. Kelly, 130 Cal. Rptr. 144 (Cal. 1976). See People v. Leahy, 882 P.2d 321 (Cal. 1994). This test is discussed at length in Chapter 10.

[3]10 Cal. Rptr. 2d at 732.

[4]People v. Axell, 1 Cal. Rptr. 2d 411 (Cal. App. 1991). For the current view of California law concerning DNA, see People v. Venegas, 954 P.2d 525 (Cal. 1998); and People v. Soto, 981 P.2d 958 (Cal. 1999).

> evidence must demonstrate that correct scientific procedures were used in the particular case.[5]

"Reliability," according to the California courts, is synonymous with the concept of "general acceptance."

The court conducted a de novo review[6] of whether the science met the general acceptance test and found—as have other courts—that the theory and technique of DNA testing meets the general acceptance tests, but that the issue of statistical interpretation poses more difficult problems. The court thus focused its discussion on this latter problem, laying out the controversy in a lengthy discussion of each side's principles.

The court held that the statistical issues are not a question of weight, but of admissibility. Quoting *Axell*, the court here stated that "since a match between two DNA samples means little without data on probability, the calculation of statistical probability is an integral part of the process and the underlying method of arriving at that calculation must pass muster under *Kelly/Frye*."[7] The court further reasoned that the jury should not be made to weigh the competing positions on statistical calculation and, in one of the better reasoned approaches to statistical interpretation and the honest difficulty it would pose for jurors, concluded:

> We would be asking jurors to do what judges carefully avoid—decide the substantive merits of competing scientific opinions as to the reliability of a novel method of scientific proof. We cannot reasonably ask the average juror to decide such arcane questions as whether genetic substructuring and linkage

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[5]10 Cal. Rptr. at 737 (citations omitted). Whether the proper scientific procedures were used in the particular case is referred to as the "third prong" of the *Frye* analysis and, while not a part of all *Frye* jurisdictions, is a part of California's jurisprudence. As the *Barney* court stated later in its opinion, "the third prong of *Kelly-Frye* is alive and well, and is not merely a question of weight but is an element of the *Kelly-Frye* admissibility determination" Id. at 746. Accord, People v. Venegas, 954 P.2d 525 (Cal. 1998). For a differing opinion, see State v. Mohit, 579 N.Y.S.2d 990 (1992), holding that this third prong goes to the weight, not the admissibility of such evidence.

[6]Like other courts using a *Frye* standard, the appellate courts conduct a de novo review of the evidence and do not employ the abuse of discretion standard generally used by courts with a relevance or "helpfulness" test. See Chapter 10, supra, for for discussion of de novo review.

[7]Id. at 742.

> disequilibrium preclude use of the Hardy-Weinberg equation and the product rule, when we ourselves have struggled to grasp these concepts. The results would be predictable. The jury would simple skip to the bottom line—the only aspect of the process that is understood—and look at the ultimate expression of match probability, without competently assessing the reliability of the process by which the laboratory got to the bottom line. This is an instance in which the scientific proof is so impenetrable that it would " . . . assume a posture of mystic infallibility in the eyes of the jury. . . "[8]

Thus, holding that the matter is one of admissibility and not weight, the court analyzed the controversy and concluded that "the debate that erupted in *Science* in December 1991[9] changed the scientific landscape considerably, and demonstrates indisputably that there is no general acceptance of the current process."[10]

Further, the court in *Barney* held that unless the proper scientific procedure was established in each case, the evidence would be inadmissible under *Kelly-Frye*, although the nature of the hearing would be limited.[11] The court in *Barney* (and in the companion action) declined to reverse the conviction, however, finding the error to be harmless.

The *Barney* rationale was upheld in a case that was decided shortly thereafter, *People v. Wallace*,[12] where the court held it was an error to admit testimony concerning DNA evidence, although the court again deemed that the admission of such evidence was harmless. In the *Wallace* case, the Attorney General urged the court to reconsider *Barney*, claiming that there are more supporters of DNA testing and that those supporters are correct. The *Wallace* court correctly noted that such an argument misconstrues

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[8]Id. at 742, citing People v. Kelly, 130 Cal. Rptr. 144 (Cal. 1976), and United States v. Addison, 498 F.2d 741, 744 (D.C. Cir. 1974).

[9]This reference is to the Lewontin-Hartl and the Chakraborty-Kidd articles, discussed earlier in the chapter.

[10]Id. at 744.

[11]See also State v. Jobe, 486 N.W.2d 407 (Minn. 1992), where the Minnesota court reached a similar holding, requiring only a limited *Frye* hearing to ensure that the laboratory in question did the testing in compliance with appropriate standards and controls, but there was no need to rechallenge the based RFLP testing procedures as a whole, since they had reached a general acceptance level.

[12]People v. Wallace, 17 Cal. Rptr. 2d 721 (Cal. App. 1993).

the issue: "[T]he point is not whether there are more supporters than detractors, or whether . . . the supporters are right and the detractors are wrong. The point is that there is disagreement between the two groups, each significant in both number and expertise. . . "[13]

In *People v. Venegas*[14] the court of appeals agreed that genetic profiling evidence and statistical probability evidence are generally admissible, but found that the FBI failed to perform analysis in accordance with accepted methodology. As evidenced by these cases, the debate seems to have turned full circle as scientific questions are resolved and techniques are refined.

In 1992, the Supreme Judicial Court of Massachusetts issued an opinion in *Commonwealth v. Lanigan*[15] which determined that the current debate concerning population substructure—as evidenced by the NRC Report—indicated that the evidence did not meet the *Frye* standard of admissibility. The court held:

> "[N]either infallibility nor unanimous acceptance of the principle need be proved to justify its admission in evidence." However, the lively, and still very current, dispute described above regarding the role of population substructure constitutes something much more than a lack of unanimity. We cannot say that the processes by which Cellmark and the FBI estimated the frequency of the defendants' DNA profiles has found "general acceptance" in the field of population genetics. Accordingly, evidence of the estimated frequencies of the defendants' DNA profiles is not admissible. Because the frequency estimates are inadmissible, evidence of a match between profiles is also inadmissible.[16]

Although the court did note that they would be inclined to follow the "ceiling principle" if it had been introduced in the case at bar, it opined: "The national call for considered, conservative approaches to DNA testing, such as the use of ceiling frequencies, and the absence of such an approach in the

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[13]Id. at 725-26, quoting *Barney*.

[14]People v. Venegas, 954 P.2d 525 (Cal. 1998),.

[15]Commonwealth v. Lanigan, 596 N.E.2d 311 (Mass. 1992).

[16]Id. at 162, quoting Commonwealth v. Lykus, 367 Mass. 191, 198 (1975).

present cases, underscore the wisdom of the motion judge in excluding the test evidence."[17]

This decision was reaffirmed the following year by the Supreme Judicial Court in *Commonwealth v. Daggett,*[18] although any error in admission was determined to be harmless. As stated earlier in the *Curnin* case, without statistical certainty, DNA evidence was meaningless. Thus, noting that Massachusetts still adhered to the *Frye* test for admissibility, the court pointed out that the failure of the DNA testing at hand was still in the significance of the statistical frequency and should be inadmissible. As the court stated, "[t]he point is not that this court should require a numerical frequency, but that the scientific community clearly does. If the relevant scientific community generally accepted some nonnumerical expression of statistical frequency, then this court would likely accept it as well."

Massachusetts subsequently followed the national trend of admitting DNA evidence when it held, in *Commonwealth v. Lanigan*,[19] that the reliability of the process had been established and the evidence of the probability of a DNA match had been properly admitted.

Perhaps the most scientifically detailed opinion to date to disallow DNA testing evidence is *State v. Bible*.[20] The *Bible* case, like other cases disallowing DNA evidence, used a de novo standard of review under *Frye* to determine whether the expert testimony is generally accepted in the scientific community.[21]

The *Bible* decision is an important review of the law concerning the appropriate standard for cases involving novel scientific evidence, aptly remarking that " *Frye* helps us determine whether new scientific principles are ready for

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[17]Id. at 163-64.

[18]Commonwealth v. Daggett, 622 N.E.2d 272 (Mass. 1993)(plurality opinion).

[19]Commonwealth v. Lanigan, 641 N.E.2d 1342 (Mass. 1994)(Lanigan II).

[20]State v. Bible, 858 P.2d 1152 (Ariz. 1993), cert. denied, 511 U.S. 1046 (1994). For an in-depth analysis of the *Bible* case, see Note, State v. Bible: The Admissibility of Forensic DNA Profiling and Statistical Probability Evidence in Arizona Criminal Proceedings, 26 Ariz St LJ 593 (1994).

