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Forensic DNA Fundamentals for the Prosecutor

Be Not Afraid

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INTRODUCTION

DNA has become an invaluable instrument in the search for justice. DNA evidence may play a significant role at various points throughout the life of a criminal case, from the initiation of a criminal investigation through post–conviction confirmation of the truth.

As the "end users" of DNA evidence, prosecutors must be "in the know." Understanding DNA, both the science and its technology, is not discretionary, but compulsory to the responsible practice of criminal law.

This publication serves as a primer for prosecutors on the basics of DNA. The application of the science and the math, trial issues and potential defense challenges that prosecutors face in DNA cases will be addressed in detail.

Never before has material like this been assembled for prosecutors. We hope prosecutors will use this publication to strengthen investigations, find the truth, serve justice and give voice to those who may not have one.

THE SCIENCE OF NUCLEAR DNA

Every human body is comprised of chemicals whose interactions and synthesis are regulated by the genetic blueprint that was drawn at the moment of conception. The genetic code determines each person's individual characteristics and in doing so, dictates that no two persons, with the exception of identical twins, are the same.

The analysis of deoxyribonucleic acid (DNA) began in medical research.[1] Scientific interest in the DNA structure arose in the early 20th century as biochemists began to define the classes of chemicals that comprise us all. Initially, it was discovered that nucleic acids were a major component of all cellular material. There are two categories of nucleic acids: ribonucleic acid (RNA) and deoxyribonucleic acid (DNA). Later, it was learned that DNA, rather than RNA, is the repository of the genetic code. In 1953 James Watson and Francis Crick published their seminal paper describing the primary structure of DNA.[2]

DNA is a polymer, i.e., a long molecule composed of only a few simple units. Those units are deoxyribose (a sugar), phosphate and four (A, C, T and G) different organic bases. These units taken together are nucleotides, which are the raw building blocks of DNA. The DNA structure has been likened to that of a long ladder that has been twisted along its long axis. The sugar and phosphate together form the outside support of the ladder and the four different bases are the rungs or steps of the ladder. (See Figure 1.)

As molecular biology research developed, several scientific truths were determined. One premise is that, among human beings, 99.99% of DNA nucleotide sequences are identical. The shared DNA creates human characteristics that are similar to all people: two hands, ten toes, blood that can be transfused and organs that can be transplanted. The .01% of

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[1] For a summary description of the forensic analysis using DNA, see *People v. Axell*, (Cal.App. 1991) 235 Cal.App.3d 836.

[2] Watson and Crick, *A Structure for Deoxyribose Nucleic Acid*, NATURE, April 2, 1953, *available at*, http://biocrs.biomed.brown.edu/Books/Chapters/Ch%208/DH-Paper.html.

DNA that is not shared is different in every individual, with only one exception: Identical twins share their DNA sequence completely. A second premise is that 100% of a person's DNA is the same within and throughout a human being's body. Whether you look at the cells of a person's blood, skin, semen, saliva or hair, the DNA sequencing will be the same.[3] Scientists have developed a methodology to identify the variations within an individual's sequencing, and these methods form the basis for DNA profiling.

Each cell with a nucleus[4] contains a copy of a person's DNA. DNA is a molecule of genetic materials that encodes a person's hereditary information. A DNA strand is shaped as a spiral staircase, also referred to as a double helix. The sides of a DNA strand are chains of sugars and phosphates. The steps connecting the two sides of the staircase are pairs of molecules called "bases." There are four bases in the DNA strand: adenine (A), cytosine (C), guanine (G) and thymine (T). Nucleotides from separate DNA strands bond in a specific form (the steps), connecting the sides of the DNA (the staircase). C bases bond or pair only with G bases and A bases bond or pair only with T bases.
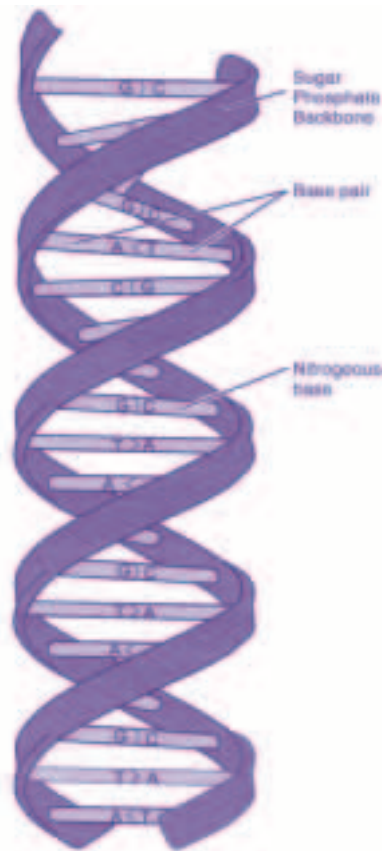
Figure 1 (Courtesy of the National Human Genome Research Institute - NIH)

The double helix is the shape that two paired strands of DNA assume when they are bonded together. The double helix is made up of sugars, phosphates and bases. The bases are adenine, thymine, cytosine and guanine.

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[3] There is one very rare exception, a genetic condition that occurs when two fertilized eggs fuse in the womb, creating a child with two full sets of genes, called a chimera. (David Baron; "DNA Test Shed Light on Hybrid Human", NPR, August 11, 2003). This condition is easily identifiable with lab testing.

[4] Not all cells have a nucleus, for example, red blood cells do not have nuclei.

(See Figure 2.) There are three billion base pairs, including thirty thousand genes, which comprise the human genome.

The three billion base pairs are grouped in 23 pairs of chromosomes: one set from the mother and one set from the father (for a total of 46 chromosomes). Specific sequences of bases that code for a characteristic are called genes. A gene's position on a chromosome is its locus. The possible sequences or variations of a gene are called "alleles." Because everyone inherits one set of chromosomes from each parent, humans have two alleles at each locus. Good examples of genes are hair color and eye color: within a person's chromosomes, there are genes for hair color and genes for eye color. A person's alleles for hair color may be for brown hair and her alleles for eye color may be for green eyes—the alleles are the variations of the gene. Genes may be "polymorphic," meaning they may take different forms or contain different sequences of base pairs. Varying alleles of the genes that differ from one person to another provide the basis for DNA identification.[5]
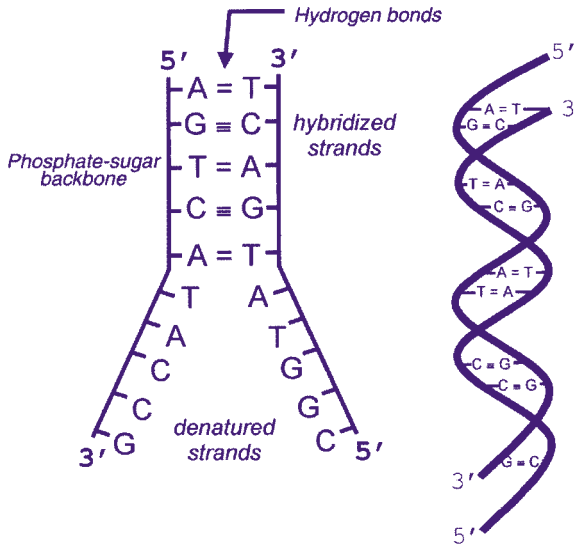
Figure 2 (Reprinted from: Butler, John M., *Forensic DNA Typing*, "Additional DNA Markers," Chapter 2, page 15, Academic Press, 2001, with permission from Elsevier.)

