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DNA IDENTIFICATION: APPLICATIONS AND ISSUES

Eric A. Fischer, Resources, Science, and Industry Division

Updated January 12, 2001

Abstract. This report provides an overview of how the genetic information contained in DNA is used for identification, and a discussion of issues associated with those uses. It begins by discussing the unique properties of genetic information that make it a powerful tool for identification and what is involved in making identifications from DNA. Next is a description of current federal programs and activities, followed by discussion of issues raised by the development of this new technology. Major issues include the use of DNA identification in the criminal justice system, impacts of technological improvement, and privacy.

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ABSTRACT

This report provides an overview of how the genetic information contained in DNA is used for identification, and a discussion of issues associated with those uses. It begins by discussing the unique properties of genetic information that make it a powerful tool for identification and what is involved in making identifications from DNA. Next is a description of current federal programs and activities, followed by discussion of issues raised by the development of this new technology. Major issues include the use of DNA identification in the criminal justice system (including sample backlogs, databases, and postconviction DNA analysis), impacts of technological improvements, and privacy. Legislative activity in the 106th Congress focused on several criminal-justice issues; for detailed discussion, see CRS Report RL30694, *DNA Evidence: Legislative Initiatives in the 106th Congress*. For discussion of genetic privacy and discrimination, see CRS Issue Brief IB98002, *Medical Records Confidentiality*, and CRS Report RL30006, *Genetic Information: Legal Issues Relating to Discrimination and Privacy*. This report will be updated at least annually.

DNA Identification: Applications and Issues

Summary

DNA technology can provide useful identifying information in many situations, such as in solving crimes, determining paternity, and identifying human remains. Research is resulting in improvements in sensitivity and power and reductions in cost. Such use and improvements are raising several policy issues.

The use of DNA in identification results from its unique characteristics: It is a complex molecule, containing much information. Each person has billions of identical copies. The structure of the molecule varies from person to person and is inherited, so the DNA of relatives is more similar than that of unrelated people. Also, DNA is easily preserved with the structure intact.

Identification requires comparing DNA whose source has not been determined with DNA whose source is known. The first step is to characterize corresponding DNA sequences from samples. The resulting profiles are then compared. If they differ, the samples did not have the same origin. If they match, then they could have come from the known source, or from someone else who has an identical profile. The science of population genetics provides ways of estimating quantitatively the chances that the matched DNA could have come from another source.

Databases or indexes are often used in DNA identification. They might contain profiles of persons whose identity is known, such as convicted felons, or whose identity is not known, such as from crime scene samples or unidentified remains. The Combined DNA Index System (CODIS), administered by the FBI, contains both kinds. When a profile is obtained from a relevant sample, the database can be searched to determine if a match is found. Thus, a suspect may be identified when a profile from a crime-scene sample is searched against profiles of convicted felons.

Congress has enacted several laws relating to DNA evidence. The DNA Identification Act of 1994 (P.L. 103-322) authorized CODIS and a grants program for state and local laboratories, and addressed quality control and privacy issues. The Antiterrorism and Effective Death Penalty Act of 1996 (P.L. 104-132) expanded CODIS and established a grants program that required states, to be eligible, to collect DNA samples from persons convicted of felony sex crimes. The Crime Identification Technology Act of 1998 (P.L. 105-521) established a grants program that funds a broad range of activities, including several related to DNA typing. The National Institute of Justice (NIJ) and the Bureau of Justice Assistance (BJA) administer those and other relevant grants programs. The National Institute of Standards and Technology (NIST), the Armed Forces Institute of Pathology (AFIP), and the Army Criminal Investigation Laboratory (USACIL) also have significant DNA identification activities.

Policy issues raised by the use of DNA in identification include how best to eliminate the large backlog of samples awaiting processing for CODIS, whether to broaden the offenses that qualify, how to respond to the increasing number of requests for postconviction DNA analysis, how to address privacy issues, and what impacts the broadening applications of the technology may have.

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Introduction

As our understanding of human genetics has become more and more sophisticated, scientists have developed increasingly powerful tools using genetic information to aid in identifying individual people. DNA can be helpful in many situations where identification is at question: For example, in criminal cases, forensic DNA evidence can link a suspect, or a weapon such as a knife, to a crime scene. It can also exclude a suspect. The best known sources of DNA evidence are blood and semen, but increasingly it can be obtained from other items, such as a bottle cap, a toothbrush, a bite mark on a piece of cake, or a fragment of a contact lens. Another use is to identify human remains, such as of a soldier killed in battle. Or it might be used to determine biological relationship, such as in paternity cases. This report focuses on using human DNA to determine individual identity, but animal and plant DNA can also be used, to identify species (for example, did a sample of meat come from a protected whale species?) or even individuals (did a seed pod found in a truck come from a particular tree at a crime scene?).[1]

Those and similar developments raise several policy issues, including the use of genetic information in the criminal justice system, the impacts of continuing technological improvements, and the effects of the technology on privacy and individual rights. This report provides an overview of how genetic information is used in identification and some of the issues associated with those uses. It begins by discussing the unique properties of genetic information that make it a powerful tool for identification and what is involved in making identifications from physical evidence. Next is a description of current federal programs and activities related to DNA identification, followed by discussion of issues raised by the development of this new technology. Legislation activity in the 106th Congress focused on several criminal-justice issues; for detailed discussion, see CRS Report RL30694, *DNA Evidence: Legislative Initiatives in the 106th Congress*.

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[1] The examples in parentheses refer to real cases. The first involved testing whale meat purchased in markets in Japan — C.S. Baker & S.R. Palumbi, "Which Whales Are Hunted? A Molecular Genetic Approach to Monitoring Whaling," *Science* 265 (1994): 1538. The second was a 1993 murder case in which the DNA in seed pods in a defendant's truck were found to match the DNA of a palo verde tree at the crime scene — G. Sensabaugh and D.H. Kaye, "Non-human DNA Evidence," *Jurimetrics Journal* 38 (1998): 1-16.

Why DNA Can Be Used in Identification

The use of DNA in identification — sometimes called DNA typing or DNA profiling[2] — results from its unique characteristics. Those characteristics also affect how it can be used and the issues that arise from using it. Key features are described below.

It is a complex molecule, containing much information. DNA is a chemical, deoxyribonucleic acid, consisting of modular components, called nucleotides, that are connected in a linear sequence. Each nucleotide contains one of four bases — called adenine, cytosine, guanine, and thymine, often designated by their initials A, C, G, and T. Each DNA molecule consists of two complementary strands, with each adenine on one strand paired with a thymine on the other, and each guanine with a cytosine. The sequence of bases strung along a DNA molecule contains the information that forms the basis of the genetic code of humans and most other organisms.[3] Much of the growing body of knowledge about DNA comes from efforts of the Human Genome Project, a major goal of which is to create a map of the code and identify the sequence of bases on the DNA molecule.[4] DNA identification technologies tap a small part of the large set of information that the molecule contains.

Each person has billions of identical copies of DNA in the cells of the body. Most of the billions of cells in a person's body contain identical sets of DNA molecules[5] — approximately 3 billion base-pairs per cell altogether. Most of the DNA is contained in 23 pairs of chromosomes in the nuclei of cells. Within each pair,

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[2] It is sometimes also called DNA testing. In this report, for clarity, that term is used only to refer to medical tests.

[3] For a more in-depth description, see Human Genome Program, U.S. Department of Energy, *Primer on Molecular Genetics* (Washington, DC, 1992), [http://www.ornl.gov/hgmis/publicat/primer/primer.pdf].

[4] The Human Genome Project is an international effort performed with both government and private funding. The U.S federal effort began in 1988 with the signing of a memorandum of understanding between the Department of Energy (DOE) and the National Institutes of Health (NIH). At DOE, the program is housed in the Office of Biological and Environmental Research (OBER) within the Office of Science (see the DOE genome project website at [http://www.sc.doe.gov/production/ober/hug_top.html] for more information). At NIH, the program resides in the National Human Genome Research Institute, NHGRI (see the NHGRI website [http://www.nhgri.nih.gov:80/index.html] for more information). NHGRI was established by statute, under the name National Center for Human Genome Research, in the National Institutes of Health Revitalization Act of 1993 (P.L. 103-43). The DOE genome efforts do not have separate statutory authorization.

[5] The major exceptions are germ cells (eggs, sperm, and their precursors) which have 23 single, not paired, chromosomes, and red blood cells, which have no DNA. DNA extracted from blood comes from white blood cells. The DNA sequences in different germ cells are not identical, because each contains half the full DNA complement, partially mixed through a process called recombination. Also, rare changes, called mutations, can occur in a sequence through damage, errors in replication, or other means. Only mutations that occur in the germ cell line can be inherited — they are called germ-line mutations; all others are called somatic mutations.

one chromosome is inherited from the mother and the other from the father. Some DNA, inherited only from the mother, is also contained outside the cell nucleus, in structures called mitochondria, which are small bodies with many copies in each cell. Because the human body contains so many copies of DNA, even a very small amount of body fluids or tissues, such as blood or skin, can yield useful identifying information.