[21]858 P.2d at 1181, citing to *Barney*, *Vandebogart*, and *Cauthron*, all discussed at length in this section.

the courtroom and, conversely, whether the courtroom is ready for new scientific principles."[22]

In *Bible*, the court declined to adopt a different standard than *Frye*, although noting that it believed the evidence would be inadmissible—in its opinion—even under the *Daubert* standard.[23] The court's opinion on the scientific evidence and the role of the *Frye* standard is worth repeating:

> It is impossible for our system of justice to ignore scientific and technological advances. Nevertheless, scientific evidence is "a source of particular judicial caution." [citation omitted]. "Because, 'science' is often accepted in our society as synonymous with truth, there is a substantial risk of overweighing by the jury." Morris K. Udall, et al., Arizona Practice—Law of Evidence sec. 102, at 212 (3d ed. 1991). Similarly, because neither judge nor jury may be able to separate "junk science" from good science, *Frye* helps guarantee "that reliability will be assessed by those in the best position to do so: members of the relevant scientific field who can dispassionately study and test the new theory." [citation omitted]. *Frye* helps protect courts from unproven, and potentially erroneous and misleading, scientific theory "until a pool of experts is available to evaluate it in court." 1 John W. Strong, et al., McCormick on Evidence sec. 203, at 873 (4th ed. 1992).[24]

With the above caveats in mind, the court went on to analyze the evidence to determine whether DNA testing evidence met the *Frye* standard for general admissibility

The *Bible* court, like other courts, found that there was no significant scientific controversy over Cellmark's analysis of DNA fragments and its method for declaring a match. But, like numerous other courts, the calculation of a the probability of a random match troubled the court.

The court focused on three concerns: whether the database from which the statistical calculations were to be made was a truly random sampling; whether the DNA segments tested were actually in linkage equilibrium; and whether the

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[22]Id. at 1181.

[23]The court did indicate that it might be amenable to changing its standard to a different one, but that DNA proved a particularly bad subject on which to create such a change.

[24]Id. at 1181.

population engages in truly random mating, such that the Hardy-Weinberg equilibrium is established.[25]

A point troubling to this court—and generally not mentioned by other courts—was that not only did a larger percentage of scientist disapprove than approve of the forensic use of DNA testing, but that "the ratio of critics to supporters is higher among scientists whose work is better known in the field of population genetics."[26]

Thus, based upon the "bitter dispute" ongoing among scientists concerning the statistical probability of calculations used by Cellmark and the fact that several other courts[27] also found a lack of general acceptance on that point, the Arizona Supreme Court held that the "Cellmark method of deriving the random match probability figures is not generally accepted in the relevant scientific community."[28] The court determined the probability calculations were flawed in three ways: "(1) they are impermissibly based on the dis puted assumptions of linkage equilibrium; (2) the database relied on is of disputed statistical validity; and (3) the database relied upon is not in Hardy-Weinberg equilibrium."[29]

The court determined error had been committed in the case by the admission of such evidence, although noting that it was difficult to term the judge's ruling erroneous, in light of the fact that most of the dispute over DNA occurred after the trial court's ruling. The conviction, however, was not dismissed, since the court found that the quantum of evidence against the defendant was overwhelming and thus any error was harmless.

As a final note, the court acknowledged that while some courts found that without statistical interpretation of the meaning of a match between two DNA profiles, DNA testimony is meaningless, other courts "uncoupled" the statistical evidence from the match evidence. Thus, testimony could conceivably be admissible to establish—without statistical evidence—that the sample found at the crime

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[25]Id. at 1185-86.

[26]Id. at 1188, citing inter alia Thompson & Ford, DNA Testing: Debate Update, 28 Trial 52, 58 (Apr. 1992).

[27]Those other decisions are reviewed in this section.

[28]Id. at 1188.

[29]Id.

scene *could* have come from the defendant (or victim, if that was the case). The court, however, did not express any opinion on whether such evidence would be admissible in another case.

Curiously, unlike most other cases that were published after the NRC Report, the *Bible* decision makes no mention of the viability of the ceiling principle or its application to the case in question.[30]

In *State v. Cauthron*,[31] the defendant was accused and convicted on seven counts of first-degree rape, relating to a series of rapes that had occurred—with an identifiable *modus operandi* —over a two year period. Five of the semen samples of the seven cases in which semen was recovered were matched to the defendant's DNA sample. Additionally, there was a rare enzyme found in the defendant's blood that was also found in the semen and was present in less than one percent of the population.

The Supreme Court of Washington accepted the case on certification from the lower court and conducted a review of the case according to the *Frye* standard. The *Cauthron* court did not confine itself to reviewing just the lower court's decision for error, but rather reviewed the "record, available literature of law reviews and other journals, and the cases of other jurisdictions."[32] In *Cauthron*, as in many other significant DNA cases, the trial court had heard several days of hearings, with thousands of pages of transcripts as well as extensive briefs.

The Supreme Court of Washington followed the lead of Massachusetts in deciding to disallow evidence of the RFLP type of DNA testing. The NRC Report came out after the court heard oral argument, but before the court issued its

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[30]The court's citation to the *Vandebogart*, *Cauthron*, and *Barney* cases would suggest that it was aware of the ceiling principle. In 1996, the Washington Supreme Court, in State v. Copeland, 922 P.2d 1304 (Wash. 1996), held that DNA evidence was admissible and there was no need to use the ceiling principle. So too, the Arizona Supreme Court upheld the admission of DNA evidence without the use of any ceiling principles. See State v. Boles, 933 P.2d 1197 (Ariz. 1997).

[31]State v. Cauthron, 846 P.2d 502, 505 (Wash. 1993), abrogated on other grounds, State v. Copeland, 922 P.2d 1304 (Wash. 1995).

[32]Id. at 506. Significantly, the Supreme Court of Washington also undertakes a *Frye* determination de novo, and not under an abuse of discretion standard. Id. at 507, n.4.

opinion. Accordingly, the court requested additional briefing on the applicability of the Report.[33]

The court in *Cauthron* conducted a complete analysis of the *Frye* standard of admissibility, noting that Washington was disinclined to accept a newer, more liberal test and stating that "the court is less inclined to admit evidence which is still disputed in the scientific community [citations omitted]. Thus, in making the initial determination to allow novel scientific evidence, we do not examine its reliability, but instead focus on whether it is generally accepted in the scientific community."[34]

The court noted that the DNA commentary had identified a variety of potential problems with RFLP tests performed on forensic samples: contamination of the sample; degradation of the sample due to the passage of time; partial digestion of the fragments by the restriction enzyme; cuts by the enzyme in too many places; cross-contamination and human error in the laboratory.[35]

These potential problems with DNA testing did not trouble the court in their *Frye* analysis. Rather, these were the types of problems that the court should properly let the two sides introduce expert testimony about before the jury and ask the fact-finder to resolve the dispute. These issues were not whether the *science* of DNA and the *method* of testing were generally accepted, but rather whether there were errors that occurred in this testing procedure of which the jury should be apprised. Specifically challenged were the processes used by the Cellmark laboratory and whether the autorads were inconclusive.

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[33]This court, as well as the Supreme Court of New Mexico in State v. Anderson, 881 P.2d 29 (N.M. 1994), unlike the Sixth Circuit in United States v. Bonds, 12 F.3d 540 (6th Cir. 1993), was more willing to consider the importance and impact of the NRC Report on the viability of the defendant's conviction.

[34]846 P.2d at 505 n.2. Like the Supreme Court of New Hampshire in *State v. Vandebogart*, the Washington court focused its *Frye* analysis only on (1) whether the theory of the DNA forensic testing is generally accepted and can produce reliable results, and (2) whether the technique of forensic DNA testing is generally accepted in the scientific community.

[35]846 P.2d at 511, citing Thompson & Ford, DNA Typing: Acceptance and Weight of the New Genetic Identification Tests, 75 Va L Rev 45, 93-95; and Hoeffel, Note, The Dark Side of DNA Profiling: Unreliable Scientific Evidence Meets the Criminal Defendant, 42 Stan L Rev 465, 493 (1989-90).

What the court did become troubled over, nonetheless, was the statistical evidence that the prosecution wished to introduce into its case. The defendant challenged the evidence on two fronts: first, whether testimony that the DNA taken from the crime scene matched the DNA taken from the defendant; and second, whether the statistical evidence presented at the hearing was invalid.[36]

The court discussed each of these challenges thoroughly. Correctly, it noted that the probes used in RFLP must actually detect sites that are polymorphic (variable in individuals) and not monomorphic (the same in all individuals), or else the concept of "match" means nothing. For example, if the probes were detecting the genes for legs, eyes, arms, and mouth, all DNA tests would match, as if they came from the same person.

Additionally, once the polymorphic aspect of the DNA is established, then the proponent of the evidence must establish that the alleles tested are each independent. That is, that there is no relationship among the various alleles (such as hair color and eye color, which are not independent genes). This issue, referred to as the "linkage equilibrium" problem, proved to the court to be a difficult issue.[37] "It has not been sufficiently established that the various probes used detect independent alleles. Various scientists have raised concerns that the databases used do not adequately address the problem of population substructures."[38]

The other problem found by the court was the "Hardy-Weinberg equilibrium" assumption—that statistical calculations are based on a truly random population which mates randomly and mixes the gene pool evenly.[39] The court noted that "[o]ur decision rests on the existence of a controversy, not on its resolution."[40] In so noting, the court quoted from NRC Report:

> Substantial controversy has arisen concerning the methods for estimating the population frequencies of specific DNA typing patterns. Questions have been raised about the adequacy of

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[36]846 P.2d at 512.