A DNA strand is structurally comprised of bases that when paired with other bases form a double helix. The base pairs are held together by hydrogen bonds.

[5] *New Jersey v. Harvey*, 151 N.J. 117, 1997 (Supreme Court of NJ).

When a DNA sample is analyzed, the results are called profiles. Samples can come from either a crime scene or a person; when analyzed they produce either an evidence profile or a suspect (or known reference) profile.

DNA AND STR TECHNOLOGY

Nuclear DNA is found in blood, sperm, vaginal secretions, mucus, sweat, saliva, hair roots, earwax, bone and teeth. It is found in organs, muscles, and/or skin. Nuclear DNA is found in every cell and tissue of the body, except for red blood cells. Also, the DNA found in body fluids can be in either liquid or dried form. DNA is durable and long lasting. Scientists have progressed in their ability to find DNA suitable for testing in smaller and more degraded samples than ever before. Nonetheless, the authenticity requirement that ensures the reliability of evidence applies to DNA: The evidence must be what is claimed and not the product of corruption or tampering.

Historically, scientists needed large evidence samples to enable them to extract DNA. The earliest method of forensic DNA analysis, known as restriction fragment length polymorphism (RFLP), involved a comparison of lengths of specific DNA fragments. This method required the evidentiary DNA to be relatively non-degraded, a condition not always met by biological material from a crime scene. Also, producing a DNA profile through RFLP analysis requires a great deal of labor, time and expertise.[6] To improve their ability to analyze DNA from a crime scene, scientists developed a method of replicating exact copies of DNA from the biological evidence found.[7] Their underlying motivation was to produce more samples to enable more testing so that other scientists could find the same results obtained by the initial scientist.[8] Because of the accuracy and the durability of the copies, scientists less frequently face the dilemma of exhausting all of the evidence during analysis. Once the crime scene evidence is copied, more than one scientist may test it and confirm accuracy.

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[6] Butler, John M., *Forensic DNA Typing*, "Overview and History of DNA Typing*,"* Chapter 1, page 4, Academic Press, 2001.

[7] In 1993, the inventor of this technique, Dr. Kary Mullis, was awarded the Nobel Prize in Chemistry for his discovery.

[8] National Research Council (NRC-II), *The Evaluation of Forensic DNA Evidence*, National Academy Press, Washington DC, 1996.

The amplification/replication process is known as polymerase chain reaction (PCR). PCR allows laboratories to develop DNA profiles from extremely small samples of biological evidence.[9] PCR is a three step process: First, the DNA strand is denatured, which means the strand is pulled apart by heating. Annealing is the second step in the process, where the sample is cooled and the primers bind to the target sequence of the DNA molecule. (A primer is synthetic or manufactured DNA.) Lastly, the DNA strand is heated again, activating a polymerase (enzyme) that will produce the mate to the single strand to form a complete copy. Each time the PCR process is done, the number of new DNA strands doubles, theoretically generating a billion copies after 30 cycles.[10] (See Figure 3.) The development of PCR was crucial to forensic identification made with DNA because frequently it enables both the prosecution and the defense to analyze the evidence. It also allows for sample retention if retesting is later deemed necessary.
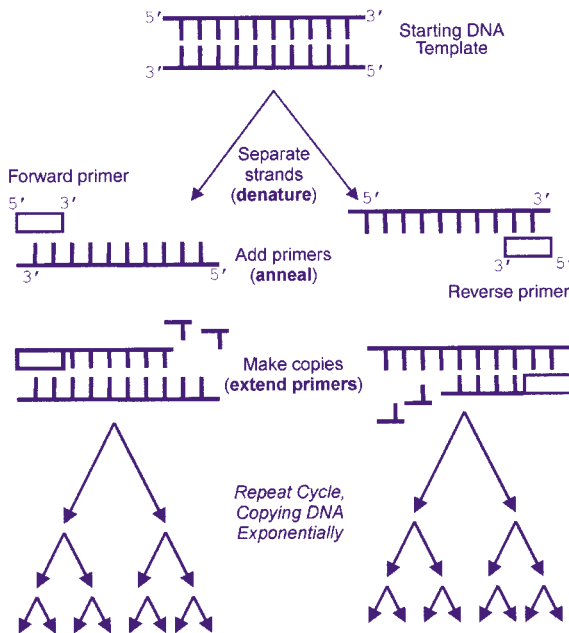
Figure 3 (Reprinted from: Butler, John M., *Forensic DNA Typing*, "Additional DNA Markers," Chapter 4, page 40, Academic Press, 2001, with permission from Elsevier.)

Polymerase Chain Reaction—the DNA replication process.

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[9] National Institute of Justice, Special Report, *Using DNA to Solve Cold Cases*, *PCR Analysis*, U.S. Department of Justice; July 2002.

[10] Butler, John M., *Forensic DNA Typing*, "The Polymerase Chain Reaction," Chapter 4, page 39, Academic Press, 2001.

A second significant development in the science of DNA was proficiency in the testing of short tandem repeats (STR). STR testing is a PCR-based technology. As described earlier, genes are specific sequences of nucleotides located at a particular position (locus) on a particular chromosome, and the variant forms of the genes are called alleles. The different alleles are distinguished either by length polymorphisms or sequence polymorphisms. Short Tandem Repeats or STRs are one type of length polymorphism. STRs are a core sequence of two to seven bases that are repeated consecutively a variable number of times, e.g., ACTGACTGACTGACTG.

In the most modern method of DNA profiling, scientists exploit interpersonal genetic variation found in short tandem repeat (STR) sequences. While those repeats are constant in an individual person's DNA, the repeats vary by individual. Comparing the number of repeats is STR testing. Taking advantage of PCR technology, STR testing can be performed with smaller and even degraded samples and is the fastest testing technology presently available. Slab gel and capillary electrophoresis are the two separation methods used in the STR process to extract the DNA for visual analysis and comparison.