The structure of the molecule, and therefore the information it contains, varies from person to person. DNA sequences from any two people will be the same at many points along the DNA molecule, but the overall nuclear DNA sequence of each person is unique, except for identical twins, who have identical DNA.[6] On a single chromosome, individual *alleles,* which are discrete components of a DNA sequence, are inherited intact. Each pair of chromosomes has many pairs of alleles[7] (the total number is as yet unknown), with one member of the pair inherited from the father and the other from the mother. The region of a pair of chromosomes containing a pair of alleles is called a *locus.* The DNA of the two alleles inherited at any particular locus may have identical or different base-pair sequences.[8] It is the substantial variation in DNA among people that is characterized with the technologies used in DNA identification.

The structure is inherited, so the DNA of close relatives is more similar than that of distant relatives or unrelated people. Since half of a person's DNA comes from each parent,[9] full siblings also share half their alleles, on average, and grandparents and first cousins, one quarter. However, since a son receives his Y chromosome from his father, all the alleles on that chromosome are identical to the father's and are inherited through the paternal line alone.[10] Similarly, all alleles in mitochondria are identical to the mother's and are inherited through the maternal line alone.[11] Therefore, the mitochondrial DNA of a male, for example, will be identical to that of his maternal grandmother, and his Y-chromosome DNA identical to that of his paternal grandfather. The inheritance patterns of DNA mean that analyzing a person's DNA can also provide identifying information about a relative.

Most of a person's DNA has no known biological function. Genes are segments of DNA that contain the code for making specific chemicals (mostly proteins). Humans have tens of thousands of genes (the exact number is not yet known), but

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[6] except for mutations and certain other minor variations.

[7] except for the sex chromosomes in males (see below).

[8] The technical term is *homozygous* if they are identical and *heterozygous* if they are different.

[9] Exceptions are mitochondrial DNA and the sex chromosomes in males, in whom the Y chromosome is much smaller than the X and contains many fewer alleles.

[10] The power of using this male-line inheritance of the Y-chromosome was demonstrated in the genetic research that provided strong support for the assertion that Thomas Jefferson fathered at least one son by Sally Hemings — Eugene A. Foster and others, "Jefferson Fathered Slave's Last Child," *Nature* 396 (1998) 27–28.

[11] except for mutations.

they comprise only a small part of a person's DNA, most of which has no known function. However, many nonfunctional segments of a person's DNA can be characterized with the techniques of molecular biology; those segments are called *markers*. The distinction between genes and markers has implications for use in identification that will be discussed later.

DNA is easily preserved with the structure intact. DNA is a surprisingly stable chemical, and sequences can be easily preserved intact in dried or frozen samples. However, DNA can be degraded, particularly in warm or moist environments or in the presence of many common chemicals. The ability to use DNA in identification depends both on the size and the condition of the sample. That has consequences for sample collection, handling, and storage in applications such as law enforcement.

How DNA Is Used in Identification

Using DNA in identification requires comparing DNA whose source has not been determined (such as from a crime scene or from a child in a paternity case) with DNA whose source is known (such as from a suspect or from a putative father). Four basic steps are involved: characterization, comparison, calculation, and interpretation. They are each discussed below, along with implications for applications and issues.

Characterization

The first step is to characterize or profile corresponding DNA sequences in the samples to be compared. For forensic evidence in a criminal case, one or more samples of blood, semen, or other sources of DNA related to the crime will be processed, as will usually a sample from one or more suspects. It is not possible with current technology to characterize the entire DNA sequence. Instead, alleles at specific loci are characterized. The technique used depends on the particular kind of marker. The major kinds of markers in use today are VNTRs, STRs, mtDNA, and certain simpler sequences.

For most of the fifteen years during which DNA typing has been used in forensics, VNTRs (variable number of tandem repeats) have been the major kind of marker used. They have the greatest potential power to identify or exclude, because they vary more from person to person than any other DNA system used in identification. They consist of sections of DNA in which a sequence of about 15–70 bases is repeated many times. Analysis of a sample using VNTRs measures the approximate number of repetitions in each marker examined. That number varies substantially from person to person. Analysis of VNTRs uses RFLP[12] technology, which requires that substantially more DNA be present, and in good condition, in the

[12] RFLP stands for *restriction fragment length polymorphism.* A chemical called a restriction enzyme cuts the DNA molecule in certain (restricted) places corresponding to particular base sequences. The result is pieces of DNA called *restriction fragments* that vary among people — are *polymorphic* — in *length.* RFLP and VNTR are sometimes used interchangeably to refer to the analysis of VNTRs using RFLP technology.

sample than do the other systems described below. Therefore, many samples that are degraded or have very small amounts of DNA cannot be processed using VNTRs.

STRs (short tandem repeats) also consist of repeated sequences, but the number of bases repeated is smaller (2–4), as is the total length of DNA comprising an allele (approximately 100–300 bases for STRs versus 500–10,000 for VNTRs). STRs are not as variable as VNTRs, and therefore more loci must be typed to obtain the same resolving power as with VNTRs.[13] Nevertheless, STRs can be examined with much smaller samples (for example, requiring a bloodstain the size of a pinhead rather than one the size of a quarter coin), for two reasons. First, DNA-amplification procedures (known as PCR — the polymerase chain reaction) can be used. The process uses the ability of DNA to replicate itself to make many identical copies from a small initial amount of DNA. The procedure does not yet work with VNTRs. Second, because the sequences are shorter, they are less likely to be damaged if the sample is degraded. Therefore, such samples can often yield more usable results with STRs than with VNTRs. STRs also have some other technical advantages over VNTRs. In particular, they can be processed in the laboratory much more quickly and they are easier to interpret. For those reasons, STRs, which first became available for forensic use a few years ago, are quickly replacing VNTRs as the standard marker for typing.

Mitochondrial DNA (mtDNA) can be used in even smaller or more degraded samples than STRs. That is because the relevant DNA sequences are moderately short (approximately 1,200 bases or less), there are thousands of copies per cell, and they can be amplified. This kind of DNA can be extracted even from skeletal remains and has been used, for example, in identifying the remains of armed forces personnel from conflicts as far back as World War II.[14] Because of the way it is inherited, mtDNA from remains must be compared with samples obtained from maternal relatives. Therefore, it cannot be used to distinguish among maternally related persons. Also, mtDNA is not as variable as STRs and VNTRs, and it is therefore not as powerful a tool for making positive identifications. It also takes much longer to analyze than STRs.

Some other nuclear DNA markers, such as DQA and Polymarker, are also used to aid in identification. Those consist of simpler DNA sequences than STRs or VNTRs. They can be amplified and require only small amounts of DNA, but they are less variable than STRs or VNTRs, and some of the loci used are closely linked to genes or are genes themselves. However, they can be processed very rapidly and are often used to determine quickly whether a potential source of DNA should be eliminated or investigated further using more sensitive marker systems. They are also used extensively in paternity cases.

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[13] Twelve STR loci provide about the same power to identify as five VNTR loci for most populations (Dennis Reeder, National Institute of Standards and Technology, conversation with the author, 9 June 2000). The current standard set of STR loci established by the Federal Bureau of Investigation for use in law enforcement contains 13 loci.

[14] Armed Forces DNA Identification Laboratory, "AFDIL…about us…mtDNA," [http://www.afip.org/oafme/dna/mtdna.htm], 22 October 1999.

Comparison

Once DNA from the samples is characterized, the resulting profiles are compared. If one or more alleles differ in the two samples, they are said not to match. In that case, if the analysis was performed correctly, the samples did not have the same origin. In the case of a criminal suspect, that means that the suspect did not produce the DNA found in the evidence. In a paternity case, it means that the putative father was not the biological father. If an attempt is being made to identify remains using mtDNA, it means that the person whose remains were typed is not related to the supposed maternal relatives. This use of DNA as a means of exclusion is a powerful and important use, particularly in the criminal justice system. A common estimate is that one-quarter of named suspects are excluded in cases where DNA evidence is used.[15] Also, in the past few years, more than 60 people convicted of violent crimes in the United States have been subsequently exonerated as a result of DNA evidence.[16]

If the profiles match — that is, if they are identical at every locus — then they could have come from the same source. Alternatively, the source could be someone else who has an identical profile for the markers that were examined. The way such a match is treated in DNA evidence has usually been different than for other sources of identifying information, such as fingerprints. In the latter, a match has usually been considered either a positive identification or inconclusive — for example, either the suspect left the fingerprints or could not be ruled out — depending on the quality of the print. For DNA, in contrast, the science of population genetics provides in many cases a way of estimating quantitatively the chances that the DNA could have come from another source. The chances of such a coincidental match depend on both the number of markers used and the variability exhibited by those markers. Therefore, results of DNA analysis have usually been given in terms of the probability that such a match could be coincidental rather than a conclusion about identity.[17]

Calculation

For several years, there was controversy about how best to perform calculations to estimate probabilities in DNA identification, but that issue is now largely, although not completely, settled. The specific procedures can be complex and will vary depending on the circumstances and the system used. However, there are two basic steps:

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[15] Louis J. Freeh, *Ensuring Public Safety and National Security Under the Rule of Law: A Report to the American People on the Work of the FBI 1993 - 1998*, Federal Bureau of Investigation, 2000, 36, available at [http://www.fbi.gov/library/5-year/5YR_report_.PDF].