[37]This problem is discussed at length at § 11:27.

[38]846 P.2d at 513.

[39]This concept is discussed at length at § 11:28, supra.

[40]Id. at 514.

> the population databases on which frequency estimates are based and about the role of racial and ethnic origin in frequency estimation.[41]

In addressing these concerns, the *Cauthron* court quoted from various scientific publications which confirmed the existence of such problems,[42] and cited a variety of legal publications also reflecting such concerns.[43]

In the case at issue, the expert had not used any probability statistics. Rather, the prosecution experts testified that the defendant's DNA "matched" the semen samples taken from the victims and that the DNA could not have come from anyone else on earth.

The *Cauthron* court disapproved of such testimony, stating that to permit the expert to testify about a match without explaining what that means is a meaningless exercise. This is also the view taken by the Massachusetts court in the *Curnin*[44] case, the Alabama Court in *Perry v. State*,[45] the California court in *People v. Barney*,[46] the Oklahoma court in *Taylor v. State*,[47] and the NRC Report. "Testi mony of a match in DNA samples, without the statistical background or probability estimates, is neither based on a generally accepted scientific theory nor helpful to the trier of fact."[48]

The court then held that it was dissatisfied by the Cellmark handling of the evidence, especially with regard to

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[41]Id. at 514, quoting from the NRC Report at 74-75.

[42]See, e.g., Eric S. Lander, Population Genetic Considerations in the Forensic Use of DNA Typing, 32 Banbury Report: DNA Technology and Forensic Science 143 (Jack Ballantyne et al, eds 1989); Lewontin & Hartl, Population Genetics in Forensic DNA Typing, 254 Science 1745 (1991). Lander has since changed his position, see Lander & Budowle, DNA Fingerprinting Dispute Laid to Rest, Nature, Oct 27, 1994, at 735, discussed supra at § 11:34.

[43]The articles cited were: Lempert, Some Caveats Concerning DNA as Criminal Identification Evidence: With Thanks to the Revered Bayes, 13 Cardozo L Rev 303 (1992); Saks & Koehler, What DNA "Fingerprinting" Can Teach the Law About the Rest of Forensic Science, 13 Cardozo L Rev 361 (1991).

[44]Commonwealth v. Curnin, 565 N.E.2d 440 (Mass. 1991).

[45]Perry v. State, 586 So. 2d 242 (Ala. 1991).

[46]People v. Barney, 10 Cal. Rptr. 2d 731, 745 (Cal. App. 1992). But see People v. Venegas, 954 P.2d 525 (Cal. 1998)

[47]Taylor v. State, 889 P.2d 319, 337 (Okla. Crim. App. 1995).

[48]846 P.2d at 516.

the statistical database. Citing the recommendations that had been made by the NRC Report with regard to collecting databases, and for estimating population frequencies, the court reversed the defendant's conviction. On remand, the court instructed the trial court to "take additional expert testimony to determine if the empirical evidence utilized by Cellmark is valid under the criteria set for by the Committee[49] prior to allowing an expert to testify about the results."[50]

Thus, the court's holding is that "RFLP testing is admissible. However, we conclude that it was error to admit the testimony of a 'match' since it was not accompanied by valid probability statistics."[51]

The State of Connecticut reversed a conviction based in part on DNA evidence in the recent case of *State v. Sivri*.[52] The court there, recognizing the effect of the NRC Report, remarked that the Report had "significantly changed the scientific landscape."[53]

In *Sivri*, the defendant was arrested for the murder of a masseuse/prostitute, whose body was never recovered, although there were large blood stains at the defendant's home and a substantial amount of evidence pointing to fatal foul play by the defendant.[54]

Since the body was never recovered, the blood stains in question were compared to the blood of the victim's parents to arrive at a probability that the blood in question was someone's other than the victim.[55]

According the evidence put on by the prosecution, the Caucasian database used by Cellmark had samples from 300 people, taken from a Red Cross blood band in Delaware. For each of the three alleles tested, the database was consulted

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[49]This refers to the NRC Report recommendations.

[50]846 P.2d at 517.

[51]Id. at 518.

[52]State v. Sivri, 646 A.2d 169 (Conn. 1994).

[53]Id. at 191.

[54]This case, however, is extremely troubling from a legal and factual perspective. The dissents of the Chief Justice and another Justice bear reading and highlight the difficulty in discerning between circumstantial evidence and speculation.

[55]Calculating this type of probability is obviously different from calculating the probability of a match of a known DNA sample, as is typical in most cases.

to determine the probability that a match would have occurred coincidentally. Thus, six separate probabilities were created—three representing the match with the mother's DNA, three representing the match with the father's.

Next, the expert testified that using the product rule,[56] the probabilities are multiplied together for each parent. Thus, the resulting probability concerning the mother was that one in 1400 unrelated persons would have the same alleles and one in 26,000 for the father.

On defense, Dr. Laurence Mueller of the University of California at Irvine[57] testified about the problems with linkage equilibrium as well as the problems with the Cellmark database.[58]

In *Sivri*, the Supreme Court of Connecticut discussed the problems of DNA that had been raised by the defense and subsequent to conviction, recognized by the NRC Report.[59] The Connecticut court also cited to the decisions of other courts, including Massachusetts,[60] Arizona,[61] New Hampshire,[62] Washington,[63] the District of Columbia,[64] and California.[65]

Citing to the NRC Report, as well as other decisions from other jurisdictions, the court addressed three issues. First, the *Sivri* court remarked that the Report had fully endorsed

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[56]The product rule is explained at length § 11:24, supra.

[57]Dr. Mueller testified repeatedly throughout the country on the issue of problems with linkage equilibrium and Hardy-Weinberg equilibrium.

[58]Dr. Mueller conceded, however, that the issue of the Hardy-Weinberg equilibrium would be irrelevant in this case. 646 A.2d at 191, n35.

[59]As with other cases, such as *Bonds* and *Anderson* discussed supra, the NRC Report was issued after the trial court took evidence. Connecticut, like many other courts, took notice of the NRC Report in their decision. To date, the only court to disregard the NRC Report intentionally is the *Bonds* decision in the Sixth Circuit.

[60]Commonwealth v. Lanigan, 596 N.E.2d 311 (Mass. 1992).

[61]State v. Bible, 856 P.2d 1152 (Ariz. 1993), cert. denied, 511 U.S. 1046 (1994).

[62]State v. Vandebogart, 616 A.2d 483 (N.H. 1992).

[63]State v. Cauthron, 846 P.2d 502, 505 (Wash. 1993), abrogated on other grounds, State v. Copeland, 922 P.2d 1304 (Wash. 1995).

[64]United States v. Porter, 618 A.2d 629 (D.C. 1992).

[65]People v. Barney, 10 Cal. Rptr. 2d 731 (Cal. App. 1992); People v. Wallace, 17 Cal. Rptr. 2d 721 (Cal. App. 1993).

the DNA typing technology and indicated that the scientists were uniformly in accord about the procedures.

Second, the NRC Report acknowledged that there was a "substantial controversy" concerning the methods for estimating the population frequency and that there were questions about the role of racial and ethnic origin in frequency estimation. Third, the *Sivri* court stated that the Report "recommended that courts admit into evidence population frequency calculations, but it set out various recommended criteria for the admission of this evidence, including the reliance on conservative population frequency estimates, and the use of a ceiling principle, which is a method of estimating probabilities that attempts to account for population substructures."[66]

These problems had led some courts, including Massachusetts, California and Arizona to hold that the population frequency evidence did not meet the *Frye* standard and was therefore inadmissible. Other courts, such as Washington, the District of Columbia and New Hampshire, took a less rigid view, remanding the case to permit the trial court to determine whether the ceiling principles suggested do, in fact, meet the *Frye* standard of admissibility.

Thus, the Connecticut court remanded the case to the trial court for further consideration and held that

> if this issue [population substructure and the ceiling principle] again becomes relevant, the trial court should consider the conclusions and recommendations of the Committee report and any other relevant evidence, including expert testimony, and determine whether the probability calculations sought to be introduced conform to the criteria set out in the Committee report, or if not, whether the evidence nevertheless passes appropriate scientific evidence standards under the circumstances of this case.[67]

As mentioned in the analysis of the *Sivri* case, there are other jurisdictions that have remanded the case to the trial court for consideration.

One of those cases was *State v. Vandebogart*,[68] in which the Supreme Court of New Hampshire elected to keep a two-prong *Frye* test. The court noted that although many had

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[66]646 A.2d at 192.

[67]Id.