M ITOCHONDRIAL DNA

The analysis described up to this point has been based on the genetic profiling of nuclear DNA, i.e., DNA found in the nucleus of a cell. Another form of DNA that can be used for comparison is mitochondrial DNA (mtDNA), which is found in the mitochondria of a cell, outside the nucleus in the cytoplasm. (See Figure 4.) The mitochondria are the energy source for a cell. MtDNA has 16,569 base pairs and possesses 37 genes.[11] The portion that is used for analysis is a "non-coding control region, also known as the D-loop, which exhibits a fair degree of variation between individuals and is therefore useful for human identity testing purposes".[12] MtDNA can be found in bone, muscle, hair, teeth, skin, blood and body fluids, and like nuclear DNA, it can be located, extracted and copied.
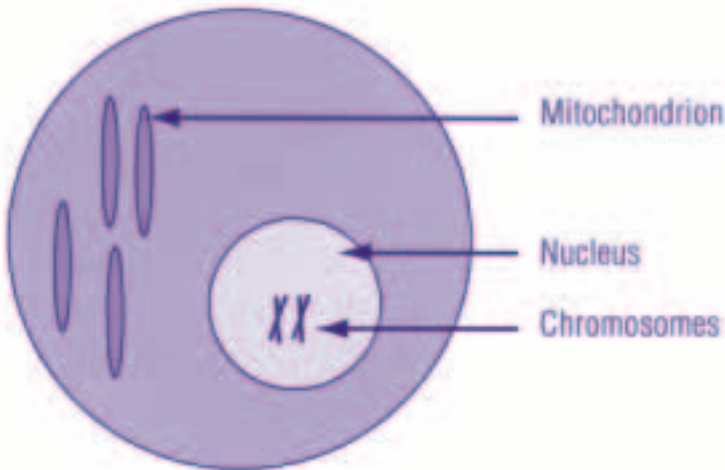
Figure 4 (National Institute of Justice, *Using DNA to Solve Cold Cases*, Washington, D.C.:U.S. Department of Justice, July 2002, p.7.)

Cell Diagram: Nucleus, chromosomes and mitochondrion.

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[11] Butler, John M., *Forensic DNA Typing*, "Additional DNA Markers," Chapter 8, page 121, Academic Press, 2001.

[12] Butler, p.121 (2001).

MtDNA can be a great source for analysis in cases where the evidence collected is so degraded that nuclear DNA analysis would not yield a profile, for example, cold cases or cases where only skeletal human remains are found. Two techniques are used to examine mtDNA: PCR, which does the copying, and mitochondrial sequencing, which does the comparative analysis. Mitochondrial sequencing is a process that looks at the sequencing of the A, C, T, and G's, the bases that make up the steps of the DNA strand. MtDNA is robust and more plentiful and durable than nuclear DNA. It is, however, less discriminating than nuclear DNA because it is transmitted only from a mother to her children and therefore there is less variation between individuals.

FORENSIC IDENTIFICATION: THE MATH

By using the 1/100% of person-specific DNA, scientists can make specific determinations that have significant forensic value to the prosecution of a case. First, they can determine the genetic profile drawn from biological evidence found at a crime scene and match it to the genetic profile from a defendant, which would tie *this* defendant to *this* charged crime. Then, a scientist can calculate the statistical probability that a random unrelated person within the human population would coincidentally have the same genetic profile as the one taken from the crime scene evidence. Such a determination helps the prosecutor to meet the burden of proving that *this person* committed *this crime*.

When performing forensic DNA testing, analysts first compare the profile generated from the crime scene evidence sample to the profile generated from the offender's sample. To do this, the analyst examines 13 locations along the chromosome, known as loci, which the relevant international scientific community has identified as suitable for comparison purposes. Each locus contains two alleles, one from each parent. When the STRs from a crime scene profile match an offender's profile, it means that there is a match at each and every one of the 26 alleles (genes) that comprise the 13 loci.[13,14] The specificity of this forensic identification is one of the most significant powers of DNA.

When scientists compare the crime scene evidence profile and the offender's profile, they look for a 100% match of the two profiles at the 13 loci. This comparison is *not* a statistical determination, but rather a scientific one. DNA analysts, however, *do* speak in terms of statistical probabilities when describing the rarity or frequency of finding a certain profile among human populations. There are approximately six billion people on the earth. Comparing DNA at 13 loci can generate a *random*

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[13] The 13 core loci used for STR comparisons are: TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, TH01, VWA, D13S317, D18S51, D21S11, and D16S539. Profiles are also developed at the Amelogenin locus for sex determination. Currently, Profiler Plus ID and CoFiler typing systems are the kits predominantly used for analysis.

[14] MtDNA analysis only looks at a single locus, in comparison to the 13 that are looked at for nuclear DNA analysis.

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match probability greater than six billion. In other words, the analyst may testify that there is no likelihood that anyone else, other than the offender, will have the same genetic profile as the profile generated from both the crime scene evidence and the offender. By calculating the random match probability, scientists can conclude from whom the DNA originated, also called *source attribution of the DNA*. In other words, these statistical formulae allow the analyst to demonstrate, using 13 loci in STR testing, that an individual profile matching the profile generated from the crime evidence will not be found in any other unrelated person on earth.

The product rule is the statistical method used to calculate the random match probability. The product rule states as follows: When events are independent, then the frequency of their combined occurrence may be determined by multiplying the individual frequency of an occurrence by one another. For example, think of a single playing card and a full deck of cards. The likelihood (or frequency of occurrence) of selecting the two of hearts from a deck on one try is 1:52. The likelihood (or frequency of occurrence) of selecting it from one deck and then selecting the same card from a second deck is 1:52 times 1:52, or 1:2,704. And, since each of the 52 cards is different, the likelihood of selecting a two of hearts and then the queen of spades from the same deck is 1:52 times 1:51, or 1:2,652. Applying this rule to the likelihood of locating the same genetic profile, the product rule is translated as follows: The frequency of occurrence of the alleles found at one locus is multiplied by the frequency of occurrence of the alleles found at a second locus, which is multiplied by the frequency of occurrences of all the other alleles in the remaining 11 loci.[15] The total *random match probability* is the probability of that exact genetic profile being found in someone, other than the suspect, within the human population.[16]

[15] In order to take advantage of the product rule, STR markers used in forensic typing were chosen to insure independence. In other words, the inheritance of a profile at one location does not influence the inheritance of a particular profile at any other locations.

