Part V

ETHICS, LAW, AND POLICY

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Forensic DNA Typing

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Introduction

Forensic DNA typing is a technique for identifying people from their organic traces – blood, semen, saliva, or hair – and their genetic idiosyncracies. It involves the comparison of small portions of DNA (deoxyribonucleic acid), the molecule containing the human genetic code, taken from different sources, e.g., from a bloodstain and a suspect, or a child and an alleged father. Its value as an identification technique arises from the fact that DNA is found in virtually all bodily residues, is extremely resistant to decay and contamination, and has many regions that are highly ''polymorphic,'' or variable among individuals. It is a versatile technology, that can help implicate or clear a criminal suspect, distinguish serial from copycat crimes with no suspect, resolve parentage disputes, and help parents find missing children (see generally, NRC 1996: chs. 1 and 2; Weedn 1996).

Since its introduction in the mid-1980s, DNA typing has been employed in thousands of cases of disputed identity, in criminal, domestic, immigration, and other proceedings. In some of these cases, it merely gilded the lily, yielding more powerful and persuasive evidence for an identification that could have been made by other means. In other cases, however, there would have been no identification, or a mistaken identification, without DNA typing. This chapter will focus on its use in American criminal cases, and address the principal issues that have been raised about its accuracy, its role as legal evidence, its impact on the criminal justice and legal systems, and its threat to privacy. As we move from technology to policy, it will become apparent that DNA typing, like other controversial applications of genetic research, has not raised new issues in law and public policy so much as intensified the debate over long-standing ones.

In its use of genetic material, DNA typing accomplishes the same task as the scientific comparison of other bodily residues. To assess its impact on criminal investigation and adjudication, we must examine it in the context of those other identification techniques, especially fingerprinting and nongenetic serology (blood-marker testing).

DNA typing was first introduced to the public by the trademarked name of ''DNA fingerprinting'' (Gill et al. 1985). While that term has since lost currency, and has

been criticized for suggesting a discriminatory potential that DNA typing does not (yet) have, the comparison is instructive. Both fingerprinting and DNA typing use highly variable characteristics of biological residues to aid in criminal identification. While a DNA match cannot identify a suspect with the certainty claimed for a fingerprint match, DNA can be obtained in a far wider variety of settings, and the presence or absence of the suspect's DNA will often be more clearly incriminating or exculpatory. DNA typing has a greater capacity to discriminate among individuals than any other serological test, and it can be used on a wider variety of residues.

But although DNA typing may be more useful or versatile than other identification techniques, its marginal value as a forensic tool can hardly explain its extraordinary popular and judicial reception. The publicity and controversy it has generated may reveal less about its potential as an identification technique than about the strength of public expectations and anxieties concerning genetic research and technology. For while fingerprint identification uses features of the human body that are readily accessible and widely assumed to be unrevealing (apart from their potential for identification), DNA typing uses features that are widely, if misleadingly, thought to be among the most private and revealing. And while fingerprinting, despite its slow judicial acceptance, generated little scientific controversy, DNA typing, as an application of cutting-edge genetic research, has encountered both rapid judicial acceptance and intense, protracted controversy.

How it Works

In theory, we could identify people with absolute certainty by examining their entire genetic sequence, or genome, since each person's genome is unique. That is not a practical possibility, however, since the genome is spread over 46 chromosomes, each containing millions of smaller molecules. DNA identification was suggested by the discovery of small regions (loci) of DNA throughout the genome, varying in length and other characteristics from person to person. The capacity to use these variable loci to identify people resulted from earlier advances in molecular biology, which made it possible to break up the DNA molecule into very small segments and detect small differences in their length and weight. In the classical typing method known as ''restriction fragment length polymorphism'' analysis (RFLP), these variations, or polymorphisms, are detected by differences in the length of the segments left when DNA is cut up by restriction enzymes. More recent techniques employ the polymerase chain reaction (PCR) to make multiple copies of DNA segments, an ''amplification'' process that permits the typing of minute amounts of DNA by fragment length or molecular sequence (see generally, NRC 1996: chs. 1 and 2).[1]

Forensic typing typically involves the comparison of several loci, since even the most polymorphic locus has a limited number of ''alleles,'' or variants. Typing is done with either a multiple-locus probe, which permits the comparison of several loci at the same time, or several single-locus probes, each comparing the alleles at a single locus, from the maternal and paternal chromosomes. While early forensic typing used multiple-locus probes, single-locus probes now predominate, for reasons that include the simplified interpretation of population data.