[68]State v. Vandebogart, 616 A.2d 483 (N.H. 1992).

criticized *Frye*, there were legitimate reasons to adhere to such a test. First, it "permits disputes concerning scientific validity to be resolved by the relevant scientific community," second, it "ensures that a minimal reserve of experts exist who can critically examine the validity of a scientific determination in a particular case," and third it "spares courts from the time-consuming and difficult task of repeatedly assessing the validity of innovative scientific techniques" and fourth, it "promotes a degree of uniformity of decision."[69]

Like the Supreme Court of Washington in *Cauthron*, discussed above, New Hampshire likewise conducted a review de novo of the novel scientific evidence in the case. "Whether a scientific theory and the technique used to implement it are generally accepted does not vary according to the circumstances of each case, and thus the determination of general acceptance is not a matter to be left to each trial judge's individual discretion."[70]

The court in New Hampshire, like all other jurisdictions, found that the DNA profiling theory and procedures for declaring a match were generally accepted as reliable. Citing the NRC Report, however, the court determined that there was no general acceptance of the population frequency calculation. It stated that the "most important question underlying the validity of using the product rule is whether significant population substructure exists."[71]

The court determined that, given the conflicting expert testimony at the *Frye* hearing as well as the NRC's recognition of the debate, the evidence concerning population frequency did not meet the general acceptance standard: "We conclude that the FBI's method for estimating population frequencies, which relies on the product rule, has not found general acceptance in the field of population genetics."[72]

Because the New Hampshire court considered a match without statistical evidence "meaningless," it found that evidence of a match would not be admissible unless accompanied by a population frequency estimate that has been produced from a generally accepted method.

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[69]Id. at 489, citing a variety of state and federal opinions.

[70]616 A.2d at 491, citing Reed v. State, 391 A.2d 364 (Md. 1978).

[71]616 A.2d at 493.

[72]Id.

The *Vandebogart* court did discuss the recognition of the ceiling principle in DNA testing and, on remand, suggested that the State may be able to demonstrate that there is general acceptance of that principle which would permit the admission of DNA testimony.

There are other cases that have disallowed DNA testing, although they have not received as much attention as have those discussed above. One is the Nebraska Supreme Court case of *State v. Houser*.[73] In that case, the court found that the State did not produce evidence establishing that Lifecodes Laboratory had appropriate written protocol or that the proper protocol had been followed in the instant case. Additionally, the court found that there was insufficient evidence in the trial court to establish the accuracy of the probability testimony in question.

Finally, the trial court's failure to weigh the probability value against any prejudicial effect further contributed to error. The defendant's conviction was reversed and the case was remanded.

§ 11:57 Jurisdictions disallowing or limiting DNA evidence—Post-1996 NRC II Report cases: toward uniform admissibility of DNA evidence

The science of DNA fingerprinting changes rapidly. As the science has changed, so have the courts' decisions on whether to admit expert testimony. Following the 1992 NRC Report, a number of courts embraced the ceiling principle and modified ceiling principle recommended by the Report. Since that time, however, scientists appear to have reached agreement that the product rule provides a more accurate analysis and that there is no need to use the ceiling principle.

Following the publication of the 1992 Report, the National Research Council formed a new committee to update and clarify principles concerning population genetics and statistics as used with DNA evidence. According to the 1996 Report, it is not necessary to apply the ceiling principle or modified ceiling principle: "The abundance of data in different ethnic groups within the major races and the genetically and statistically sound methods recommended in this report

[73]State v. Houser, 490 N.W.2d 168 (Neb. 1992).

imply that the ceiling prinicple and the interim ceiling principle are unnecessary."[1]

This change in position has been recognized by a number of Courts across the country and will likely become even more widespread barring another change in the science.[2]

In *State v. Copeland,*[3] the Supreme Court of Washington, sitting en banc, revisited the issue of the admissibility of DNA evidence. This time, unlike its holding in *State v. Cauthron*,[4] the Washington Supreme Court did not require the proponent of DNA evidence to use the modified ceiling principle. In its lengthy and well-reasoned opinion, the court held that there was no reason to continue to require use of the modified ceiling principle. The court stated:

> Although at one time a significant dispute existed among qualified scientists [concerning the product rule], from the present vantage point we are able to say that the significant dispute was short-lived. *Cauthron* was decided while the dispute raged; since that time additional empirical studies have been conducted, the FBI has collected data from around the world, and one of the most vociferous opponents of use of the product rule has joined with an FBI scientist in declaring that the DNA wars are over.[5]

Since scientists are in general agreement about the acceptibility of the product rule in the use of DNA evidence, it is likely that the vast majority of courts will soon follow the lead of the scientists.

In March, 1998, the Supreme Court of Arizona, sitting *en*

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[1]National Research Council, Committee on DNA Forensic Science: An Update, the Evaluation of Forensic DNA Evidence, 162 (1996).

[2]See, e.g., State v. Johnson, 922 P.2d 294 (Ariz. 1996). See also People v. Soto, 981 P.2d 958, 976 (Cal. 1999) (upholding the use of the unmodified product rule and collecting cases from various jurisdictions in agreement); Clark v. State, 679 So. 2d 321 (Fla. App. 1996); People v. Dalcollo, 669 N.E.2d 378 (Ill. App. 1996), appeal denied, 675 N.E.2d 635 (Ill. 1996); State v. Kinder, 942 S.W.2d 313 (Mo. 1996), cert. denied, 118 S. Ct. 149 (1997); State v. Marcus, 683 A.2d 221 (N.J. Super. 1996); Commonwealth v. Blasioli, 713 A.2d 1117 (Pa. 1998)(citing this Treatise); State v. Morel, 676 A.2d 1347, 1353 (R.I. 1996); and State v. Jones, 922 P.2d 806 (Wash. 1996).

[3]State v. Copeland, 922 P.2d 1304 (Wash. 1996).

[4]State v. Cauthron, 846 P.2d 502 (Wash. 1993).

[5]*Copeland*, 922 P.2d at 1318.

banc, decided that PCR testing was admissible, after finding that it met the *Frye* standard of scientific admissibility.[6] The court noted that both other states had approved the use of PCR testing and stated that "[t]he overwhelming consensus among scientists is that so long as proper procedures are followed, the results should be reliable."[7] Arizona is not alone in its acceptance of either the PCR method of testing DNA or the admissibility of DNA evidence without use of the ceiling principles. In *State v. Stills*,[8] the Supreme Court of New Mexico approved of the method in 1998, quoting a commentator who stated that "PCR analysis has received overwhelming acceptance in the scientific community and the courts."[9] A number of courts, both state and federal, have held PCR evidence admissible.[10]

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[6]State v. Tankersley, 956 P.2d 486 (Ariz. 1998).

[7]Id. at 492, citing the 1996 NRC Report at 23 and the 1992 NRC Report at 145-46.

[8]State v. Stills, 957 P.2d 51 (N.M. 1998).

[9]Id. at 57, quoting George Bundy Smith & Janet A. Gordon, The Admission of DNA Evidence in State and Federal Court, 65 Fordham L Rev 2465, 2470 (1997).

[10]See, e.g., State v. Burke, 2000 ND 25, 606 N.W.2d 108 (N.D. 2000); Brodine v. State, 936 P.2d 545 (Alaska App. 1997); State v. Butterfield, 2001 UT 59, 2001 WL 765821 *9 (Utah 2001); Campbell v. State, 910 S.W.2d 475 (Tex. Crim. App. 1995); State v. Isley, 936 P.2d 275 (Kan. 1997); People v. Pope, 672 N.E.2d 1321 (Ill. App. 1997), appeal denied, 677 N.E.2d 970 (Ill. 1997); Com. v. Rosier, 425 Mass. 807, 685 N.E.2d 739 (1997); Bolin v. State, 960 P.2d 784 (Nev. 1998), cert. denied, 525 U.S. 1179 (1999); State v. Harvey, 699 A.2d 596 (N.J. 1997); Commonwealth v. Blasioli, 713 A.2d 1117 (Pa. 1998) (citing this treatise); State v. Begley, 956 S.W.2d 471 (Tenn. 1997);State v. Russell, 882 P.2d 747 (Wash. 1995), cert. denied, 514 U.S. 1129 (1995); United States v. Beasley, 102 F.3d 1440 (8th Cir. 1996), cert. denied, 117 S. Ct. 1856 (1997); United States v. Hicks, 103 F.3d 837 (9th Cir. 1996), cert. denied, 117 S. Ct. 1483 (1997); United States v. Lowe, 954 F. Supp 401 (D. Mass 1990),aff'd on that ground, 145 F.3d 45 (1st Cir. 1998), cert. denied, 119 S. Ct. 270 (1998) (the district court opinion provides an extensive overview of judicial decisions recognizing RFLP, PCR, and DQ Alpha testing as reliable and generally accepted within the scientific community); State v. Brown, 949 S.W.2d 639, 641 (Mo. Ct. App. E.D. 1997); State v. Kinder, 942 S.W.2d 313, 326-28 (Mo. 1996)(en banc). United States v. Gaines, 979 F. Supp. 1429 (S.D. Fla. 1997); People v. Wright, 72 Cal. Rptr. 2d 246 (Cal. App. 1998)(review denied); Ingram v. State, 699 N.E.2d 261 (Ind. 1998); Watts v. State, 1999 WL 33867 (Miss. 1999); State v. Jackson, 582 N.W.2d 317 (Neb. 1998); State v. Roberts, 142 Wash. 2d 471, 14 P.3d 713 (2000); State