[16] The Federal Bureau of Investigations (FBI) has determined frequency of allelic occurrences at the different loci in a number of human populations. For reporting purposes, however, the FBI uses the four most common populations: Caucasians, African Americans, Southwestern Hispanics and Southeastern Hispanics.

The negative, or absence of the profile being found amongst others, is a very important distinction to make. In the forensic identification of an offender, the analyst discusses *probabilities*. The analyst is not saying the offender's profile is the only one of its kind in existence, simply because not every person on earth has been DNA profiled, so a direct comparison to all human DNA is impossible. Instead, there can only be an estimate of the probability of finding the same profile among all possible arithmetic combinations.

Prosecutors, defense attorneys, and judges frequently make mistakes in their translations or descriptions of the statistical frequencies. These errors can result in misstatements of fact, mistrials, or worse, miscarriages of justice. In answer to the question, "What is the chance of a coincidental DNA match?" one common erroneous statement is, "The numbers mean there is only a million to one chance the DNA came from someone else." A correct statement would be, "The statistical frequency that the evidence profile will be found in a population of unrelated individuals is one time *in 'X'* billion or quadrillion." Another fallacy is, "Anyone else with the same profile has an equal chance of having committed the crime." Assuming the statement could be used in a situation involving identical twins, an evaluation of all of the evidence and its applicability to each twin would significantly alter the equality of chance. Obviously, and importantly, the random match probability regarding the DNA evidence in no way projects odds or likelihood of guilt.

DNA Evidence in Criminal Investigation and Prosecution

In addition to proving identity, DNA evidence can prove and/or corroborate other elements of substantive crimes such as sexual battery, burglary, robbery, or homicide. Its constraints are only limited by a prosecutor's creativity. In proving all of the elements of a crime, all the questions of who, what, when, where, and sometimes, why, must be answered. Extrapolating meaning from the source, location and type[17] of DNA evidence found during an investigation can help answer these questions.

Where was the DNA sample found? Assume, for example, that a DNA sample, blood, is recovered from gravel in the victim's driveway. This evidence may corroborate the victim's description of being assaulted in her driveway. Or, if a DNA sample matching a victim is found in a defendant's home, this evidence can refute the defendant's claim that the victim was never there and help to prove where the crime occurred.

DNA evidence can also help determine *what* happened during a crime. Fingernail scrapings of only the victim's skin under the victim's fingernails, combined with scratches along his neck, may illustrate or corroborate the victim's attempt to remove a ligature or human hands from around his throat. As another example, saliva samples found under a bed may indicate that a victim was hiding there before she was discovered.

The location of DNA samples can also help demonstrate a sequence of events, or *when* a specific incident occurred. For example, identifying a single DNA source from blood spots on an outside wall but a mixture of sources from blood on an inside wall may support a theory that an incident began outdoors before escalating to mutual combat and justifiable force indoors. Finding a victim's DNA in a blood sample taken from the defendant's weapon could help explain *why* the victim acceded to the defendant's demands.

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[17] Type means single human source, human mixture or non-human DNA.

DNA evidence can even help demonstrate purpose or intent. For example, DNA evidence taken from the inside of a ski mask arguably indicates the intent to commit the crime—in certain circumstances, finding, taking and wearing a ski mask must have been purposeful behavior. Finding a mixture of a defendant's blood and a victim's blood on a victim's towel recovered from a garbage can may demonstrate the defendant's purposeful conduct of removing and concealing evidence. DNA evidence found inside a burglary victim's home is similar to fingerprint evidence – consistent with the absence of consent when the homeowner does not know the person who left the sample.

DNA evidence may also be used to impeach a defendant's description of events. For example, in sexual assault cases, defendants frequently deny even knowing the victim. Confronted with his DNA found in the victim's vagina, the defense theory quickly shifts to one of consent. DNA evidence can also enhance a witness's credibility. DNA evidence from the defendant, recovered from an article of clothing described by the witness, bolsters the accuracy of the witness's initial description.

In sum, DNA's evidentiary value can go far beyond proving the defendant's identity. DNA evidence should be used just as any other form or type of evidence—to corroborate, validate and/or impeach evidence or testimony.

TRIAL ISSUES

The trial issues of concern to prosecutors are admissibility, discovery, case presentation, defense attacks, and proper closing argument. The sections to follow will discuss these topics in detail.

Admissibility

Understanding DNA testing and DNA forensic identification is essential to arguing its admissibility. Fortunately, admissibility battles have been won in both courthouses and statehouses for the past 15 years.[18] Thirteen states have statutes specifically authorizing admission of DNA evidence.[19] Through case law, more than 35 states have admitted into evidence the PCR method of copying or amplifying DNA; more than 30 have admitted into evidence the results of STR testing; more than 25 states have admitted into evidence population frequency data or statistics; and more than 11 states have admitted mitochondrial DNA evidence.

In those states where DNA evidence has not been admitted, either one of two standards, or a hybrid of the two, must be met in order for the admission to be legally sufficient. One standard is that articulated in *Frye v. United States,* 293 F. 1013 (D.C.Cir. 1923). The other standard is that articulated in *Daubert Merrill Dow Pharmaceuticals, Inc.,* 509 U.S. 579, 113 S.Ct. 2786, 125 L.Ed.2d 469 (1993). Occasionally, a jurisdiction will use a variant derived from the cases or state statute, as in the Colorado Criminal Rules of Evidence 702 and 403. The *Frye* standard requires that the scientific evidence offered has been generally accepted by the scientific community to which it relates and that the testing procedures used properly applied the scientific technique. The *Daubert* standard requires a demonstration of the validity of the underlying scientific theory, the reliability of the scientific test, and the usefulness of the scientific evidence to the jury.

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[18] *Andrews v. State*, 533 S.2d 841 (3rd DCA 1988).

[19] For case or statute listings by technology and jurisdiction, contact APRI.

Generally, admissibility standards are met through the testimonial or documentary evidence specific to the case, the pertinent scientific literature and all the authority from other jurisdictions throughout the country. Because the requisite evidence may be introduced in documentary form, and because DNA evidence—be it RFLP or STR—has been admitted in the majority of the country, an argument can be made that a hearing is unnecessary. To date, mitochondrial DNA has been admitted in 11 states and the same is true—many admissibility issues have been litigated. The goal is to limit the admissibility hearing by persuading the court of the degree to which the scientific and legal communities have accepted the scientific and mathematical methods that serve as the basis for DNA testing and forensic identification.