[16] National Commission on the Future of DNA Evidence, *Postconviction DNA Testing: Recommendations for Handling Requests*, National Institute of Justice, NCJ 177626 (September 1999), 2, available at [http://www.ojp.usdoj.gov/nij/pubs-sum/177626.htm].

[17] However, those distinctions between interpretation of fingerprint and DNA analysis are beginning to blur (see section on interpretation below).

The population frequency of each allele in the profile — that is, the percentage of people who have that allele in the population examined — is identified. In most cases, those frequencies are estimates drawn from extensive data banks such as those compiled by the FBI.[18] Subpopulations within a country such as the United States vary in the frequencies of different alleles, and therefore comparisons may be made to data from the most relevant subpopulation, usually a racial or linguistic group, or, if it is not known what group the source of DNA belonged to (as is often the case with DNA from crime scenes), from two or more subpopulations.

The frequencies are multiplied together, with the aid of appropriate mathematical formulas, to produce an estimated probability that someone drawn at random from the population would have that profile. If enough loci are used, those probabilities can be very small — on the order of one chance in billions or even trillions — even though the frequency of any given allele is likely to be on the order of 1–10%.

In some cases, probability calculations may not be appropriate or useful. For some loci, the frequencies of alleles in the population as a whole might not be known, or there might be too few loci or too few alleles at a locus to yield useful probability estimates. In such a case, a match means that a putative source cannot be excluded, but there might be many other potential sources. Or the particular case might not require a calculation. For example, if the question is which of two men fathered a child, no calculation is necessary if the profile of one yields a match and the other does not. Or, in a case of identification of remains with mtDNA, it might be known that a soldier came from one of four families. If the maternal mtDNA profile of only one of the four yields a match, then the soldier came from that family. However, if more than one source produces a match in either of those two examples, then DNA evidence cannot resolve the question unless more loci can be examined. Another situation that can present problems for making useful calculations is where DNA from more than one person is in the sample. In such mixed samples, if the DNA contributed by different people cannot be separated,[19] then it might only be possible to determine if someone can be excluded.

Interpretation

There are two essential questions involved in interpreting the results of a DNA identification: Did the DNA come from the person (or family) who is thought to be its source, and what is the significance of the answer for the case at hand?

The probability calculation, when performed, is used to help answer the first question. If the probability estimate is low enough, the expert who provides it may

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[18] See, for example, Federal Bureau of Investigation, *VNTR Population Data: A Worldwide Survey* (5 volumes), (Quantico, VA: FBI Academy, 1993). The data are drawn from anonymized samples from blood banks or other sources. They should not be confused with the databanks housing DNA profiles of convicted criminals, which are discussed below.

[19] For example, if the DNA comes from different kinds of tissues or fluids, as in a vaginal swab from a sexual assault, it is often possible to separate the male and female DNA. However, if DNA from more than one male is present, separating those is often not possible.

declare a positive identification — that the person in question was in fact the source of the DNA.[20] However, the question of what probability level (or other criterion) is required to ensure a positive DNA identification is not yet settled, and in many cases, experts may be reluctant to make such a declaration, preferring to provide simply the probability estimate for the jury or other trier of fact to interpret. That is in contrast to the situation with fingerprints, which are accepted as unique (even in identical twins, unlike DNA) but for which probabilities are not calculated. Fingerprints have been used effectively for much longer than DNA, so little question remains about how they can provide positive identification. In addition, they are not as amenable to statistical analysis as is DNA evidence, although that is beginning to change as automated fingerprint analysis systems are developed and refined. However, with DNA, triers of fact may interpret a very low probability estimate as a positive identification, provided that there are no significant questions about how the evidence was handled, the quality of the laboratory analysis, or special circumstances of the case.

Once a positive identification has been made (or found very likely), its significance must be determined. That would seem straightforward but is not always. For example, in a rape case involving DNA evidence, if the probability of a coincidental match is very small, that would be strong evidence of a sexual encounter but would not of itself be proof of guilt, since the encounter might have been consensual. However unlikely, it is also possible, for example, that there was a laboratory error or even that blood or other sources of DNA might have been planted by someone wishing to frame a suspect. For those and other reasons, a match probability in a criminal case should not be interpreted as a probability of guilt.[21]

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[20] For example, in 1997, FBI experts switched from simply providing probability estimates to stating in addition that a person whose profile matches a sample is the source of the sample, provided that the calculated match probability is less than about 1 in 260 billion (Freeh, *Ensuring Public Safety*, 35; Jennifer Smith, Laboratory Director, DNA Unit 1, Federal Bureau of Investigation, "Comments regarding R&D Report," *Proceedings, National Commission on the Future of DNA Evidence*, 9 April 2000, [http://www.ojp.usdoj.gov/nij/dnamtgtrans9/trans-e.html]). For comparison, that probability is about 1/50 the chance that a person drawn at random from the entire world population would have that profile. The original scientific work that provided the basis for the use of fingerprints in identification established that the probability of a second person having the same fingerprint pattern on a given digit was about 1/40 the reciprocal of the world population at the time — National Research Council, *The Evaluation of Forensic DNA Evidence*, (Washington, DC: National Academy Press, 1996), 57. The average match probability yielded by using 12 of the 13 core STR markers used by the FBI is about 1 in 700 billion (James F. Crow, "Research and Development Working Group Report," *Proceedings, National Commission on the Future of DNA Evidence*, 28 February 1999, [http://www.ojp.usdoj.gov/nij/ dnamtgtrans4/trans-c.html]). Nevertheless, many forensic experts prefer to provide probabilities but not state firm conclusions about the source of the DNA.

[21] Such misinterpretations are sometimes called "the prosecutor's fallacy." This can be a surprisingly complex issue, and a technical discussion of it is beyond the scope of this report. For more information, see NRC, *Evaluation of DNA Evidence*, 133, 198; and David H. Kaye and George F. Sensabaugh, Jr., "Reference Guide on DNA Evidence," in *Reference Manual on Scientific Evidence*, 2nd ed. (Washington, DC: Federal Judicial Center, 2000), 539,

(continued...)

However, it does provide evidence for the jury or judge to consider in determining whether the accused was the perpetrator of the crime.

Databases

Databases or indexes used in DNA identification are of three basic kinds. One provides the allele frequencies that are used in calculations to estimate profile frequencies and match probabilities. Such population databases are drawn from anonymous samples and are separated or stratified according to the population group (usually based on ethnicity or race) of the donors, since allele frequencies, and therefore match probabilities for different profiles, may differ among such groups. Sources are various, such as blood donors or medical patients.[22]

The second kind contains profiles of persons whose identity is known. One example is databases with STR or VNTR profiles of convicted felons or of victims of unsolved crimes (such as the CODIS database system, discussed below). Another is databases with profiles of missing persons or their biological relatives, such as mtDNA profiles of maternal relatives of armed forces personnel lost in past military conflicts (see below). When a profile is obtained from a relevant sample whose source is not known, the database can be searched to determine if a match, called a *cold hit*, is found. For example, in an increasing number of cases, a suspect is identified when a DNA profile from a crime-scene sample is searched against a database containing profiles of persons convicted of violent crimes or other felonies.

The third kind of database contains profiles of persons whose identity is not known. Samples might come from crime scenes or unidentified remains. When a profile is obtained from a relevant sample whose source is known, the database can be searched for cold hits, as above. For example, a profile obtained from a suspect in another crime can be searched against a forensic database of profiles associated with crimes for which there are no suspects. In 1999, a DNA profile of a male murdered in Florida was found to match DNA evidence from nine rapes, three in Florida and six in Washington, D.C.[23]

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[21] (...continued)
available at [http://air.fjc.gov/public/fjcweb.nsf/pages/16].

[22] Such so-called "convenience samples" might seem unlikely to generate accurate frequencies of the distribution of alleles in the underlying population, but they work surprisingly well (NRC, *Evaluation of DNA Evidence*, 126).

[23] Federal Bureau of Investigation, "First 'Cold' Hit Recorded in National DNA Index System!", Press Release, 21 July 1999, [http://www.fbi.gov/pressrm/pressrel/pressrel99/coldhit.htm]; Kathleen Sweeney, "DNA testing links rapes to slain man," *Florida Times Union*, Thursday, 22 July 1999, Sec. A, 1. The index system is discussed below.

Federal Agency Programs and Activities

Federal agencies with significant involvement in DNA identification activities include the Federal Bureau of Investigation (FBI), the National Institute of Justice (NIJ), and the Bureau of Justice Assistance (BJA) in the Department of Justice; the National Institute of Standards and Technology (NIST) in the Department of Commerce; and the Armed Forces Institute of Pathology (AFIP), the Army Central Identification Laboratory, Hawaii (CILHI), and the Army Criminal Investigation Laboratory (USACIL)in the Department of Defense. Major activities are described below.