The Supreme Court of Colorado, sitting en banc, issued an important decision discussing the admissibility of PCR testing in *People v. Schreck*.[11] The defendant in *Shreck* was charged with sexual assault and other offenses and filed a motion to exclude certain DNA evidence, which was granted by the trial court. The Supreme Court of Colorado, at the prosecution's request, granted an interlocutory appeal. In this case, the DNA was tested using the PCR method of amplification and the short tandem repeats ("STR") method, which reveals length difference between chromosomes on different people with the same base pair sequence.[12] The court stated that "[t]here are thirteen locations at which the number of STRs are known to vary from person to person. Thus, if all thirteen locations of the known and questioned sample are identical, a match is considered to be made."[13]

The Supreme Court held that this form of PCR testing, using STRs, to be reliable and admissible. The court also found that the "multiplex" system of testing, which tests several loci simultaneously, was also sufficiently reliable to warrant such admission.[14]

In 2001, the Supreme Court of Washington, sitting en banc, decided that the PCR technique was reliable and properly admissible, where the tests involved the DQ-alpha, polymarker, and D1S80 systems.[15] In making this decision, the court concluded that a*Frye* hearing on the admissibility of these systems was unnecessary, since such systems were not substantially different from the DQ-alpha test (which

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v. Stills, 957 P.2d 51 (N.M. 1998); Wood v. State, 1998 OK CR 19, 959 P.2d 1, 11 (Okla. Crim. App. 1998); Wood v. State, 959 P.2d 1 (Okla. App. 1998); State v. Lyons, 924 P.2d 802 (Or. 1996).

[11]People v. Shreck, 22 P.3d 68, 90 A.L.R.5th 765 (Colo. 2001). This decision is also important in that it changed the standard of admissibility for scientific evidence. See Chapters One and Ten, discussing this issue.

[12]Id. at 71.

[13]Id.

[14]Id. at 80. For further reading on multiplex systems, see JOHN M. BUTLER, FORENSIC DNA TYPING, 61-62 (Academic Press, 2001).

[15]See State v. Gore, 143 Wash. 2d 288, 21 P.3d 262 (2001). The Washington Supreme Court has approved of the use of PCR testing of DNA. See State v. Roberts, 142 Wash. 2d 471, 14 P.3d 713, 741 (2000); State v. Gentry, 125 Wash. 2d 570, 888 P.2d 1105 (1995); and State v. Russell, 125 Wash. 2d 24, 882 P.2d 747 (1994).

was accepted by the Washington Court in 1994[16]) and were generally accepted in the field.[17] For example, the polymarker system, one witness testified, was the "identical methodology" to DQ-alpha, but tests six different genes instead of one.[18] Testing which uses the D1S80 locus involves acceptable techniques of PCR (amplification) and RFLP (using gels and an electric current). The court noted that these testing techniques (amplification and the use of gels with electric currents to produce bands) are widely accepted and have been held admissible in numerous Washington cases.[19]

The *Gore* court also determined, in keeping with most other jurisdictions, that the product rule for calculating probabilities of a random match of a genetic profile in the human population was generally accepted in the scientific community and was admissible when using PCR-based systems.[20]

Several courts have also followed the NRC II report and have eliminated the use of the any ceiling principles, deciding that the product rule provides a proper basis for statistical analysis.[21]

§ 11:58 Statutory guidance

Since 1990, a number of states have enacted statutes governing the admissibility of DNA evidence, and it is likely that more states will follow.

Virginia enacted a statute in 1990 providing that DNA testing "shall be deemed to be a reliable scientific technique

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[16]See State v. Russell, 125 Wash. 2d 24, 882 P.2d 747 (1994).

[17]Gore, 21 P.3d at 272.

[18]Id.

[19]Id. at 272-73.

[20]Id. at 275.

[21]State v. Gore, 143 Wash. 2d 288, 21 P.3d 262 (2001); People v. Pope, 672 N.E.2d 1321 (Ill. App. 1996), appeal denied, 677 N.E.2d 970 (Ill. 1997); Armstead v. State, 673 A.2d 221 (Md. 1996); Com. v. Rosier, 425 Mass. 807, 685 N.E.2d 739 (1997); State v. Kinder, 942 S.W.2d 313 (Mo. 1997), cert. denied, 118 S. Ct. 149 (1997); People v. Freeman, 571 N.W.2d 276 (Neb. 1997); Bolin v. State, 960 P.2d 784 (Nev. 1998), cert. denied, 525 U.S. 1179 (1999); State v. Harvey, 699 A.2d 596 (N.J. 1997); Commonwealth v. Blasioli, 713 A.2d 1117 (Pa. 1998)(citing this treatise); Hepner v. State, 966 S.W.2d 153 (Tex. App. 1998) (holding the admission of random match probability harmless); State v. Copeland, 922 P.2d 1304 (Wash. 1996). The California Supreme Court, in People v. Soto, 981 P.2d 958(Cal. 1999), recently upheld the use of the unmodified product rule.

and the evidence of a DNA profile comparison may be admitted to prove or disprove the identity of any person."[1] This statute was upheld against constitutional challenges in *Satcher v. Commonwealth*.[2]

Maryland[3] followed suit by enacting a similar statute in 1991, as did Minnesota,[4] Washington,[5] and Louisiana[6] in 1992.

In the last few years, more states have also enacted DNA legislation, in order to simplify the process of admission of such testimony into court.[7]

IV. SOME CRITICAL THOUGHTS ON DNA EVIDENCE

§ 11:59 New technology; new questions

Forensic DNA evidence relies upon a combination of modern science and technology, with new insights creating new methods. Along with this rapid development, however, comes the risk of new questions concerning the validity of both the scientific method and the technical methodology.

One newer development in forensic DNA has been the use of automated equipment to analyze short tandem repeats (STRs).[1] However, when this new methodology has been chal-

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[1]Va Code § 19.2-270.5.

[2]Satcher v. Commonwealth, 421 S.E.2d 821 (Va. 1992), cert. denied, 507 U.S. 733 (1993), rev'd in part on other grounds, Satcher v. Pruett, 126 F.3d 561 (4th Cir. 1997).

[3]Md Cts & Jud Proc Code § 10-915.

[4]Minn Stat §§ 634.25, 634.26.

[5]Wash Rev Code §§ 43.43.752 through 43.43.758.

[6]La Rev Stat § 15:441.1.

[7]Alabama, Code of Ala § 36-18-30; Alaska, Alaska Stat § 12.45.035; Connecticut, Conn Gen Stat § 54-86k; Delaware, 29 Del C § 4713; Idaho, Id St § 19-5505; Indiana, Ind Stat § 35-37-4-13; Lousiana, La Rev Stat 15:441.1; Maryland, Md Cts & Jud Proc Code Ann § 10-915; Minnesota, Minn Stat §§ 634.25, 634.26; North Dakota, ND Cent Code, § 31-13-02; 22; Oklahoma, Okla Stat § 751.1; Tennessee, Tenn Code Ann § 24-7-117; Virginia, Va St § 19.2-270.5.

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[1]See <http://www.scientific.org/news-notes/news/html>, discussing the issue.

lenged, a few trial courts have not admitted the evidence.[2] The Supreme Court of Colorado, however, has approved of such technology.[3] While this issue is still to be addressed by appellate courts, it illuminates a significant concern about technologically driven scientific evidence — namely, methodological validity must be proved, not assumed.

The following sections present a candid discussion of the issues that raise concerns in DNA litigation.

§ 11:60 New technology; new questions—Financial interests of DNA experts

The legal community is entirely dependent in DNA cases upon a small group of experts, many of whom have an enormous amount of money or personal interest at stake.

The laboratories that have brought us forensic DNA testing, such as Lifecodes and Cellmark, have a huge financial stake in the viability of DNA testing. The motives of their employees, therefore, to support the science cannot be entirely academic and pure. Their future employment and livelihood depends on the acceptance of the science in the courtroom. Understandably then, the "impartiality" we would hope for in experts is lacking. While no one is suggesting that these scientists are falsifying information or changing results, there is a need to look critically at the messenger in these cases, and not just the message.

Second, the FBI is another of the large laboratories currently pushing hard for the admission of its evidence. Yet, even more so than the commercial laboratories, the FBI is actually a party in interest. Consider for a moment if a commercial laboratory were the expert in a case of a novel scientific theory in which it was also a party. Most judges would have difficulty accepting the testimony of such experts, without being overly affected by the bias issue.

Yet, in DNA cases, the FBI has been both a party and the laboratory trying to convince the court that their methods

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[2]See opinions found at <http://www.scientific.org/news-notes/news/html>.