Discovery

Integral to the legal sufficiency of the discovery in a case is the communication and coordination between the laboratory analyst, the prosecutor, and law enforcement. A prosecutor must meet two responsibilities: compliance with criminal procedure and ethical rules. Generally, the facts subject to appellate review in pretrial discovery matters are: (1) facts describing the State's efforts to make available scientific test reports and relevant raw data used in a given case, and (2) facts describing the State's efforts to maintain and preserve the evidence.[20]

To ensure criminal procedure compliance, it may be useful for prosecutors to work with the laboratory to coordinate a generic discovery response, independent of a specific case. Subsequently, the prosecutor may supply the discovery, or parts thereof, and confidently invite the defense attorney to visit the lab, at the mutual convenience of the analyst and the attorney, to obtain copies of discoverable materials that are specifically available.

The prosecutor's ethical responsibilities pertaining to biological evidence are (1) to preserve evidence that possesses both an apparent exculpatory value *and* that cannot be obtained by other reasonably available means,[21]

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[20] *Arizona v. Youngblood*, 488 U.S. 51, 102 L.Ed.2d 281, 109 S. Ct. 333 (1988).

[21] *California v. Trombetta*, 467 U.S. 479, 81 L.Ed.2d 413, 104 S.Ct. 2528 (1984), citing *Brady v. Maryland*, 373 U.S. 83, 10 L.Ed.2d 215, 83 S.Ct. 1194 (1962).

and (2) to ensure that the defendant has access to the "basic tools" or "raw materials integral to the building of an effective defense."[22] The best practice for successful discovery is clear communication between the lab and the prosecutor about evidence availability during the investigation and before the commencement of the case. Investigators, doctors, and scientists may investigate cases vigorously, as long as they act in good faith. It is possible that evidentiary samples are exhausted through the testing processes in the course of an investigation, such that no evidence is available for testing by the defense. Prosecutors should disclose this fact in their initial response. Consistently, appellate courts look to the factual record to find support of reasonable acts by the prosecution *done in good faith*.[23]

The Case-in-Chief

Less is more, generally speaking, in the courtroom presentation of DNA evidence. There are two important goals to achieve with the direct examination of the state's DNA expert witness, the analyst: (1) to assure the jury they can rely upon DNA by educating them about its widespread use and accuracy, and (2) to explain to the jury how the DNA evidence incriminates *this* defendant in *this* crime. Too often time is wasted, confusion is caused, or collateral issues are injected in a direct examination that is too broad and too long, including, for example, a lengthy explanation of the underlying science, the mechanisms of the testing machinery, or the historical development of national proficiency standards. Compare the direct examination of the DNA analyst to that of a medical doctor, who is also an expert witness: Would you ask the doctor about all aspects of pathology, how x-ray machinery works, or the historical development of medical licensing requirements? In other words, if you know your lab is accredited, why create in the mind of a juror the idea that accreditation must be "proven?"

The first goal, jury persuasion, can be accomplished easily by reviewing the many uses of DNA—e.g., to determine paternity, identify missing persons or remains of the dead, isolate or prevent disease through

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[22] *Ake v. Oklahoma*, 470 U.S. 68, 84 L.Ed.2d 53, 105 S.Ct. 1087 (1985).

[23] For a more detailed review of these cases, see APRI's *The Silent Witness*, Winter 2003.

genome typing, protect endangered animal species, and exonerate or exclude individuals based on collected crime scene evidence. To assure the jury they can rely upon this evidence, it is necessary to demonstrate the specific qualifications of your witness: his or her education, training, and experience examining DNA in school; training and experience with forensic DNA typing; ongoing education and professional development through scientific associations or conference participation; and a thorough description of the analyst's current employment as a forensic scientist in a forensic laboratory. An analyst employed in a forensic laboratory, whose job responsibility is to conduct forensic identification testing, is the best person to testify about forensic identification results.

The second goal, jury education about the incriminating meaning of the DNA evidence, is accomplished through pretrial preparation of the DNA analyst. In the courtroom presentation, ask the analyst to explain the meaning of the 100% match between the crime scene profile and the offender profile on specific pieces of evidence. How the analyst responds can be powerful. To say that "the profile generated from testing the saliva swabbed from the bite mark on the victim's breast matches the profile generated from the offender sample at each and every one of the 26 spots examined" more powerfully explains the evidence than to say that "no exclusion could be made between sample 1(A) and sample 3." When both analyst and prosecutor talk about evidence in the complete context of the crime, the value of the DNA evidence is enhanced.

Questions to the analyst about population frequency data also need to be discussed in advance. For example, the prosecutor might ask, "What are the chances that this profile would occur in a randomly selected population of unrelated people?" Also, "What is the world's human population?" Followed by, "So, the probability that the profile generated from testing this *crime scene evidence* is identical to the profile generated from testing the *defendant's sample*, is so small that, in order to find it again, a population larger than the world's entire population would be necessary?"

It is also important to discuss, before trial, the analyst's willingness to attribute the source of the crime scene evidence to the defendant, within a reasonable degree of scientific certainty. If testing excluded someone

else as the source of the sample, the direct testimony of the analyst should say so. Finally, questions about the remaining sample, or lack thereof, should be addressed in the analyst's direct testimony to explain the reason for preserving the remaining sample, i.e., to provide for re-testing or further testing as a quality control measure. That fact speaks to the certainty of results everyone can have.[24] The analyst can then reinforce the value of re-testing and the consequent confidence in the test results when responding to cross-examination and re-direct questioning.

Defense Experts

Learning as early as possible what a credible defense attack of the DNA evidence could be is important to effectively responding. When the DNA analyst provides a report, then is the time to ask if there are any foreseeable criticisms, attacks, concerns, or problems. When there have been no identifiable issues relating to the DNA (or lack thereof), prosecutors have been successful in limiting the defense expert's testimony or even excluding it from trial.[25] It may be possible to exclude or limit the expert's testimony by questioning his credentials or the relevance of the testimony in the context of this case.[26] Is the expert a forensic DNA examiner, a non-forensic scientist, an academic, or a population geneticist? Has the expert worked in a *lab*? Is he or she testifying about an issue in the case or about arguments academics can and should have elsewhere?

If the defense expert is allowed, it is important to limit the witness's testimony to a specific attack on the case *evidence*. A soft beginning to a cross-examination, however, can often induce the defense witness to agree with the reliability and accuracy of the science or the method of analysis. If the defense witness attacks the statistics but agrees that the science is accurate, the match between crime scene evidence and offender sample is not discredited. If he or she attacks the science, compare and contrast sharply the specific scientific, forensic, and non-forensic work experience of your analyst with that of the defense expert. Which

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[24] Additionally, the testimony regarding sample preservation and sample availability enhance the security of the conviction from successful post-conviction attack.