Federal Bureau of Investigation

Most forensic DNA evidence is developed and used by local or state law enforcement agencies. However, the FBI provides many important services to those agencies and is responsible for processing DNA evidence for cases under federal civilian jurisdiction.

FBI Laboratory. Major activities of the FBI Laboratory include training of federal, state, local, and foreign law enforcement and crime laboratory personnel; research and development in DNA typing technologies; development of an integrated national DNA database program; and providing expert testimony in the courts.[24] The laboratory was the first public crime laboratory in the United States to perform analysis of forensic DNA evidence, creating its DNA Analysis Unit in 1988. It is currently the only such laboratory performing mtDNA analyses.

The laboratory also administers the Combined DNA Index System. CODIS is a distributed system of local, state, and national DNA databases that are linked electronically, permitting the comparison of profiles stored in different locations. Begun as a pilot program in 1990, it was authorized in the DNA Identification Act of 1994 (P.L. 103-322). More than 40 states now participate. CODIS has several indexes. One, a convicted offenders index, contains DNA profiles of persons convicted of qualifying crimes. Current law does not specify qualifying federal crimes. However, section 811(b)(2) of the Antiterrorism and Effective Death Penalty Act of 1996 (P.L. 104-132) required that states, to be eligible for grants to improve their capacity to perform forensic DNA analyses and certain other activities,[25] collect DNA samples from persons convicted of sexual felonies. All 50 states now require

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[24] See the laboratory Web site at [http://www.fbi.gov/programs/lab/labhome.htm] for more information.

[25] Specifically, the grants are made "to carry out all or part of a program to establish, develop, update, or upgrade…computerized identification systems…, the capability to analyze…DNA…, and automated fingerprint identification systems…," provided that they are compatible with the relevant corresponding FBI systems (Sec. 811(b)(1)). Those State Identification Systems formula grants are administered through the Bureau of Justice Assistance.

samples from such persons. Most also collect samples from persons convicted of murder or other violent crimes, and several from those convicted of any felony.[26]

Other indexes are a forensic index, which contains profiles of DNA samples taken from crime scenes (especially from cases without any suspects); a population file, which contains information on allele frequencies to be used in calculating match probabilities; and a missing persons index containing profiles from unidentified remains.

The national component of CODIS, called NDIS, the National DNA Indexing System, has been in operation since 1998. Laboratories in 24 states currently contribute DNA profiles to NDIS.[27] While CODIS initially used VNTR markers, they are largely being replaced with the more powerful STRs (see section on sample backlogs below). NDIS uses thirteen core STR markers that have been established as a standard set by the FBI.

DNA Advisory Board. DNA typing is technology intensive. That makes issues of quality control and assurance especially important. To help address such issues, P.L. 103-322 required that the FBI Director establish a DNA Advisory Board (DAB) to recommend quality assurance standards for forensic DNA analysis. Following submission of DAB recommendations, the director established standards effective October 1, 1998. They replaced standards that had been established by the Technical Working Group on DNA Analysis Methods (TWGDAM), a practitioners' group representing federal, state, and local forensic laboratories and supported by the FBI. As of 1998, most of the publicly funded crime laboratories in the United States followed DAB or TWGDAM standards, and about half were accredited by an official organization.[28] DAB is scheduled to dissolve at the end of 2000, at which time its functions will be transferred to the renamed TWGDAM, now called the Scientific Working Group on DNA Analysis Methods (SWGDAM).

National Institute of Justice

The National Institute of Justice (NIJ), a research agency within the Office of Justice Programs, engages in several kinds of activities related to DNA evidence. The institute supports research to improve speed, reliability, and sensitivity of DNA profiling and to reduce its cost. There are three main activities, administered through the NIJ Office of Science and Technology: the DNA Five Year Research Program, the Forensic DNA Laboratory Improvement Program, and the National Commission

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[26] Dwight E. Adams, Statement, Legislative Hearing on H.R. 2810, the "Violent Offender DNA Identification Act of 1999", H.R. 3087, the "DNA Backlog Elimination Act", and H.R. 3375, the "Convicted Offender DNA Index Systems Support Act"; Subcommittee on Crime, House Committee on the Judiciary, 13 March 2000, [http://www.house.gov/judiciary/adam0323.htm].

[27] Adams, Hearing Statement.

[28] Greg W. Steadman, *Survey of DNA Crime Laboratories, 1998*, Bureau of Justice Statistics Special Report NCJ 179104, February 2000, 3, available at [http://www.ojp.usdoj.gov/bjs/abstract/sdnacl98.htm].

on the Future of DNA Evidence. The DNA Five Year Research Program (1999–2003), is awarding $5 million per year to support research aimed at reducing the cost and time of processing DNA samples, developing technologies to enhance the reliability of DNA analysis and perform analyses at crime scenes, and developing standard test materials and new markers.[29]

The Forensic DNA Laboratory Improvement Program was initiated in FY1996 with DNA Identification Grants, authorized in P.L. 103-322 (Sec. 210302). Appropriations for the program have grown annually (see table). From FY1996–FY1999, the program awarded grants to state and local governments, up to 75% of the total cost of the project, to develop and improve the abilities of forensic laboratories to analyze DNA evidence. In FY2000 and FY2001, funds were awarded under a new series of grants authorized by the Crime Identification Technology Act of 1998 (P.L. 105-121), with half allocated by NIJ to the DNA Identification Program and half to the elimination of sample backlogs (see below). That program can fund up to 90% of the total cost of a project.[30]

Appropriations for State and Local DNA Laboratory Support, FY1996–FY2001

(in millions of current dollars)

Year	Amount
FY1996	1.0
FY1997	3.0
FY1998	12.5
FY1999	15.0
FY2000	30.0
FY2001	30.0

Note: FY2000 includes funds for addressing sample backlogs. Source: FY1996, P.L. 104-134; FY1997, 104-208; FY1998, P.L. 105-119; FY1999, P.L. 105-277; FY2000, P.L. 106-113; FY2001, P.L. 106-553.

A 1996 NIJ-funded report[31] led Attorney General Reno to charter, in September 1997, the National Commission on the Future of DNA Evidence (hereinafter called

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[29] National Institute of Justice, *Technology Development Portfolio: Investigative and Forensic Sciences,* [http://www.ojp.usdoj.gov/nij/ sciencetech/invest.htm], 16 January 2000.

[30] Information on NIJ grant programs can be found on the agency's Web site at [http://www.ojp.usdoj.gov/nij/funding.htm].

[31] Edward Connors and others, *Convicted by Juries, Exonerated by Science: Case Studies in the Use of DNA Evidence to Establish Innocence After Trial,* National Institute of Justice Research Report, NCJ 161258 (June 1996), [http://www.ncjrs.org/pdffiles/dnaevid.pdf].

the DNA Commission). This four-year NIJ commission is examining several topics, including the postconviction use of DNA, legal concerns, training and technical assistance, and future technological developments. Its members include representatives from federal, state, and local law enforcement agencies, the judiciary, defense lawyers, and other groups and areas of expertise. Rather than producing a single final report, the commission is developing reports on specific issues and making recommendations on an ongoing basis. In 1998, the commission first identified the need for a special effort to address a backlog of hundreds of thousands of DNA samples, taken from convicted persons and from crime scenes, that have not yet been processed (see section on sample backlogs below).[32] A 1999 report[33] recommended procedures for handling postconviction DNA-typing requests.

Bureau of Justice Assistance

The Bureau of Justice Assistance supports state and local criminal justice programs. It administers formula grants, including Byrne grants (42 U.S.C. 3751), which can be used, among other purposes, to develop or improve the DNA-analysis capabilities of forensic laboratories; and State Identification Systems grants, which can be used, among other purposes, to help laboratories develop their capabilities with respect to CODIS.[34]

National Institute of Standards and Technology

The National Institute of Standards and Technology (NIST) has played a major role in the development of standards for DNA profiling, as part of its long-standing role in developing technological standards and measurements generally.[35] The standard reference materials that NIST has produced, both for VNTR and STR analysis, are used by laboratories to test the accuracy of their analyses.[36] They are therefore important components of quality-assurance and control activities. NIST also performs research on new DNA-typing technologies, both through the Biotechnology Division (within Scientific and Technical Research and Services) and the Advanced Technology Program (within Industrial Technology Services). Many of the DNA-forensic activities in which NIST engages are performed in collaboration

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[32] Paul Ferrara, "CODIS Backlog Elimination Report," *Proceedings, National Commission on the Future of DNA Evidence*, 8 June 1998, [http://www.ojp.usdoj.gov/nij/dnamtgtrans2/trans-f.html]. Specific actions to eliminate the backlog were later recommended to the Attorney General.

[33] DNA Commission, *Postconviction DNA Testing*.

[34] Information on BJA grant programs can be found on the agency's Web site at [http://www.ojp.usdoj.gov/BJA/html/fund1.html]. For information on Byrne grants, see also Garrine P. Laney, *Crime Control Assistance Through the Byrne Program*, CRS Report 97-265, 8 August 2000.