Consider a case in which a semen stain is found on the clothing of a rape victim. DNA typing can test whether the stain came from a suspect by comparing the DNA from his blood with the DNA extracted from that stain. The failure to obtain a match ''excludes'' the suspect as a source of the semen; a match ''includes'' the suspect in a subpopulation of potential sources. The more loci at which matches are obtained (and the rarer the matching alleles), the smaller the probability that someone besides the suspect was the source of the semen.

DNA typing can rule out identity categorically: if alleles from two samples do not match, those samples cannot have the same source. A match, however, yields only a probability of identity between suspect and source. A simple product rule will give the probability that the DNA could have come from anyone besides the suspect, if (1) a match is *correctly* found for the maternal and paternal alleles at each locus; (2) the alleles at each locus can be assumed to be statistically independent of each other and of the alleles found at other tested loci (e.g., the probability of finding a given allele at one locus must not depend on the probability of finding a given allele at another), and (3) the frequencies of the alleles at each locus can be estimated *for the appropriate population*. To continue with our example, if the suspect's DNA matches the semen for each pair of alleles at three tested loci, the alleles can be regarded as independent, and the frequency of each allele at each locus is 1 in 20, then the probability that the source DNA came from someone else will be 1 in 64,000,000: $[20 \times 20] \times [20 \times 20] \times [20 \times 20]$. The legal controversies over the admission and presentation of DNA matches have focused on the validity of the assumptions needed to yield such staggering odds.

Sources of Error and Uncertainty

The soundness of the theory and technique underlying DNA typing has never been in serious dispute; the controversy over the admission of DNA typing results has focused on the criteria for declaring a match, and the statistical interpretation of a match. The first issue was prominent in the early debate over the admissibility of DNA evidence, with critics concerned that the comparison of DNA typing from different sources left too much room for error, interpretation, and bias, notably in adjustments for ''band-shifting,'' a phenomenon associated with certain methods of RFLP analysis (e.g. Neufeld and Colman 1990; Lander 1992). That concern has receded as techniques for comparing DNA fragments have become more precise and the criteria for declaring a match have been standardized.

Since the early 1990s, the second issue has predominated: the statistical interpretation of DNA matches. The vanishingly low odds often given for a chance match, as in our example above, rest on disputed assumptions about the frequency of specific alleles across population subgroups and the independence of alleles at different loci. They also rest on the assumption that a match has been correctly made, i.e., that the laboratory claiming a match has not done so erroneously – an assumption that laboratory errors in blind tests call into question, and that the absence of a standardized testing programs renders highly problematic. I will begin with the first concern, although some critics consider the second the more important.

Because of inbreeding, a racial, ethnic or other subgroup may have a significantly higher frequency for a given allele than the population average. If it does, and if any potential contributor of the source DNA comes from that subgroup, then the odds of obtaining a chance match on that allele will be significantly higher than the frequency of the allele in the general population.

Two distinct questions present themselves: do subpopulations differ in allele frequency? If so, what is the appropriate subpopulation to consider in a given case? The first is a scientific question, which has generated sharp disagreement among population geneticists, particularly about the validity of various tests for subpopulation heterogeneity. Proponents of forensic typing argue that current databases, based on broad population estimates, yield adequate frequency estimates, while some critics call for more refined subgroup data (see NRC 1992). The second question is evidentiary, because it concerns the population of potential contributors: if not the suspect, then who? If the suspect in a Crown Heights rape of a Hasidic woman is a Hasidic Jew, should the statistical interpretation of a match reflect the frequency of the matched profile in New York City, among Jews, among Hasidic Jews, among Crown Heights residents, or among some other subgroup? The choice of the most appropriate subgroup will depend on what is known or assumed about the offense or the offender, e.g., on whether the race or general appearance of the offender is known, on whether the rape occurred in an alley or a mikvah.[2] Some commentators argue that these uncertainties make it appropriate to use the general population frequency in all cases, others that the suspect's own racial or ethnic subgroup should be used, if adequate population data is available. Others question why the suspect's subgroup is appropriate unless the evidence limits potential contributors of the source DNA to that group; they suggest that the choice of subgroup must be left to judges or juries, on a case-by-case basis. Finally, some regard the multiplicity of possible subgroups, and the uncertainties about which is most appropriate, as militating against the use of frequency data or any statistical interpretation of a DNA match.