[25] See *Maryland v Gross*, 134 Md.App. 528, 580 (Md. 1999).

[26] Contact APRI's DNA Forensic Program for resources relating to defense DNA experts.

expert works solely on forensic science cases in a lab that is accredited or working towards accreditation? Which expert is in a lab every working day of the year? Who works daily with other qualified scientists available to review the expert's work? Who has examined the evidence in the case? When did the defense expert learn about the case?

DNA is an easily validated and trustworthy science. Statistics is not new or fuzzy math. Consequently, a defense expert cannot attack the fields of science and statistics credibly. To be relevant, experts should challenge facts in a case. Prepare your response strategically, bearing in mind that the DNA evidence is merely one piece of evidence in your entire case.[27]

Closing Argument

While a number of improper closing arguments can result in a conviction reversal, there are essentially two that relate to DNA evidence. One potential problem occurs with the prosecutor's discussion or description of the statistics in the case. The random match probability pertains to the likelihood of reoccurrence of the *crime scene profile* in another unrelated person in the population. This probability, cannot be characterized as proof of the defendant's guilt at trial, but merely as evidence in the case—powerfully persuasive, but only evidence nonetheless. The second issue that has been raised successfully is argument pertaining to the defendant's actual testing or burden of re-testing the DNA evidence. It is permissible argument that remaining sample is a quality control of the lab.[28] Approximately a dozen states have found the following argument permissible: that there is an absence of defense evidence that contradicts or conflicts with the DNA evidence presented.[29]

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[27] For a more detailed discussion about preparation, see APRI's *The Silent Witness*, Fall 2002.

[28] National Research Council (NRC-II), *The Evaluation of Forensic DNA Evidence*, National Academy Press, Washington DC, 1996 and *See also State v. Saleh*, 2001 Wash.App. LEXIS 1461 (Div.1)(2001)(Allowing a prosecutor to permissibly argue that a defendant had an opportunity to independently test or re-test DNA evidence without burden shifting).

[29] *Seager v. Iowa*, 2002 US LEXIS 6343 (2002); See *State v. Varnado*, 753 So.2d 850 (La.App. 4 Cir.)(1999); *See also State v. Faison,* 59 S.W.3d 230 (Tex. 2001) and *State v. Ledet*, 2001 WL856433 (Finding proper rebuttal to argue defendant could have hired his own lab to substantiate allegations of error).

CONCLUSION

Maximizing the value of forensic DNA evidence requires considerable education, preparation and work, but the benefits are readily apparent. DNA technology has the potential to vastly improve the administration of justice and to assure public confidence and trust in the criminal justice system. For further educational and resource materials, please contact the American Prosecutors Research Institute's DNA Forensics Program.

A CKNOWLEDGEMENTS

APPENDIX I
GLOSSARY OF DNA TERMS[30]

ADENINE—One of the four bases that are found in nucleotides – the subunit of DNA. Adenine, abbreviated "A," binds only to Thymine. See also *Base, Nucleotide, Thymine*

ALLELE—A specific sequence of nucleotides, the variant forms of a gene. Alleles within a gene, depending upon their sequence, determine traits. Humans have two alleles at each locus – one inherited from each parent. See also *Diploid, Gene, Loci*

ALLELE FREQUENCY—The proportion of a particular allele among the chromosomes carried by individuals in a population.

AMELOGENIN—A system for determining the gender of the donor of a sample by rendering different sized bands or peaks for the X and Y chromosomes. See also *Chromosome, X Chromosome, Y Chromosome*

AMINO ACID—Any of a class of 20 molecules that are combined to form proteins in living things. The sequence of amino acids in a protein and hence protein function are determined by the genetic code.

AMPLIFICATION—Using the PCR process to create many copies of a specific DNA fragment. See also *PCR*.

AUTORADIOGRAPH (Autorad)—A photographic recording on X-ray film on which radioactively or chemiluminescently labeled probes have left a mark determining the positions of particular DNA fragments on a gel. See also *Gel Electrophoresis.*

AUTOSOME—Any chromosome other than the sex chromosomes X and Y. Humans have 22 autosomes. See also *Chromosome, X Chromosome, Y Chromosome.*

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[30] Definitions were adapted from the following sources:
Federal Bureau of Investigation Forensic Science Systems Unit, 1998 CODIS DNA Laboratory Survey; Center for Health Policy Research, A Glossary of Terms Associated with DNA Typing and Genetic Testing; National Research Council, The Evaluation of Forensic DNA Evidence; Office of Technology Assessment, Genetic Witness: Forensic Uses of DNA Tests (July 1990); Birgid Schlindwein, A Hypermedia Glossary of Genetic Terms, http://www.weihenstephan.de/~schlind/genglos.html; Cancer Web, The On-line Medical Dictionary, http://www.graylab.ac.uk/omd/index.html; MedicineNet.com, Medical Dictionary, http://www.medicinenet.com; Department of Energy, *Primer on Molecular Genetics*, in HUMAN GENOME 1991-92 PROJECT REPORT (1992); National Institute of Justice, The Future of Forensic DNA Testing: Predictions of the Research and Development Working Group 2000; Inman and Rudin, An Introduction to Forensic DNA Analysis. Boca Raton. CRC Press, 1997. Some of these definitions were taken from *DNA Technology in Forensic Science*, (1992) National Research Council, Washington, D.C.: National Academy Press.

BAND—The visual image representing a particular DNA fragment on an autoradiograph. See also *Autoradiograph*

BAND SHIFT—An artifact of gel electrophoresis by which DNA fragments of the same size migrate at different rates through a gel. See also *Gel, Gel Electrophoresis*.

BASE—Component part of DNA nucleotides. Two of the DNA bases are pyrimidine in nature (cytosine and thymine), and the other two are purine (adenine and guanine). See also *Adenine, Base Pair, Cytosine, Guanine, Nucleotide, Thymine*

BASE PAIR—Two complimentary nucleotides (A & T; C & G) held together by a weak hydrogen bond. A series of base pairs forms nucleotides. See also *Nucleotide*

BASE SEQUENCE— The order of nucleotide bases in the alleles of genes that combine to create the chromosomes contained in a DNA molecule.

BASE SEQUENCE ANALYSIS—A method, sometimes automated, for determining the base sequence.