[35] For general information on NIST, see Wendy H. Schacht, *The National Institute of Standards and Technology: An Overview*, CRS Report 95-30, 6 July 2000.

[36] For more information on STRs, see John M. Butler and Dennis J. Reeder, "Short Tandem Repeat DNA Internet Database," [http://www.cstl.nist.gov/biotech/strbase/], 24 May 2000.

with other agencies, such as the NIJ and Department of Defense, and with private industry.

Department of Defense

The two major uses of DNA identification by the Department of Defense (DOD) are in criminal investigation (see below) and in the identification of remains of military personnel. To aid in such identification, DOD established in 1988 the Office of the Armed Forces Medical Examiner within the Armed Forces Institute of Pathology,[37] under the Assistant Secretary of Defense for Health Affairs. DNA was first used to identify combat fatalities in 1991 in Operation Desert Storm. At that time, the DNA Registry[38] was formed, consisting of two components. The Armed Forces Repository of Specimen Samples for the Identification of Remains (AFRSSIR) collects and stores DNA samples taken from active duty and reserve personnel.[39] Armed Forces personnel are required to provide DNA samples for deposit in the repository. Currently, the repository holds more than 3 million specimens. When a casualty occurs that requires DNA identification, the Armed Forces DNA Identification Laboratory (AFDIL) processes relevant samples to produce nuclear (STR and other PCR-based systems) or mtDNA profiles. AFDIL also performs analyses of samples in other selected cases.[40] Two examples of the latter are assisting the FBI in identifying remains after the fire at the Branch Davidian compound in Waco, Texas, in 1993, and assisting the National Transportation Safety Board in identifying passengers who died in the crash of TWA Flight 800 in 1996.

Another DOD unit involved in DNA identification of remains is the United States Army Central Identification Laboratory, Hawaii (CILHI).[41] The laboratory recovers and identifies remains of military personnel lost in past conflicts and unaccounted for. AFDIL performs mtDNA analysis on the recovered remains. AFDIL maintains a database of mtDNA profiles from maternal relatives who volunteer to provide samples, for matching against profiles from remains. As of June 1999, 154 matches had been obtained (including 112 from Vietnam and 34 from World War II). The most prominent was the identification of First Lieutenant Michael J. Blassie, USAF, whose remains had been interred in 1984 as the Vietnam Unknown in the Tomb of the Unknowns in Arlington National Cemetery. Lt. Blassie had been lost in 1972 in Vietnam. Samples of mtDNA from maternal relatives in seven families involved in the

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[37] See Department of Defense, "Armed Forces Institute of Pathology (AFIP)," DOD Directive 5154.24, 28 October 1996, available at [http://web7.whs.osd.mil/pdf/ d515424p.pdf].

[38] See Department of Defense DNA Registry, "Welcome to…," [http://www.afip.org/oafme/dna/history.htm], 22 October 1999.

[39] The target date for completion of collection from reserve personnel is December 2002 (AFRSSIR, "Repository History," [http://www.afip.org/oafme/dna/History.htm], accessed 27 June 2000). Specimens may be retained for up to 50 years. However, personnel may request destruction of specimens once they have completed their service.

[40] For guidelines, see "AFDIL...DNA Services," [http://www.afip.org/oafme/dna/outsidedna.htm], 22 October 1999.

[41] See "The United States Army Central Identification Laboratory, Hawaii," [http://www.cilhi.army.mil/], 19 June 2000.

investigation were compared with mtDNA from a bone fragment taken from the tomb, and the samples from the Blassie family provided a very close match.

The United States Army Criminal Investigation Laboratory (USACIL) performs DNA analysis for criminal investigative agencies within the Department of Defense. The laboratory analyzes approximately 500 cases per year and recently converted from VNTR to STR analysis using the 13 core loci. USACIL participates in CODIS, providing profiles for NDIS of evidentiary samples for specific cases and searching for matches in cases under investigation, where appropriate. However, the armed forces do not currently collect samples from convicted offenders (see the section below on issues). USACIL works only on cases with a military connection.[42]

Other Agencies

Three other federal agencies support research that has contributed to the scientific basis for advances in DNA identification. The Office of Biological and Environmental Research, in the Department of Energy, and the National Institutes of Health, in the Department of Health and Human Services, are the lead agencies for the Human Genome Project. They also support research on ethical, legal, and social aspects of DNA identification and other applications of advances in genomics.[43] The National Science Foundation, an independent agency, supports relevant basic research in molecular biology and in the social sciences at universities and other research institutions.[44]

Relevant Public Laws

When DNA evidence first became available in the United States, questions often arose about the quality of analyses and the absence of widely accepted standards.[45] Also, the typing of specimens was expensive,[46] and its availability to many state and local law enforcement agencies was therefore uneven. The DNA Identification Act of 1994, a subtitle of the Violent Crime Control and Law Enforcement Act of 1994 (P.L. 103-322), addressed quality control and privacy issues. It authorized the DNA

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[42] This description is based on information provided by Larry Chelko, Director, USACIL, email communication with the author, 25 August 2000.

[43] Details can be found at the program Web sites — for DOE, see [http://www.ornl.gov/hgmis/elsi/elsi.html], and for NIH, see [http://www.nhgri.nih.gov/About_NHGRI/Der/Elsi].

[44] For general descriptions of research programs in these agencies, see the following CRS reports: Richard E. Rowberg, *Department of Energy Research and Development Budget for FY2001: Description and Analysis,* CRS. Report RL30445, 12 September 2000; Pamela Wolfe Smith, *The National Institutes of Health: An Overview,* CRS Report 95-96, 15 September 2000; Christine M. Matthews, *U.S. National Science Foundation: An Overview,* CRS Report 95-307, 20 September 2000.

[45] National Research Council, *DNA Technology in Forensic Science,* (Washington, DC: National Academy Press, 1992), 97–110.

[46] Ibid., 153–154.

Identification Grants program administered by NIJ (see above). The law authorized appropriations for the program through FY2000. It also authorized use of Drug Control and System Improvement Grants for similar purposes (42 U.S.C. 3751; those grants are part of the Edward Byrne Memorial State and Local Law Enforcement Assistance Programs, or Byrne grants). The DNA Identification Act required that forensic laboratories receiving the grants follow specified quality assurance and privacy provisions. Recipients are to meet current quality-assurance standards, as specified by the FBI director, and undergo regular proficiency testing in DNA analysis. The use of DNA samples analyzed by recipients are restricted to use in law enforcement, judicial proceedings, and criminal defense. However, anonymized samples can also be used in population databases, research, and quality control activities.

The act also provided for the establishment of the FBI's DNA Advisory Board, to recommend quality-assurance and proficiency-testing standards to the director (Sec. 210303), and required that FBI personnel engaging in DNA analysis undergo regular proficiency testing (Sec. 210305). It also authorized the establishment of CODIS indexes containing profiles of persons convicted of crimes and samples recovered from crime scenes or unidentified remains (Sec. 210304). The Consolidated Appropriations Act of 2000 (P.L. 106-113) additionally provided for an index of profiles from "samples voluntarily contributed from relatives of missing persons" (Sec. 120).

The Antiterrorism and Effective Death Penalty Act of 1996 (P.L. 104-132) authorized the application of CODIS to federal crimes and those committed in the District of Columbia (Sec. 811(a)(2)). It also authorized grants to state and local government for participation in CODIS. To be eligible, states must collect DNA samples from persons convicted of felony sex crimes (see above). Also, the National Institutes of Health Revitalization Act of 1993 (P.L. 103-43) established as one of the purposes of the National Human Genome Research Institute "reviewing and funding proposals to address the ethical and legal issues associated with the genome project."

The Crime Identification Technology Act of 1998 (P.L. 105-521, 112 Stat. 1871) established the State Grant Program for Criminal Justice Identification, Information, and Communication. Grants can be awarded for a broad range of activities to, among other things, improve state capabilities in crime identification and promote compatibility and integration among local, state, and federal identification systems, and including accreditation and certification programs relating to DNA analysis. Funding is authorized through FY2003.

Current and Emerging Issues

Some of the issues discussed below, particularly those related to law enforcement, were the subject of legislation in the 106th Congress. See CRS Report RL30694 for a discussion of those legislative initiatives.

Law Enforcement and Criminal Justice

Sample Backlogs. DNA samples are now collected in all 50 states from persons convicted of certain crimes. Also, DNA evidence is routinely gathered from crime scenes and victims in cases of rape, murder, and other violent crimes. As DNA technology has improved and states have increased its scope in criminal justice activities (see next section), the workload in forensic laboratories has increased. For example, from 1996 to 1997, casework increased 40%, from a total of about 15,000 to 21,000, and convicted-offender samples increased more than 60%, from 72,000 to 116,000.[47] Given limited resources, forensic laboratories must prioritize the analysis of those and other samples they receive. Therefore, many samples, such as from scenes of crimes for which there are no suspects, and from convicts who are not suspects for additional crimes, are given lower priority. Currently, there is a backlog in the United States of several hundred thousand such samples that have not been analyzed and entered into CODIS databases. That means that profiles from those samples are not available for database searches. Given that "cold hits" have been identified through such searches, the DNA Commission and others have proposed that funding be increased to process that backlog. Also, the $30 million appropriated by Congress in FY2000 for DNA grants included funding for processing backlogged samples.