[3]People v. Shreck, 22 P.3d 68, 90 A.L.R.5th 765 (Colo. 2001). Other state courts have likewise approved of the use of the multiplex systems, which test multiple loci at one time. See State v. Butterfield, 2001 UT 59, 2001 WL 765821 (Utah 2001).

are worthy of scientific acceptance. Not one court to date has remarked on the fact that the government is sponsoring both the prosecution and the expert testimony to establish such evidence as acceptable to the courts. Given the allegations that the Government is attempting to strong-arm those scientists in disagreement with the official FBI position,[1] the courts need to be taking a stronger, more involved role in the direction that this jurisprudence takes.

§ 11:61 [Reserved]

§ 11:62 New technology; new questions—Trial by mathematical probability

Are we creating trial by mathematical probability when we allow figures like "one in a billion" into evidence?

Some have raised concerns about the appropriateness of using both statistical probability as evidence of crime and using overwhelming statistical evidence to identify and convict defendants. The courts[1] as well as commentators have long wrestled with the issue of the appropriate use of statistical evidence in trials.[2]

In some recent cases, the only evidence to link the defen-

[Section 11:60]

[1]See Neufeld, Have You No Sense of Decency?, 84 J Crim L & Criminology 189 (1993).

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[1]The most well-known case discussing the use of the product rule as well as Bayesian analysis is People v. Collins, 68 Cal. 2d 319, 66 Cal. Rptr. 497, 438 P.2d 33, 36 A.L.R.3d 1176 (1968), a case referenced in most evidence courses and in dozens, if not hundreds of law review articles. In a contemporary case, the Court of Special Appeals of Maryland discussed the use of the product rule in a case involving the likelihood of more than one child in a family dying of Sudden Infant Death Syndrome (SIDS). See Wilson v. State, 136 Md. App. 27, 764 A.2d 284 (2000), cert. granted, 363 Md. 662, 770 A.2d 169 (2001), cert. denied, 770 A.2d 169 (Md. 2000).

[2]Among the original widely-referenced articles are Michael O. Finkelstein & William B. Fairley, A Bayesian Approach to Identification Evidence, 83 Harv. L. Rev. 489 (1970); Laurence H. Tribe, Trial by Mathematics: Precision and Ritual in the Legal Process, 84 Harv. L. Rev. 1329, 1344-50 (1971); Michael O. Finkelstein & William B. Fairley, The Continuing Debate over Mathematics in the Law of Evidence: A Comment on "Trial by Mathematics," 84 Harv. L. Rev. 1801 (1971); and Laurence H. Tribe, A Further Critique of Mathematical Proof, 84 Harv. L. Rev. 1810 (1971). More contemporary articles include Jonathan J. Koehler & Daniel

dant to the crime has been DNA evidence, which courts have held to be sufficient evidence of guilt.[3] In 2000, the Supreme Court of Arkansas upheld a conviction that was based primarily on DNA evidence, stating:

> This court is, therefore, satisfied that the testimony of even one DNA expert that there is a genetic match between the semen recovered from the victim of a rape and the blood of the defendant, a total stranger, and the statistical probability that anyone else was the source of that semen are 1 in 500 million is legally sufficient to support a guilty verdict.[4]

There is little doubt that juries and courts are satisfied that the testimony of one eyewitness is sufficient evidence to convict—even when the parties are strangers, the lighting is poor, and the identifi cation is cross-racial.[5] Yet, many are troubled by technical evidence resting on mathematical probability.

As our forensic capability becomes more discerning and more prevalent in the court, the issue of the appropriate use of statistical probability becomes more focused.

§ 11:63 New technology; new questions—Establishing protocol

What kind of protocols should there be for DNA testing and who should oversee the process?

One of the suggestions of the NRC Report is to create a standardized method to govern the protocol of the laborator-

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N. Shaviro, Veridical Verdicts: Increasing Verdict Accuracy Through the Use of Overtly Probabilistic Evidence and Methods, 75 Cornell L. Rev. 247, 274-75 (1990); Robert S. Thompson, Decision, Disciplined Inferences and the Adversary Process, 13 Cardozo L. Rev. 725 (1991); and Robert Timothy Reagan, Supreme Court Decisions and Probability Theory: Getting the Analysis Right, 77 U. Det. Mercy L. Rev. 835 (2000).

[3]See, e.g., People v. Soto, 39 Cal. Rptr. 2d 406, 890 P.2d 1115 (Cal. 1995), aff'd, 21 Cal. 4th 512, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999);People v. Rush, 165 Misc. 2d 821, 630 N.Y.S.2d 631 (Sup 1995), judgment aff'd, 242 A.D.2d 108, 672 N.Y.S.2d 362 (2d Dep't 1998); Springfield v. State, 860 P.2d 435 (Wyo. 1993).

[4]Roberson v. State, 16 S.W.3d 156, 170 (Tex. App. Austin 2000), petition for discretionary review refused, (Sept. 13, 2000).

[5]All of these factors affect the reliability of eyewitness identification. For more on the problems associated with eyewitness identification, see §§ 13:54 -13:56.

ies using DNA testing. There needs to be standards and such standards need to be rigorously applied.[1]

The major issue with protocol standards and standardization is acknowledging that in a process this novel and radical, the courts should not be a testing grounds for discovering what is right with the process and what is wrong. Rather, uniformity and standardization in the process are absolutely necessary to maintain the certainty of the science.

§ 11:64 [Reserved]

V. GUIDES AND CHECKLISTS

§ 11:65 Prosecutor's guide to DNA evidence

If you are a prosecutor and you intend to use DNA evidence, you will have by far the easier job in using such evidence than will defense counsel. Because there is a great deal of help available to the prosecution on this subject and because the greatest difficulty with DNA evidence is in the challenge to its use, the following sections need provide only a brief analysis.

If you have a case in which the DNA at the crime scene appears to match the accused's DNA sample and your jurisdiction permits the introduction of DNA evidence, the following sections detail the issues you will need to address in consultation with your expert.

§ 11:66 Prosecutor's guide to DNA evidence—Make certain the expert confirms the match

Always check with your expert to make certain that there is no hesitancy or vacillation about whether the control sample matches the crime scene sample. In the event there is a problem with the match, you would do better to go without the DNA testimony than to have your case blow up before the jury and possibly be destroyed.

Additionally, check with your expert about how the expert will be able to withstand a challenge to the conclusion of a

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[Section 11:63]

[1]The need for standardizations and controls in all forensic laboratories is truly an issue for those involved with forensic evidence. This issue is discussed at length in Chapter 12.

match. If the expert is hard pressed to provide you with an appropriate explanation, you can imagine how poorly a jury will receive such an inadequate response.

§ 11:67 Prosecutor's guide to DNA evidence—Establish proper protocol

Can your expert articulate the appropriate procedures for DNA testing and testify that they were followed in this case? If not, the expert's conclusion concerning the match may be put into question. It is beyond question that the proper protocol is an essential element of establishing your case in DNA testing.

In some jurisdictions, for example, it is the prosecution's burden to establish that proper procedures were followed in the case. Thus, a failure to establish appropriate methods in the case at bar may result in the evidence being excluded.

In the event the evidence survives exclusion, but problems exist with the protocol, the defense will have an opportunity to exploit those weaknesses on cross-examination so as to convince the jury that the evidence is not worth the paper it is blotted upon.

§ 11:68 Prosecutor's guide to DNA evidence—Keep the explanation simple

One time while writing this book I found myself explaining linkage equilibrium to non-lawyers at a dinner party. The blank stares I was getting finally brought me back to reality, where I became aware that I had lost my audience.[1] Although a dinner party is not a courtroom, the same principle applies: If the subject is technical and boring, people tune out quickly. When your witness is explaining DNA evidence, make sure that the explanations are simple, short and to the point.

Additionally important is the use of "toys" for the jury during the explanation. The most helpful tools to use are models of DNA that can be taken apart, as well as color diagrams and charts to help explain such issues as the modified ceiling principle.

[Section 11:68]

[1]Not to mention that I had lost my mind if I really thought discussing DNA at a dinner party was "having a good time."

Whatever you do, avoid boring your jury to death with explanations that are too technical. On the other hand, do not make your explanation so simplistic that you will be unable to prove the elements of your case. Understandably, it is a fine line dividing simple from simplistic. For that reason, a written direct examination, reviewed ahead of time with your witness is particularly important for this type of evidence.

§ 11:69 Prosecutor's guide to DNA evidence—Know the law and keep the testimony within its limits

As with every other subject in the law, failure to know the law in your jurisdiction may result in total failure in the courtroom. The law on DNA testing has been in constant flux since 1991. Do not assume that you know the law in your jurisdiction until you have reviewed this chapter (many jurisdictions are included) and have updated the research to check for the most recent developments. Once you are comfortable with the state of the law, then you are able to structure the testimony in accordance with those limits.

§ 11:70 Prosecutor's guide to DNA evidence—Who should be an expert

In many forensic cases, experts are often the technicians who perform the testing to obtain the results. As a rule of thumb in DNA cases, try to use experts who have been qualified as such in prior cases. There are people who testify frequently on DNA and your case will most likely proceed more smoothly with those experts.

Also, if the defense is going to present expert testimony, you will need to make sure that your expert's qualifications do not pale in comparison to the opposition's experts. Be careful not to let your expert be outdone by a better qualified expert.