In 1992, the Committee on DNA Technology in Forensic Inference of the National Research Council (NRC) issued a report that called for using the highest allele frequency for any population subgroup if there were any significant differences among groups.[3] Under this ''ceiling'' principle, the probability that someone besides the suspect contributed the bloodstain would be assessed using the frequencies for the subgroup in which the matched alleles were most common, even if there was no reason to think that someone from that subgroup was involved in the incident. This proposal, intended to resolve the controversy by its simplicity and conservatism, only sharpened it, with critics finding the ceiling to be either overly conservative or ad hoc (e.g. Devlin et al. 1993; Kaye 1994). A new NRC panel issued a revised report on statistical issues in 1996, which rejected the ceiling principle in favor of much more modest downward adjustments in frequency when there is evidence of subpopulation differences. That proposal provoked less criticism that the one it replaced, and the 1996 Report helped shift the focus to other controversies in statistical interpretation (Symposium 1997: Introduction).

Several commentators have pointed out that the preoccupation with subpopulation differences had obscured a more important threat to the reliability of DNA typing results and their value as legal evidence: the prospect of laboratory error (Lempert

1991; Symposium 1997: 405–54). Sample-switching, contamination, and other laboratory errors, found to occur with disconcerting frequency in one highly publicized test of California crime laboratories, may be a more significant source of error than mistaken frequency estimates. Some critics have argued that the probability presented to the fact finder that someone other than the defendant was the DNA source can be no lower than the false-positive rate of the laboratory doing the testing. The debate over this proposal leads to the next general topic, the issue of integrating DNA typing results with nonquantitative evidence into the framework of legal proof.

DNA Typing Results as Legal Evidence

Even if DNA typing is reliably performed and analyzed, the significance of its results may be misunderstood by juries and judges. The statistical interpretation of a DNA match introduces a conspicuously large (or small) numerical probability into a criminal trial characterized by informal, nonquantitative evidence. The integration of DNA evidence into legal proof presents several challenges that go beyond the usual doubts about lay comprehension of scientific and quantitative evidence.

The probability of a match vs. the probability that the suspect was the source of the DNA

The statistical interpretation of a DNA match is usually given in terms of the probability that someone picked at random from the relevant population would match the source DNA. In our example, we calculated that probability as 1 in 64,000,000. But that impressive statistic does not give the probability that the fact finder is interested in – the probability that the suspect contributed the source DNA. Establishing that probability is more complex.

On the prevailing Bayesian approach, the match is seen as a piece of evidence that modifies the prior probability, whatever it was, that the suspect contributed the source DNA. The modification is made by multiplying the prior probability by the ''likelihood ratio,'' which compares the probability of a match if the suspect was the DNA source with the probability of a match if he was not. The former probability can be assumed to be 1 (with no false negatives); the latter is just the random match probability. So the likelihood ratio will just be the reciprocal of the match probability. That ratio indicates that a match was 64,000,000 times as likely if the suspect was the DNA source than if he was not, *not* that the suspect is 64,000,000 times more likely than anyone else to be the source. It is easy to confuse the two claims, and treat the match probability as indicating the latter. This error has been called the ''prosecutor's fallacy,'' and it will yield a mistakenly large probability that the suspect was the source whenever the prior odds that he was the source are less than 50:50.

The complementary ''defendant's fallacy'' involves the assumption that anyone in the reference population with the same DNA profile as the suspect is as likely to be the source (both terms are from Thompson and Shumann 1987). This would mean that if the match probability in our example had been 1 in 640,000, and the reference population 6,400,000, the suspect would have had only a 1 in 10 chance of being the

source, since we would expect there to be 9 other people in the population with the same profile. The assumption will be mistaken, and the odds substantially higher, in any case where the suspect was initially identified by evidence other than the DNA match. In cases where the suspect is identified only through the search of a DNA data bank containing his profile, there is no prior evidence linking him to the specific offense, and the match will therefore have far less probative value. The simplest way to deal with this problem would be to attempt to match the DNA of the data-bank suspect to the source DNA at several different, independent loci. If this is not feasible, the 1996 NRC report proposes a downward adjustment of the match probability that reflects the greater likelihood of a coincidental match in larger databases.

The laboratory false-positive rate and the probability that the suspect was the DNA source

Some commentators have proposed that the statistical interpretation of a match incorporate the false-positive rate of the crime laboratory performing the typing: the frequency with which it mistakenly declares a match (Symposium 1997: 405–64.) They argue that the probative value of a match reflects the probability that a match would have been declared if the suspect was not the source (this is the probability expressed by the denominator of the likelihood ratio). But there are two ways that could happen. First, the lab could accurately declare a match with the suspect's DNA when someone other than the suspect was in fact the source. Second, the lab could declare a match mistakenly. The probability of such an error, given by the laboratory's false-positive rate, may be vastly greater than the probability of a coincidental match, and it must be factored into any statistical presentation of the match.