An additional factor is the conversion of existing profiles from VNTRs to STRs. Some states have not converted to using the core STR markers, and profiles that use other markers cannot be searched against NDIS or CODIS STR records. Conversion requires that a DNA sample be retyped — reanalyzed with STR technology. More than 200,000 existing profiles may need such retyping. Also, there are many "owed" samples — that is, samples that can be taken under existing law but have not been. Those include many paroled or released convicts. The number of such owed samples nationwide may exceed the number currently backlogged.[48]

Failure to process backlogs may have several consequences. Crimes that might be solved with the help of a database match may remain unsolved. That is of particular concern in cases where a perpetrator is likely to perform additional crimes, or where a database match would prevent an innocent person from being wrongly suspected or perhaps even charged with the crime. Also, crime-scene samples from unsolved crimes may eventually be destroyed as statutes of limitations expire, permanently eliminating any possibility of typing any DNA evidence.

The size of the backlog makes the question of prioritization particularly important, but it is not straightforward. For example, typing a person's DNA is usually much less expensive than typing DNA from a crime scene, because in the latter case, several samples must usually be processed and, unlike with convicted-offender samples, processing cannot usually be automated with existing technology. That might suggest that the highest priority should be given to typing convicted

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[47] Steadman, *Survey*, 6.

[48] See "CODIS Offender Database Backlog Reduction Discussion," *Proceedings, National Commission on the Future of DNA Evidence*, 23 November 1998, [http://www.ojp.usdoj.gov/nij/dnamtgtrans3/trans-k.html]

persons, since many more samples could be processed per dollar invested. However, to make a successful cold hit requires that crime-scene samples also be typed, so that they can be compared with the profiles of convicted persons. Also, logistically, it is often easier to obtain a sample from someone newly in custody than from someone who has been released. However, a person while in prison is not a threat to the community, whereas someone who has been released might be; nevertheless, a prisoner might be discovered through DNA analysis to have committed other crimes before having been imprisoned. Finally, solving old crimes with the help of DNA evidence serves justice and might help prevent future crimes, but it might also have negative consequences. For example, reopening a case that is several years old might retraumatize victims or their families who have worked to recover from the effects of the crime.

Additional federal funding to help reduce the backlog could substantially increase the speed with which backlogged samples are processed, easing uncertainties about how best to prioritize the samples and increasing the rate at which crimes are solved. Also, the existence of the backlog could be attributed in part to the success of the DNA Identification Act grant program, and the grant-eligibility requirements in the Antiterrorism and Effective Death Penalty Act of 1996 discussed above. In addition, the processing of backlogs would have benefits across states, especially with respect to "travelling offenders" who commit crimes in more than one state.

Databases. A central issue relating to the kinds of crimes for which DNA is collected from convicted persons for inclusion in a profile database or index. States vary in the crimes for which they collect DNA samples. Qualifying offenses include, at a minimum, felony sex crimes, but several others are included by different states: offenses against children (40 states), murder (36), assault and battery (27), kidnapping (22), robbery (19), burglary (14), and all felonies (6). Also, 24 states collect samples from juveniles convicted of qualifying offenses, most collect retroactively from incarcerated convicts, and some collect from those previously paroled or on probation.[49] In the United Kingdom, the Forensic Science Service, an executive agency of the Home Office, maintains a national database with DNA profiles of "suspects charged, reported, cautioned or convicted for a recordable offence," which is any crime punishable by imprisonment, plus certain other specified offenses.[50] Profiles are removed if a suspect is exonerated or acquitted. As of July 2000, the U.K. database held approximately 700,000 profiles and had yielded more than 77,000 matches of suspects to crime scenes since its inception in 1995, with almost 130,000 profiles removed following acquittal.[51]

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[49] Adams, Hearing Statement. Figures cited are as of December 1999 from an FBI survey of laboratories participating in CODIS. States have continued to pass laws expanding the list of qualifying crimes, so the numbers cited for some categories have since increased.

[50] Among the additional recordable offenses are public drunkenness, taking part in a prohibited assembly, and certain kinds of illegal hunting — Government of Great Britain, *The National Police Records (Recordable Offences) Regulations 2000,* Statutory Instrument 2000 No. 1139, 28 April 2000, available at [http://www.hmso.gov.uk/si/si2000/20001139.htm].

[51] The Forensic Science Service, *Annual Report and Accounts 1999–2000,* 25 July 2000, (continued...)

In determining whether to broaden the range of qualifying crimes, questions might be raised such as the following: What is the cost-effectiveness of profiling those convicted of a particular class of crime? For example, are the resources needed to profile those convicted of nonviolent crimes more effective if spent on profiles or on other aspects of crime solving and prevention?[52] What is the proper balance between using profiles to help protect citizens from crime, on the one hand, and the need to protect the civil liberties and privacy of those who might be subject to profiling, on the other? The power of DNA evidence has led some to call for indexing profiles of all arrestees, or even of all citizens at birth, while others have raised concerns about the effects of such measures on civil liberties.[53]

Postconviction Analysis. A powerful use of DNA evidence is in exonerating the innocent, including in some cases where people have been wrongfully convicted. Several issues are associated with postconviction DNA analysis. Among them are when such procedures are appropriate, and what is the proper role of the federal government.

There are several potential reasons why DNA analysis might not have been done when a case was first prosecuted. One is that the identity of the suspect might not have been an issue at the trial — for example, the involvement of a suspect in a sexual encounter might not have been in question, but rather whether the encounter was consensual. In such a case, DNA evidence would probably not be relevant. Another possibility is that no DNA evidence was found at the time, but turned up later. A third is that there was DNA evidence, but the technology to analyze it was not available when the case was prosecuted. The first use of DNA typing in the United States was in the late 1980s, and it was not widely available until a few years ago.

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[51] (...continued)
available at [http://www.forensic.gov.uk/forensic/corporate/annual_rep/annual_report2000.pdf], 20–21.

[52] The answer to these two questions depends on several factors. One is the frequency with which those who commit nonviolent crimes also commit other crimes that DNA evidence would help to solve. There are few data on this topic so far, but the experience of Virginia might be illustrative. Using a convicted-offender database of approximately 118,000 profiles as of June 2000, Virginia obtained 156 matches of offenders to crimes. The state collects DNA samples from everyone convicted of a felony. Dr Paul Ferrara, Director of the Virginia Division of Forensic Sciences, has estimated that about half of those "hits" would not have occurred had the database been limited to violent offenders (personal communication with the author, 28 August 2000). Another factor is the cost of collecting samples and analyzing the DNA for a convicted offender. The DNA Commission has estimated the latter at approximately $50 per sample with current technology, but it can vary significantly depending on circumstances. A third factor is cost-effectiveness of other methods of crime solving and prevention. These and other factors involved can be difficult to measure and compare accurately.

[53] Rose Marie Arce, "Surveillance and DNA testing are among the latest police weapons. But how will we balance fighting crime and preserving civil rights?" *Newsday*, 30 May 1999, sec. A, 17. See the section on privacy below for further discussion of this issue.

In some cases, relevant DNA evidence might have been found and analyzed at the time of the original prosecution but yielded inconclusive results because of the limitations of the technology at the time. The much more sensitive STR technology did not become an established standard until the late 1990s, and many states still use the older, less sensitive VNTR markers. STRs or the potentially even more sensitive (but less powerful) mtDNA can provide useful profiles from much smaller or more degraded samples than VNTRs. Consequently, an analysis that was inconclusive with VNTR technology could lead to either a definitive exclusion or, alternatively, a strong match if a more sensitive system is used. Improvements in DNA technology are likely to continue into the future, potentially making even more samples amenable to typing.

Most states currently do not permit new trials, based on newly discovered evidence, more than three years after conviction.[54] However, DNA evidence, properly handled, is very stable and can often provide useful information even ten years or more after it was initially deposited.[55] This confluence of advances in the technology, the stability of DNA evidence, and its strong and growing exclusionary power raise questions such as whether the time limit should be extended for cases where DNA evidence newly discovered or analyzed can be probative, and whether postconviction legal procedures should be changed to accommodate the particular features presented by DNA evidence.[56]

To date, a few states have passed laws that specifically permit postconviction DNA analysis for convicted persons claiming actual innocence. In considering proposed federal legislation, Congress may consider questions including the following: Should such legislation apply only to crimes under federal jurisdiction, or should it also apply to states? What evidence standards should a petitioner be required to meet for the procedure to be permitted? Should there be a requirement for evidence to be preserved beyond exhaustion of appeals, and if so, for how long should it be preserved? Under what circumstances should elimination samples from victims or other third parties be required? What, if any, accommodation should be made for retyping when new advances are made in DNA technology? Should the government pay for analysis requested by an indigent inmate? Should wrongfully convicted persons receive compensation?[57]

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[54] DNA Commission, *Postconviction DNA Testing*, 9.