§ 11:71 Defense lawyer's guide to using DNA

Unless you are using DNA evidence to exculpate your client—a task that should not prove overly burdensome—DNA evidence poses a much bigger challenge for defense lawyers. For that reason, the defense lawyer's guide is somewhat more in depth than the prosecutor's guide.

In the event you are challenging DNA evidence that indicates that the forensic sample matches the DNA sample found at a crime scene, the following sections provide a guide for you to follow.

§ 11:72 Defense lawyer's guide to using DNA—Organize a strategy

In order to focus on how to use DNA evidence, the following hypothetical will suggest a typical set of facts that you could confront in a DNA case.

Assume that the following circumstantial evidence links your married, male client with the married, female victim who has been murdered: they worked together, some people at work thought they were having an affair, and she was stabbed with a knife that is consistent with a hunting knife owned by the defendant (although without any evidence of blood on it). The time of death is between 8:00 and 10:00 p.m. on a Sunday night, during which time your client claimed to be at a movie by himself. In addition, there is DNA evidence which could come into evidence to establish that a small spot of blood found on your client's pant leg matches the blood of the victim, according to DNA profiles. Finally, there is evidence to suggest that (under the modified ceiling principle), the chances of such a match are one out of 85,000.

There are several possible defenses that could be available, including the most obvious choices of: (1) claiming the blood is from someone other than the victim; or (2) claiming the blood may be from the victim, but that it may have come from a minor cut she received at work.

However, how you choose to mount a defense will affect whether and how you are challenging the evidence. One of the factors in your decision making will obviously be how overwhelming the odds of the match are. For instance, if your client is from a small rural location in Iowa, the number one out of 85,000 will have a different impact than if your client is a resident of New York City, where there are nine million residents and therefore numerous other possible assailants within walking distance.

Additional considerations to use in the planning of your strategy include determining (with an expert's assistance) how good the DNA match really appears, how good do you

anticipate the expert to be, and how vulnerable is the laboratory's protocol to challenge.

Finally, perhaps you believe that an error was made and that the DNA found on the pants really does not match the victim's blood at all. What to do? Is there any way to have another test performed? Can you have another expert review all the data that the prosecutors' experts have? What other ways are there to challenge the test results?

In any event, before you decide how to handle the DNA evidence, make sure you have put it into the context of the entire case.

§ 11:73 Defense lawyer's guide to using DNA—Know the law in the jurisdiction

If you have read any of Part 1 of this treatise, you have heard repeatedly how important it is to know the state of the law in your jurisdiction. Although this book includes the law for the vast majority of states, as stated earlier, the law on DNA admissibility has been in a state of constant flux.

Thus, make sure you review the law in this chapter as well as doing an electronic research check to make sure you have not missed any new case that has been decided since the time of this publication.

§ 11:74 Defense lawyer's guide to using DNA—Take the time to learn the science

Without question, the science of DNA testing is difficult to grasp and is not the most scintillating issue with which you have ever had to become conversant. Nevertheless, there is no substitute for teaching yourself everything you need to know about the subject, both with the help of this chapter as well as the source materials cited. The NRC Reports are written in clear and accessible language and should help in those areas where the subject is not well understood.

Additionally, there are other lawyers who have a well-developed knowledge of DNA testing who may be willing to help you out should you have a case involving DNA evidence.

Finally, discuss the DNA issues in your case with an expert, who should be able to explain the confusing aspects of the case to you. Do not neglect to read any of the latest studies on DNA that are written for the lay person. A good place to start is *Judicature* or the *National Law Journal*,

which generally will contain pertinent discussions.

§ 11:75 Defense lawyer's guide to using DNA—Determine whether you need an expert

Having determined the strategy of your case, the question of whether you will need to hire an expert becomes much clearer. In the event you are directly challenging either the admissibility of the evidence and/or the accuracy of the evidence in your case, you will absolutely need to hire at least one expert, if not several.

However, (using the hypothetical above) if you are admitting that the blood in question may be the victim's, you may not need an expert at all. The questions that need to be answered include the following:

- Is there sufficient money for an expert or does your jurisdiction permit the appointment of DNA experts? Some jurisdictions have found that indigent defendants are entitled to DNA experts[1] while other jurisdictions have disagreed.[2]
- How significant is DNA in your case? If the blood is the crucial bit of testimony, you need to at least consult with an expert and preferably call one to testify (if the expert is able to provide helpful testimony).
- How significant are the statistics? If you are in a jurisdiction that allows the expert to opine that "the chances of a match are 1 in 2 billion" you definitely need an expert who can at least reduce the percentages to a more reasonable level.
- Is this a case in which the defendant will stand a better chance with a plea, rather than a trial? If so, perhaps the time and money is better spent on working out a better plea for the client.

[Section 11:75]

[1]See, e.g., State v. Bloom, 516 N.W.2d 159 (Minn. 1994), providing that an indigent defendant has a right to "reasonable access to expert support at public expense." Id. at 169. Accord Taylor v. State, 889 P.2d 319 (Okla. Crim. App. 1995).

[2]See, e.g., State v. Harris, 866 S.W.2d 583 (Tenn. App. 1992).

§ 11:76 [Reserved]

§ 11:77 Defense lawyer's guide to using DNA—Challenging the admissibility of DNA evidence

You may be able to challenge the admissibility of DNA evidence in court on a few grounds. For example, the following grounds may be pursued: the prosecutor's failure to establish a match; the total contamination of the sample; or the failure of the laboratory to establish that it followed proper protocol in performing the testing.

§ 11:78 Defense lawyer's guide to using DNA—Deciding whether to file a motion in limine or request a voir dire hearing

There are a few procedural avenues available to challenge the admissibility of DNA evidence. You can file a motion in limine or request a voir dire hearing during the prosecution's case in chief.

Many defense lawyers are hesitant to file a motion in limine, since that provides the prosecution with: (1) too much notice of the defense strategy; (2) the ability to investigate and brief the issue; (3) too much time to change its witness's approach to the evidence. Nevertheless, if you are in a court that requires matters of admissibility to be raised in a motion in limine, you may be required to do so.

Another factor to consider is whether the grant of a motion in limine is appealable by the prosecution. In some jurisdictions, if the prosecution certifies that the allowance of the motion would substantially hinder or effectively end their prosecution, they may stop the case and file an interlocutory appeal on such issue.[1] In the event such an issue is raised during trial however, jeopardy would have attached, significantly limiting the prosecution's ability to do anything about the court's ruling, should it be adverse to the prosecution.

In the event you are intending to challenge the admissibility of DNA test results, you can request a voir dire hearing

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[Section 11:78]

[1]See Commonwealth v. Deans, 610 A.2d 32 (Pa. 1992).

to have the court rule on the admissibility of the evidence.[2] In the event you do not believe you will be successful in convincing the court to exclude the evidence, you may want to forgo the voir dire hearing and use your ammunition on cross-examination.

In taking this latter course, you will be unable to keep the evidence away from the jury (although you might be able to have the testimony stricken, if you are really lucky), but you will be able to seriously damage the prosecution's use of such evidence in front of the jury. Additionally, if you do have a voir dire hearing and lose, the prosecution and its witness are prepared for your likely cross-examination, which is generally harmful to your case.

As with many other matters at trial, it is worth planning your strategy in advance given what you know about the case, the prosecution and the court. As with other decisions about evidence, do not wait until the very last minute to analyze the situation and determine your strategy.

§ 11:79 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert

There is no cookbook recipe for how to cross-examine each expert on DNA. It depends entirely on what the expert has done and what the expert is able to say. However, the following sections provide a few guidelines that should help in your preparation for cross-examination.

§ 11:80 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Using the pretrial statement

First, pursuant to most procedural[1] or evidence rules, the prosecution is generally required to provide the defense with

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[2]See, e.g., Fed R Evid 103(c), which provides:

In jury cases, proceedings shall be conducted, to the extent practicable, so as to prevent inadmissible evidence from being suggested to the jury by any means, such as making statements or offers of proof or asking questions in the hearing of the jury.

[Section 11:80]

[1]See e.g., Fed R Crim P 16(E), which provides:

At the defendant's request, the government shall disclose to the defendant a written summary of testimony the government intends to use under Rules 702, 703, or 705 of the Federal Rules of Evidenceduring its case in chief at trial.

a pretrial statement in response to the defense's request for an expert's opinion. Do not forget to ask for one. Generally, the report should include the name and qualifications of the expert, a list of every publication that the witness has authored and every case in which the expert was a witness, as well as a complete summary of the witness's testimony.[2]

That pretrial statement should be the basis of your cross-examination preparation. First, have a law student or associate review the publications to determine whether anything is possibly useful for cross-examination. The same strategy should be applied to prior testimony. Contact any of defense lawyers in the cases on the resume and find out whether there are any transcripts available on the witness.

§ 11:81 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Using your own expert to prepare

Have your expert (assuming you have one at least to consult with) review the statement and determine where there are vulnerabilities in the expert's opinion. As discussed earlier in this chapter, it is very difficult to challenge such technical information without the benefit of an expert's opinion. Also, depending on the laboratory, there may be ways to specifically challenge that laboratory's procedures in the specific case.