CAPILLARY ELECTROPHORESIS—DNA samples are placed in a small, thin (capillary) tube filled with a gel or polymer. When the capillary is subjected to a high voltage current the DNA fragments migrate through the tube. See also *Gel, Electrophoresis*

CEILING PRINCIPLE—A conservative procedure in calculating the likelihood of a random match whose proponents claim it should be used to account for population substructures. One hundred persons from each of 15-20 genetically homogeneous populations spanning the range of racial groups in the United States are sampled. For each allele, the highest frequency among the groups sampled or 5%, whichever is larger, is used in the calculation. See also *Allele, Interim Ceiling Principle, Population, Population Substructure, Random Match Probability*

CELL—Basic units of living organisms, which can be either unicellular or multicellular. An animal cell contains the nucleus, cytoplasm, mitochondria, and other organelles. Cells self-replicate through a process of cell division that includes copying all of its contents and then dividing in half. See also *Mitochondria, Nucleus*

CHEMILUMINESCENCE—The process of labeling RFLP sequences with alkaline phosphatase, rather than ethidium bromide. This is chemical

rather than radioactive tagging. See also *Random Fragment Length Polymorphism*

CHROMOSOME—Structures housed in the nucleus of cells on which genes are arranged in linear order. A full compliment of chromosomes is 46 – 22 pairs of autosomes and two sex chromosomes. See also *Autosome, Cell, X Chromosome, Y Chromosome*

CODIS—See *Combined DNA Index System*

COMBINED DNA INDEX SYSTEM (CODIS)—CODIS refers to the hardware and software that links a network of local (LDIS), state (SDIS), and national (NDIS) databases housing DNA samples of convicted offenders and crime scene samples. CODIS also refers to the FBI's own DNA database.

COMPLEMENTARY SEQUENCES—Nucleic acid base sequences that form a double-stranded structure by matching base pairs; the complementary sequence to G-T-A-C is C-A-T-G.

CROSSING-OVER—When genes from the parents combine to create the child's chromosomes during cell division such that the child's cell has a different genotype than either of the parents' cells. See also *Cell, Gene, Genotype*

CYTOSINE—One of the four bases that are found in nucleotides – the subunit of DNA. Cytosine, abbreviated "C," binds only to Guanine. See also *Base, Nucleotide, Guanine*

DQ ALPHA—See *Human Leukocyte Antigen DQ Alpha*

DEGRADATION—The breaking down of DNA by chemical or physical means.

DENATURATION—The separation of double-stranded DNA into two, single strands of DNA. See also *Double Helix*

DEOXYRIBONUCLEIC ACID (DNA)—Genetic material present in the nucleus of a cell. This molecule contains all of the information necessary to code for all living things. Half of the material is inherited from each biological parent. DNA is organized into a double helix composed of two complementary chains of paired nucleotides. See also *Cell, Double Helix, Nucleotides, Nucleus*

DIPLOID—Having two sets of paired chromosomes. After the haploid egg and sperm (or gametes) combine, the resulting cell has a full complement of chromosomes, half from each parent. See also *Cell, Chromosome, Gamete, Haploid*

DNA—See *Deoxyribonucleic Acid*

DNA sequence— The relative order of base pairs, whether in a fragment of DNA, a gene, a chromosome, or an entire genome.

DOUBLE HELIX—The shape that two paired strands of DNA assume when bonded together. A double helix is visually described as a twisting ladder.

ELECTROPHORESIS—The technique for separating large molecules by placing them in a medium (usually a gel) and applying an electric current. Molecules travel through the medium at different rates depending on their size. See also *Capillary Electrophoresis, Gel Electrophoresis*

ENZYME—A protein that is capable of speeding up, but not changing the nature of, a specific chemical reaction; a biological catalyst. See also *Restriction Enzyme*

EPITHELIAL CELLS—Body surface cells such as skin cells, vaginal cells, and buccal (inner cheek) cells. Epithelial cells are found on both outer body surfaces and inner body cavity surfaces. See also *Cell*

GEL—A semisolid medium used to separate molecules by electrophoresis. Forensic analysis usually utilizes an agarose or acrylamide gel to separate DNA molecules. See also *Electrophoresis*

GENE—The fundamental unit of heredity. A gene is an ordered sequence of nucleotides located at a particular position on a particular chromosome. See also *Allele, Chromosome, Nucleotide*

GENETICS— The study of the patterns of inheritance of specific traits.

GENOME—The total genetic makeup of an organism, usually denoted by the number of base pairs. The human genome is approximately 3 billion base pairs long. See also *Base Pair*

GENOTYPE—The genetic constitution of an organism, as distinct from its expressed features or phenotype. See also *Phenotype*

GUANINE—One of the four bases that are found in nucleotides – the subunit of DNA. Guanine, abbreviated "G," binds only to Cytosine. See also *Base, Nucleotide, Cytosine*

HAPLOID—Having one set of chromosomes (half, the full set of genetic material), as a gamete. See also *Chromosome, Diploid, Gamete*

HARDY-WEINBERG EQUILIBRIUM—Refers to a population with random mating. In a human population, Hardy-Weinberg equilibrium results in independent association, a condition required in order to

apply the product rule. See also *Allele, Independent Association, Population, Product Rule*

HETEROZYGOUS—Having different alleles at a particular locus. See also *Allele, Locus*

HOMOZYGOUS—Having the same allele at a particular locus. See also *Allele, Locus*

HYBRIDIZATION—The process of pairing a single strand of DNA with its complementary strand by matching base pairs, usually with the assistance of a primer. See also *Base Pair, Primer*

INDEPENDENT ASSOCIATION—In a diploid organism, the frequencies with which an organism inherits alleles from each parent are unrelated. See also *Allele, Diploid*

LINKAGE—The tendency for certain genes to be inherited together because they are in close proximity on the same chromosome. These genes would be less likely to separate during crossing-over. See also *Chromosome, Gene, Crossing-Over*

LINKAGE EQUILIBRIUM—When all possible genotypes of a locus appear in a population with equal frequency. See also *Genotype, Locus, Population*

LOCUS (Loci)—*s.* LOCUS, *pl.* LOCI The physical location of a gene on a chromosome. Any one of the possible alleles for a gene may be present at the gene's locus or along the genes' loci. See also *Allele, Chromosome, Gene*

MARKER—A gene of known location on a chromosome and phenotype that is used as a point of reference in the mapping of other loci.

MITOCHONDRIA (Mitochondrion)—Small organelles located in the cytoplasm of a cell that are responsible for energy production and cellular respiration. See also *Cell*

MITOCHONDRIAL DNA (mtDNA)—DNA organized on small, rounded chromosomes inside the mitochondria of a cell. Mitochondrial DNA is maternally inherited. See also *Cell, Chromosome, Mitochondria*

MULTIPLEXING—A test kit for analyzing several loci at once.