[55] In some cases, convicted persons who were actually innocent have served more than ten years before being exonerated by DNA evidence. For examples of those and other cases of postconviction exoneration, see Edward Connors and others, *Convicted by Juries, Exonerated by Science: Case Studies in the Use of DNA Evidence to Establish Innocence After Trial*, National Institute of Justice Report NCJ161258, June 1996.

[56] DNA Commission, *Postconviction DNA Testing*, 10. For example, evidence containing DNA would usually not be newly discovered but would likely already be in the control of the prosecution; however, a DNA analysis might not have been done or might have been inconclusive because of earlier technological limitations. Also, some law enforcement agencies destroy evidence in a case after all appeals are exhausted (Connors, *Convicted by Juries*, 26).

[57] See Eric A. Fischer, *DNA Evidence: Legislative Initiatives in the 106th Congress*, CRS Report RL30694, 12 January 2001, for discussion of these issues.

Paternity Challenges

As more powerful DNA-typing techniques have become more affordable, their use in paternity analysis has grown. An emerging issue involves cases where men who have legally acknowledged paternity, sometimes for several years, are shown by DNA typing not to be the father of the child. A central question is whether the men in such cases, who may claim not to be responsible for child support since they are not the child's biological father, should nevertheless continue to be held responsible. A concern of child advocates is the potentially negative impacts on children if such challenges are allowed. States have varied in their treatment of this issue.[58]

Future Directions of the Technology

Current research on improving DNA identification is performed or supported mainly by NIST, NIJ, the FBI Laboratory, AFDIL, and private industry. Such research has several broad goals. Improvements in sensitivity of analyses would make useful typing possible from even smaller or more highly degraded samples than at present. That could permit more powerful identification (or exclusion) from DNA in trace evidence from, for example, saliva, tears, and skin cells. Coupled with further improvements in specificity, such as via use of a larger set of markers, it would also increase the ability of DNA evidence to make positive or unique identifications. Even identical twins possess minor genetic differences that could eventually be detected. Reducing the time required to complete typing could lead to more timely following of leads as well as more quickly removing from further consideration those persons excluded by the evidence. As the costs of performing DNA analysis has come down, its use has increased. Further reducing cost would make use of DNA identification more widely available. Research on automation and miniaturization of the typing process may lead to cost reductions and further improvements in quality control. Conceivably, an automated, portable DNA-typing system could eventually be developed that would permit on-site analysis and identification through comparison against a database via wireless communication.

Such major improvements in the technology will take several years at least to perfect. It is generally believed that STR markers will remain the standard for DNA identification over the next decade, with mtDNA increasingly used to analyze highly degraded samples. Research to develop ways to amplify longer sequences may, however, lead to more use of VNTR or other more variable systems in the near future. Also, the Human Genome Project and related efforts are increasingly identifying very small genetic differences, even at the level of a single base (single nucleotide polymorphisms, or SNPs). Such research may lead to eventual development of better marker systems. In some cases, relevant physical characteristics, such as for eye color, might even be deducible from genetic sequences and could help, for example, in identifying suspects.[59]

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[58] See Amy Argetsinger, "Court Opens Door to New Paternity Challenges," *Washington Post*, Thursday, 29 June 2000, sec. A, 1, 19.

[59] These and other potential developments are being considered by the DNA Commission and (continued...)

There are several challenges raised by the likely future improvements in DNA typing. Improvements in forensic typing will need to be validated by the scientific and law enforcement communities and accepted by the courts before they become widely available for use in cases. Therefore, any given case is likely to involve technologies that are technically sound but not the most recently developed. Furthermore, significant pressures exist to maintain a substantial degree of stability in the systems used. Not only is adopting a new technology costly, but frequent change can lead to longer and more costly proceedings and to uncertainty about the most appropriate approach.[60] One concern raised is that technological advances could lead to a lengthening of the appeals process in cases involving DNA evidence, or a flood of postconviction petitions for typing or retyping in situations where it would not actually be helpful. Such concerns will need to be balanced against whatever added ability the advances provide in reversing or avoiding wrongful convictions.

As the power of DNA profiling to identify a person continues to improve, the question arises, can a person be positively or uniquely identified from a DNA profile? FBI experts will currently testify that a person is the source of a DNA sample, provided that the match probability is low enough (see the section on interpretation of DNA evidence above). However, it has not yet been settled generally what probability, or alternatively how many loci, are needed to effectively eliminate the possibility that a match could be coincidental. One complication is that match probabilities do not take into account the possibility of misidentification resulting from errors at the laboratory or in the evidence custody chain. Both experts and the courts have generally agreed that such possibilities are best addressed in other ways.[61]

The stability of DNA evidence makes it potentially useful not only in postconviction typing; it also raises the question of whether statutes of limitations should be extended for crimes in which such evidence is potentially important. That question will likely increase in importance as the number of DNA profiles from "cold cases" grows in databases and indexes such as CODIS. The benefits of using DNA evidence to bring effective prosecutions after a longer period than currently feasible will need to be balanced against factors such as the desire to avoid retraumatizing victims who have recovered from the effects of crimes and the need to prioritize the use of limited law-enforcement resources.[62]

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[59] (...continued)
are described on the commission's website at [http://www.ojp.usdoj.gov/nij/dna/welcome.html].

[60] For example, when the first NRC report on DNA evidence proposed a new method of calculating match probabilities (the ceiling principle — NRC, *DNA Technology*, 82–85), considerable controversy was generated in the courts and was not settled until the second NRC report was released (NRC, *Evaluation of DNA Evidence*).

[61] Those approaches include proficiency testing, laboratory accreditation, and providing opportunities for retyping of evidence by the defense. For a discussion, see NRC, *Evaluation of DNA Evidence*, 85–87, 179–185.

[62] For discussion of this and other legislative issues, see Fischer, *DNA Evidence*.

Relationship of DNA Identification to Medical Genetic Testing

Both similarities and differences exist between the use of DNA for identification and for medical genetic tests — with respect to techniques, applications, and the issues raised. The most fundamental similarity is that both rely on genetic differences among people. The most fundamental difference is in the characteristics of the DNA sequences that each currently uses — in particular, variability, functionality, and independence.

Variability. A genetic marker used in identification should be highly variable — that is, there should be many alleles, and none of them should be very common. The more variable the markers, the fewer are needed for a positive identification. In contrast, a gene examined in a genetic test is unlikely to be highly variable. That is because genetic tests are most often used in medicine, to diagnose or predict the likelihood of a disease or condition caused by a genetic abnormality, which most people will not have.[63]

Independence refers to whether different loci tend to be inherited together. Two loci that occur close together on a chromosome will usually tend to be inherited together — they will be linked, not independent. Two loci that occur on different chromosomes will usually be inherited independently — they will be unlinked. In genetic testing, only one locus is usually of interest, so linkage is not usually important. In contrast, use of DNA to identify people requires examining several loci, and the mathematics that is used works best if the loci are independent.[64]

Functionality. A sequence is of interest in genetic testing specifically because it is a gene that codes for a particular chemical product. However, in identification, a noncoding sequence or marker is of most interest.[65] That is because the mathematics that is used in identification works best with noncoding loci.[66] Although most loci used in identification are noncoding, it is possible that functions for at least

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[63] There are other potential uses of genetic tests, such as to predict how a patient is likely to respond to a particular drug, but variability at any given locus will usually be low in such cases as well. Also, genetic tests often use techniques other than direct identification of sequences — such as visual examination of chromosomes (karyotypes), or examination of gene products.

[64] In the simplest case, the frequencies of a particular genotype for each locus are simply multiplied together to get an overall likelihood (see section on calculation above). While most medical genetic tests do not currently involve more than one locus, there will likely be an increased focus on multilocus testing as medical genetic technology becomes more sophisticated. However, it is only for identification that independence of the loci is an advantage.

[65] See section on why DNA can be used in identification at the beginning of this report.

[66] For nonfunctional loci the effects of natural selection, which are difficult to quantify, do not need to be taken into account when calculating the likelihood that someone will have a particular combination of alleles; the probability can be calculated directly from the frequencies of those alleles in a population (if certain other assumptions apply). For example, in the simplest case, if the frequency, x, of a particular allele is 10%, then x^2, or 1%, of the population will have only that allele.

some will be discovered in the future. Furthermore, some, in particular STRs, are thought to be linked to coding loci that may be implicated in genetic diseases or conditions.[67]

Regulation and accreditation of laboratories performing medical genetic tests and DNA identification are accomplished through different mechanisms. Clinical laboratories, which may perform medical genetic tests, are regulated and must be certified by the U.S. Department of Health and Human Services through the provisions of the Clinical Laboratory Improvement Amendments of 1988, as amended (P.L. 100-578). Standards are developed by the Health Care Finance Administration and the Centers for Disease Control and Prevention. Medical research laboratories, if they are supported by federal funds or are otherwise subject to regulation, are subject to federal policies relating to the protection of human subjects (45 C.F.R. 46, 21 C.F.R. 50 and 56). Forensic laboratories do not require federal certification, but to be eligible for DNA Identification Grants or Byrne Grants, they must adhere to standards set by the FBI and undergo regular proficiency testing (P.L. 103-322, Sec. 210302). Also, in criminal and civil cases, DNA evidence must pass the scrutiny of the judicial process, where custody-chain and quality-control procedures, as well as other aspects of typing, may be challenged.[68] Consequently, new DNA technologies are likely to be adopted more slowly for forensic use than for medical testing.