§ 11:82 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Exploiting the expert's bias

Do not overlook the importance of bias questions with DNA cross-examination. Unlike some other areas where there are

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This summary must describe the witnesses' opinion, the bases and the reasons therefore, and the witnesses' qualifications.

Do not forget to file such a request in all your cases.

[2]One area in which criminal trial lawyers could benefit from civil trial lawyers' experience is in how to effectively limit the testimony of the expert to what is contained in the pretrial expert summary. Generally, anything that is not in the "four corners of the report" is inadmissible. In civil cases, the issue of expert's reports is often a key evidentiary matter which civil lawyers spend substantial effort focusing upon. If you are attempting to limit the testimony of an expert in your case, you may want to consider reviewing the decisions in the Federal Rules Decisions Reporter and checking in some civil trial manuals for some good strategy tips.

rather independent witnesses, the vast majority of witnesses in DNA litigation are either employed by the laboratory that performed the test or are FBI employees. Bias is a useful avenue to pursue, but really scoring points on bias occurs only if you are able to suggest that the basis of the expert's opinion is somewhat questionable. In other words, bias has less impact if the test results are solid as a rock. Thus, if you are going to use bias, it is more impressive when you are able to couple it with a good claim of bad test results.

It is rare that a jury will believe, without overwhelming evidence, that a laboratory witness will make up evidence out of whole cloth. What is more believable, however, is that in marginal test results the witness would "shade" the results to favor the laboratory.

Additionally, do not forget that most of the testing in DNA is not done "blind." Rather, the laboratory is often told what the prosecution is looking for—namely, a match with a certain forensic sample. Studies have shown that knowing the desired outcome ahead of time sometimes skews the results in that favor when matters of interpretation are at stake.

Finally, it is important to keep in mind that, if nothing else, showing that the expert has always testified for the prosecution can lead to a handful of useful questions in front of the jury, questions that may not win the case, but may put some uncertainty in the jury's mind. Also, if you can establish that the expert has always found a match when asked to, you are in a position to suggest that the expert would find a match whether one existed or not.

§ 11:83 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Know how to discuss the problems of DNA

Before you cross-examine a DNA expert, it is always helpful to review the literature on where DNA testing can have problems. In a nutshell, the following areas are frequently the most important:

- Crime scene contamination
- Sample is too small for proper testing
- Destruction of the sample, so no control test
- The problem of shifting bands

- The possibility of false assumptions
- Hardy Weinberg equilibrium problem
- Poor quality laboratory procedures
- Database is too small

These specific issues are discussed earlier in the chapter and information about handling forensic problems is contained in Part 3.[1]

§ 11:84 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Challenging the expert's credentials/knowledge

Throughout this treatise, repeated warnings have been given about not trying to "outsmart the expert." Well, like all good rules, there are good exceptions. One exception is in the case where the prosecution uses a laboratory technician as an expert. If the witness does not have at least a master's degree, you may be in a position not only to hammer on the witness's lack of credentials, but also to strike a damaging blow based upon the lack of sophisticated knowledge.

Essentially, you have a great ability to challenge the expert's conclusions on the grounds that "he can test for it, but he sure does not understand it." In other words, if you have read all the information you can on DNA and have a good expert, you may be able to outsmart the technician.

Working with your expert, you need to find a variety of authoritative treatises on genetics, DNA testing, and such ancillary fields as population genetics. It is your mission to establish, in front of the jury, that this person has no idea about the complexity of DNA testing, has no clue as to what "junk DNA" is and what might be lurking in those base pairs, cannot explain population substructure, and cannot explain why a "match" has a range of acceptable variation.[1]

If you can, use the NRC Report in your examination—several courts have recognized it in their opinions—to underscore the expert's limited knowledge. As you might

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[Section 11:83]

[1]See §§ 11:25-11:30, supra, and Appendix 3C, infra.

[Section 11:84]

[1]Many people might have trouble concluding that a match need not match, but need only be within a certain percentage point of matching.

guess, this is a very dangerous tactic if your knowledge is not solid and you are working without a net (i.e., an expert sitting next to you). Also, make sure you are not being sandbagged by the prosecution who may be using an expert short on credentials and long on actual knowledge. You need to feel your way around with the expert and make sure you are not going to get buried.

However, you can make great use of an expert's limited knowledge and underscore with the jury how important the test is and how shallow the witness's understanding of the science is. In a case where DNA is the pivotal issue, you can create reasonable doubt with such a cross-examination.

§ 11:85 Defense lawyer's guide to using DNA—Cross-examination of the DNA expert—Use their expert as foundation for yours

In conjunction with your expert, plan for your cross-examination to lay a foundation for your own expert to testify. For example, if there is a great passage from an authoritative treatise you want to use with your expert, have their expert agree that it is an authoritative text— just be sure to pick a book you are sure will give you the answer you want.

If you need to establish certain facts for your expert, try first to do it (if there is no great danger of disagreement) with the other side's expert. The reason for such a tactic is to buttress your own expert's opinion with the opinion of the opposition's expert. Thus, by the time you get to your expert's significant and differing opinion, the jury will perceive that the prosecution expert has testified in agreement with your expert all the way along the way.

§ 11:86 Defense lawyer's guide to using DNA—What to do with an unshakable expert

Do not get into a battle with an unshakable expert. You will lose and your credibility will suffer. If the expert is unmovable on his or her position, shift gears and either terminate your cross-examination before the expert has another chance to explain his conclusions to the jury or move to a less dangerous topic, such as vulnerable credentials, bias or lack of testimonial experience.

§ 11:87 Defense lawyer's guide to using DNA—The safe areas to question

When in doubt, you can always ask the witness whether he or she was responsible for securing the crime scene (the answer is no) and whether he or she was responsible for making sure the blood was not contaminated or switched anywhere along the way (most likely, the answer is no).

Additionally, you can inquire about what the witness was told about the case. If he or she was told nothing, no harm done. If he or she was told something about what the prosecution wanted, you have a new area to establish bias. Furthermore, if there were any problems at the laboratory where the expert works (for example, Lifecodes failed a proficiency test in matching and was taken to task for errors in the *Castro* case, discussed at § 11:43), you can spend a long time on those problems and the deficiencies in the laboratory.

In any event, when you are doing no good for your case, sit down. Simply digging in and letting the expert be in charge is not a good strategy. All you will do is affirm the testimony in the minds of the jurors.

§ 11:88 Prosecutor's checklist

☐ Make sure you have a good handle on the law of admissibility in your jurisdiction before you try to use DNA evidence. Know the limits—if any—on DNA before you base your prosecution on such evidence.

☐ Take the time to learn the science, including its shortcomings. Do not go into court unless you are conversant with the concepts in this chapter and have sufficiently prepared to handle any attacks on the science.

☐ Choose your expert carefully. Do not try to proceed with DNA unless you really believe that you will be able to use the expert that you have procured. Not all experts are created equal and make sure that yours is of good quality.

☐ Spend enough time with your expert to polish the testimony so that it will be believable to the jury and will not be shot down on cross-examination. Make sure that your expert is prepared amply for cross-examination and can withstand the attack

☐ Use DNA as one part of your arsenal of evidence. If all you have is DNA and the defense is ready with a good

cross-examination and a decent alibi, your case may come undone. Caution suggests that, if possible, you should not put all your eggs in the DNA basket.

☐ Know where the problems are in your case with respect to the DNA evidence. Consider carefully whether to explain such problems during the direct examination or whether you would be better off letting your expert explain such matters on cross-examination.

☐ When you conduct a direct examination, keep it simple and to the point. Do not try to provide too much detail to the jurors. For a test, try out the direct exam on the secretaries in your office and ask them for suggestions and comments after you have finished.

§ 11:89 Defense checklist

☐ Plan your strategy ahead of time. Do you want to concede that the DNA is that of your client (for example, in a consensual-question rape case)? Do you want to challenge the evidence head on? Plan well.

☐ Make sure you have a good handle on the law of admissibility in your jurisdiction before you try a case with DNA evidence. If your jurisdiction is one of those that either limits DNA or has questioned DNA, be prepared to argue against admissibility.

☐ If you will be handling a DNA case for the first time, make sure to discuss the science and the law thoroughly with an expert. Better yet, retain an expert to assist you in the preparation of your case.

☐ Know the science well before you attempt to cross-examine an expert. In the event you are confused about certain issues, make sure that you are clear on them before trial.

☐ If you are not making any headway on cross-examination, move to the safer subjects or simply stop the examination. When in doubt, stick to subjects such as bias and self-promotion for challenges.

☐ Do not try to outsmart a DNA expert unless (1) you are sure that the expert is only a technician who does not understand DNA, and (2) you have assistance in your cross-examination from an expert.

☐ Lay the foundation for your own expert's opinion (if appropriate) with the opposition's expert. It is a way of reinforcing what your expert will say and lending immediate credence to your expert's opinion.