NUCLEOTIDE—A component part of DNA consisting of a base, a phosphate molecule, and a sugar molecule. Nucleotides are the raw building blocks of DNA. Nucleotides are paired according to the particular base and then linked to form alleles. See also *Base, Base Pair*

NUCLEUS—A compartment within a eukaryotic cell that houses the chromosomes. The nucleus is separated from the cytoplasm and other organelles in the cell by the nuclear envelope. See also *Cell, Chromosome, Eukaryote*

PCR—See *Polymerase Chain Reaction*

POLYMARKER (PM)—A PCR-based test (Amplitype PM PCR Amplification and Typing Kit and Amplitype PM + DQ Alpha PCR Amplification and Typing Kit) commonly used since 1994 for human DNA identification testing. The kit types five specific regions of the DNA: LDLR (low density lipoprotein receptor), GYPA (glycophorin A), HBGG (hemoglobin G gammaglobin), D7S8, and GC (group specific component)

POLYMERASE—In DNA typing procedures, an enzyme that initiates the synthesis of double-stranded DNA. See also *Enzyme*

POLYMERASE CHAIN REACTION (PCR)—A process for amplifying (copying) DNA. Two primers target a particular DNA sequence (one primer for each complementary strand of DNA) to be amplified. In a series of cycles with varying temperatures, the DNA strand is denatured and copied with the help of a polymerase enzyme. Since each copy is denatured and copied in subsequent cycles, the DNA is amplified exponentially. See also *Amplification, Denaturation, Enzyme, Polymerase, Primer*

POLYMORPHISM—The existence of more than one possible allele at a given locus; genetic variance. A polymorphism occurring in more than 1 percent of a population would be considered useful for genetic analysis. See also *Allele, Locus*

POPULATION—A stable group of randomly interbreeding individuals relatively isolated from other groups of the same species.

POPULATION SUBSTRUCTURE—The existence of small mating groups within a larger community.

PRIMER—A short, pre-existing chain of nucleotides to which a polymerase can attach complementary nucleotides and replicate the strand of DNA. See also *Nucleotides, Polymerase*

PROFICIENCY TESTING—A test to evaluate the competence of technicians and the quality of performance of a laboratory. Testing can be open or blind (depending on whether the person being tested is aware that the sample is part of a test) and internal or external (depend-

ing on whether the test is administered by the laboratory itself or an out-side agency).

PRODUCT RULE—When two or more loci are tested, the allele frequency at each locus is multiplied in order to estimate the overall frequency of that person's genetic profile. This formula assumes both linkage equilibrium and independent association. See also *Locus, Independent Association*

PROTEIN—A large molecule composed of one or more chains of amino acids in a specific order; the order is determined by the base sequence of nucleotides in the gene coding for the protein. Proteins are required for the structure, function, and regulation of the body cells, tissues, organs, and each protein has unique functions.

RANDOM MATCH PROBABILITY—The probability that the DNA in a random sample from the population will have the same profile as the DNA in the evidence sample. See also *Population*

RESTRICTION ENZYME—An enzyme that recognizes a specific series of nucleotides and cuts a DNA molecule wherever the series appears. See also *Enzyme*

RESTRICTION FRAGMENT LENGTH POLYMORPHISM (RFLP)—Variation in the length of DNA fragments produced by a restriction endonuclease (an enzyme) that cuts at a polymorphic locus.

RFLP—See *Restriction Fragment Length Polymorphism*

ROBUST—In genetics, referring to the fact that a person's genetic profile, or DNA sequence, remains constant throughout that person's life.

SEQUENCING—Determination of the order of nucleotides (base sequences) in a DNA or RNA molecule or the order of amino acids in a protein.

SHORT TANDEM REPEAT (STR)—Small regions of the DNA that contain short segments (usually 2,3,4, or 5 bases long) repeated several times in tandem (side-by-side). Thirteen STR sequences have been selected for the Combined DNA Index System (CODIS). See also *CODIS*

STR—See *Short Tandem Repeat*

SUBSTRATE—In forensics, the material on which a biological sample is deposited at a crime scene – for example a pair of pants, a shirt, or bed sheets.

SWGDAM—See *TWGDAM*

THYMINE—One of the four bases that are found in nucleotides – the subunit of DNA. Thymine, abbreviated "T," binds only to Adenine. See also *Base, Nucleotide, Adenine*

TWGDAM—Technical Working Group on DNA Analysis Methods. An organization made up largely of individuals from the FBI and public crime laboratories that recommend guidelines for DNA identification testing. The working group recently changed its name to Scientific Working Group on DNA Analysis Methods or "SWGDAM".

VALIDATION—A process for the scientific community at large to properly assess whether a particular procedure can reliably obtain a desired result, determine the conditions under which such results can be obtained, and determine the limitations of the procedure.

VARIABLE NUMBER TANDEM REPEATS (VNTR)—Repeating units of a DNA sequence; a class of loci utilized in Restriction Fragment Length Polymorphism testing. See also *Loci, Restriction Fragment Length Polymorphism*

X CHROMOSOME—A sex chromosome, present twice in female cells and once in male cells. See also *Autosome, Cell, Chromosome*

Y CHROMOSOME—A sex chromosome present once in male cells, and transmitted directly from a father to all his sons. See also *Autosome, Cell, Chromosome.*

APPENDIX II
RESOURCE LIST

1. Butler, John M., "Forensic DNA Typing," *Overview and History of DNA Typing*, Academic Press, 2001.

2. National Research Council (NRC-II), *The Evaluation of Forensic DNA Evidence*, National Academy Press, Washington DC, 1996.

3. National Institute of Justice, Special Report, "Using DNA to Solve Cold Cases," U.S. Department of Justice; July 2002.

The following websites will provide information about the forensic application of DNA:

4. www.ndaa-apri.org – National District Attorneys Association and American Prosecutors Research Institute (NDAA-APRI)

5. www.ojp.usdoj.gov – Office of Justice Programs (OJP)

   OJP, a division of the United States Department of Justice, supports training, programs, statistics and research.

6. www.ojp.usdoj.gov/nij – National Institute of Justice (NIJ)

   NIJ is the research, development, and evaluation agency of the U.S. Department of Justice and is solely dedicated to researching crime control and justice issues.

7. www.ncjrs.org – National Criminal Justice Reference Service (NCJRS)

   NCJRS is a federally funded resource offering justice information to support research, policy, and program development worldwide.

8. www.dnaresource.com – Smith Alling Lane, P.A.

   Smith Alling Lane provides a website sponsored by Applied
   Biosystems that contains information about the latest developments in
   forensic DNA policy and statistics.

9. www.denverda.org – Denver (CO) District Attorney's Office

   The Denver District Attorney's Office maintains a website that cata-
   logs opinions concerning DNA evidence admissibility and use.

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