Privacy and Discrimination

There is currently no federal law governing genetic privacy and discrimination per se, although Congress has considered several bills addressing such concerns from a medical perspective. The executive branch has also taken some actions, as have several states.[69] The Privacy Act of 1974 (5 U.S.C. 552a) places restrictions on agencies with respect to the disclosure of personally identifiable information in their possession, including any "identifying particular assigned to the individual, such as a finger or voice print or a photograph." However, it applies only to federal agencies. Executive Order 13145 prohibits genetic discrimination against executive branch employees; it applies to medical genetic tests and does not cover the use of DNA in identification per se. Other federal laws and guidelines provide privacy protections

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[67] One, VWA, is actually a noncoding segment of the human von Willebrand factor gene, which is associated with a blood condition (James F. Crow, "Research and Development Working Group Report," *Proceedings, National Commission on the Future of DNA Evidence*, 27 September 1999, [http://register.aspensys.com/nij/dnamtgtrans7/trans-k.html]).

[68] For a discussion of those and other legal issues and cases, see NRC, *Evaluation of DNA Evidence*, 166–211.

[69] For discussion of legislative issues and federal and state activities relating to genetic discrimination and medical records privacy, see Nancy Lee Jones, *Genetic Information: Legal Issues Relating to Discrimination and Privacy*, CRS Report RL30006, 2 October 2000; and C. Stephen Redhead, Harold C. Relyea, and Gina Marie Stevens, *Medical Records Confidentiality*, CRS Issue Brief IB98002, 2 October 2000.

for certain other kinds of personal information relating to health and medical research.[70]

Current federal and state laws also provide safeguards against the misuse of DNA profiles collected in law enforcement. Specifically, the DNA Identification Act of 1994 (P.L. 103-322) required grantees to certify that DNA samples and analyses "be made available only —

> (A) to criminal justice agencies for law enforcement identification purposes;
> (B) in judicial proceedings, if otherwise admissible pursuant to applicable statutes or rules;
> (C) for criminal defense purposes, to a defendant, who shall have access to samples and analyses performed in connection with the case in which the defendant is charged; or
> (D) if personally identifiable information is removed, for a population statistics database, for identification research and protocol development purposes, or for quality control purposes….

The act also applies those privacy requirements to federal, state, and local participants in CODIS. However, state laws vary with respect to how such samples can be used. Some disagreement exists over whether state protections are adequate.[71]

Samples deposited in the Armed Forces Repository of Specimen Samples for the Identification of Remains are limited to the following uses: "Identification of human remains; …[i]nternal quality assurance activities…; [a] purpose for which the donor… (or surviving next-of-kin) provides consent;" or, when specifically authorized, criminal procedures for which "[n]o reasonable alternative means for obtaining a specimen for DNA profile analysis is available…." (DODD 5154.24, Sec. 3.5).

Since most genetic markers currently used in DNA identification are noncoding, the privacy and discrimination issues raised are somewhat different than with medical genetic testing. For example, knowing someone's DNA profile for the 13 core STR loci can provide information about paternity but provides no information at this time about physical traits such as a propensity to a particular genetic disease.[72] However, the issues may begin to converge as new advances in genomics are developed and applied, or if current identification technologies are applied in the context of genetic testing. For example, in some cases clinical research laboratories have reportedly used STR typing of samples as an added protection against the possibility of potential mislabeling.

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[70] See Redhead, *Medical Records Confidentiality,* 4–8.

[71] For two different views, see Adams, "Hearing Statement," and Barry Steinhardt, Statement, Legislative Hearing on H.R. 2810, the "Violent Offender DNA Identification Act of 1999", H.R. 3087, the "DNA Backlog Elimination Act", and H.R. 3375, the "Convicted Offender DNA Index Systems Support Act"; Subcommittee on Crime, House Committee on the Judiciary, 13 March 2000, [http://www.house.gov/judiciary/stei0323.htm].

[72] It is, however, possible that some relationships will be discovered in the future, as the functions of human DNA sequences become better understood.

More generally, as DNA identification becomes more sophisticated, its potential applications are likely to broaden, potentially increasing privacy concerns. For example, it is already possible for parents to purchase kits for obtaining DNA samples from their children and to have profiles developed from those samples and placed in a database to be used potentially if the children become missing. Such private-sector practices are not covered by federal laws and judicial rulings that provide privacy or other protections against misuse or abuse of the information.

Government agencies in other countries have also become involved in DNA-identification activities that would likely be limited to the private sector in the United States. Britain's Forensic Science Service (FSS) is an executive agency of the British Government but is permitted to operate as a nonprofit corporation that offers services not only to the government but also to the public. Among its services to corporations is the development of DNA profiles of employees who might be at risk of being kidnapped. The profiles could then be compared to any biological material provided by kidnappers. FSS also provides paternity-analysis services to the public.[73] The privacy of genetic information obtained or used in such services would presumably be protected by a European Union directive on privacy of personal data.[74]

Such broadening applications may raise concerns about "function creep,"[75] the gradual widening of an application to uses not originally intended. One example often given is the slowly broadening range of uses over the years of Social Security numbers. The identifying power of DNA, the decreasing cost of typing, and the increasing ability to obtain a useful sample without drawing blood, make DNA potentially attractive for a wide range of uses requiring verification of identity.[76]

As long as DNA typing uses noncoding loci, privacy issues arising from its use in identification should remain limited. However, three potential issues might deserve particular attention as the use of the technology increases. First, as genomic research leads to increasingly sophisticated technologies for detecting genetic differences, it may become possible to use coding loci (genes) to provide identification. Use of coding DNA for identification could raise issues of privacy and discrimination similar to those that have raised concerns with respect to medical testing — if, for example, such information became publicly available during a judicial proceeding.

Second, DNA samples obtained from a person — and in many cases from crime-scene evidence, remains, or other sources — contain the person's entire genetic code,

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[73] See the FSS website, [http://www.forensic.gov.uk/forensic/entry.htm].

[74] Directive 95/46/EC of the European Parliament and of the Council of 24 October 1995 on the protection of individuals with regard to the processing of personal data and on the free movement of such data, available at [http://europa.eu.int/eur-lex/en/lif/dat/1995/en_395L0046.html].

[75] Steinhardt, Hearing Statement.

[76] For a general discussion of such issues for biometric technologies, of which DNA typing is one example, see Congressional Research Service, *Biometric Science and Technology for Personal Identification: Devices, Uses, Organizations, and Congressional Interest*," by William C. Boesman, CRS Report RL30084, 8 March 1999.

not just the profile information. Therefore, the disposition of the samples themselves, after profiling, is potentially an issue. That is especially a potential concern with respect to private-sector activities where disposition of profiles or samples is not necessarily regulated by current law. A case involving electronic commerce illustrates the concern. Toysmart.com collected information about customers under a privacy policy that claimed the information would not be shared with third parties. However, when the company filed for bankruptcy, it included the database of customer information among the assets it was selling. The Federal Trade Commission unsuccessfully opposed the sale of the database.[77]

Third, a DNA sample and profile contain information not only about the subject, but also about that person's biological relatives. Therefore, consideration of privacy issues related to DNA identification, as with genetic testing in medicine, must take into account potential impacts on family members. That can raise potentially difficult issues, as illustrated by the following hypothetical example. Suppose that a DNA profile from a convicted offender is similar but not identical to that obtained from a crime scene. Is it appropriate based on that information for a sibling of the convicted offender to be arrested as a suspect? Alternatively, suppose that a person is suspected of committing a crime but there is insufficient evidence to make an arrest. Suppose further that the person has a sibling who has a profile in CODIS. Is it appropriate to examine the profile of the sibling to determine how similar it is to the crime-scene evidence? Such examples are likely to arise in real cases as DNA becomes more widely used in identification.[78]

The growing use of DNA as an effective identification tool, and its increasing overlap with aspects of medical genetic testing, are likely to create a range of policy challenges over the next several years. While this report has discussed several current and emerging issues, new ones may well develop as the technology evolves. The biological role of DNA, the information it contains about family members, and other features of the molecule and the technology may make some of those issues, and the appropriate legislative response, especially challenging.

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[77] Matt Richtel, "FTC Moves to Halt Sale of Database at Toysmart," *New York Times,* 11 July 2000, sec. C, 2; "Judge Shelves Plan for Sale of Online Customer Database," *New York Times,* 18 August 2000, sec. C, 2.

[78] See Michelle Hibbert, "DNA Databanks: Law Enforcement's Greatest Surveillance Tool?" *Wake Forest Law Review* 34 (1999): 782–787 for a discussion of this issue and an application to an actual case.