Other commentators point out, however, that information on false-positive rates is not available in the absence of routine blind-proficiency testing of crime laboratories, and they argue that even if such testing were routine, the false-positive rates it yielded could not be generalized to the laboratory's ordinary case work. They propose that evidence of laboratory error be presented separately from the statistical interpretation of the match, with the fact finder invited to discount the latter by the former in some substantial but unspecified way, a recommendation adopted by the 1996 NRC Report (ch. 3). Critics, however, doubt that judges or juries will discount adequately; research on eyewitness testimony suggests that lay fact finders tend to take little account of the reliability of identification evidence (Symposium 1997: 405–54).

The integration of nonquantitative evidence and the neglect of ''softer'' variables

If DNA evidence is difficult for lay fact finders to interpret in isolation, it is also difficult to integrate with the standard kinds of evidence produced at a criminal trial – eyewitness testimony, evidence of motive, means, and opportunity, character evidence – where, for example, a DNA match confronts an airtight alibi, or where a DNA exclusion confronts strongly incriminating eyewitness and circumstantial evidence. It is possible that judges and juries will give too much weight to DNA evidence in cases

of conflict, but it is also possible that they will give it too little weight. There are several reports of juries having convicted defendants implicated by eyewitness or circumstantial evidence in the face of clear exclusions, a subject I will take up in discussing the exculpatory potential of DNA typing. There are few reports of DNA evidence prevailing in the face of a strong alibi or other strong exculpatory evidence; this may be because prosecutors are less likely to use DNA evidence to plug the gaps in weak cases than to reinforce strong ones.

A second concern is that the complexities and controversies surrounding the introduction of DNA evidence may divert attention from critical issues to which DNA is not material. Inclusion cannot establish guilt, only source identity; exclusion cannot establish innocence, only noncontribution. A match will have limited inculpatory value when there are other disputed issues besides identity, such as intent. Conversely, a failure to match will have limited exculpatory value where the offense was likely to have been committed by a number of people, or where there are likely to have been ''innocent'' sources for the tested residue, such as consensual sexual partners.

The Legal Reception of DNA Typing

The reception of DNA typing evidence by criminal courts in the United States has three striking features. The first is the short interval between the introduction of typing and the admission of its results in criminal trials. The second feature is the vigor and persistence of the challenges to its admissibility. The final feature is the extent to which those challenges have been resolved outside the usual confines of adversary litigation.

DNA typing was taken up by the criminal justice system far more quickly than either fingerprinting or conventional serology. It was almost 30 years from the first scientific use of friction ridge patterns on the fingertips for identification purposes to the routine admission of fingerprint evidence in criminal cases. There was a similar lag between the discovery of ABO blood-group typing around 1900 and the admission of blood-type evidence for identification purposes in the 1930s. In contrast, it was less than two years between the first published scientific discussion of the use of DNA typing for identification purposes, in 1985, and the introduction of typing results in an American criminal trial, in 1987.

Some of this difference may be due to the greatly increased pace of scientific testing and validation between the turn of the century and its final two decades. But that is only part of the story. The enormous cachet of genetic research and technology helps explain both the rapid acceptance of forensic DNA typing and the vigor of the challenges to it. A survey of court cases in 1992, when the admission of scientific evidence in federal and many state courts was still governed by the restrictive *Frye* standard (discussed below), suggested both the extent of judicial acceptance and the magnitude of the challenge. Forensic typing results had been admitted in well over 700 cases in 49 states, but they had been subject to full-dress evidentiary hearings in almost 10 percent of these (Wasserman and Weedn 1992).[4]

This tally, however, does not fully capture the intensity of the challenge to typing evidence. In several highly publicized cases in the late 1980s and early 1990s, the

courts conducted extensive evidentiary hearings, in which some of the nation's leading geneticists and forensic scientists offered sharply conflicting testimony on the reliability and interpretation of DNA matches. The duration, acrimony, and repetitiveness of these hearings convinced many observers that the controversies about DNA typing would be better resolved in an extrajudicial setting, where the admissibility of scientific evidence would not rest on the findings of individual judges and the vagaries of adversary combat.

There was precedent of a sort for this approach in the informal ''consensus conference'' held by prosecution and defense experts in the *Castro* (1989) case, the first criminal case in the US in which DNA typing was subjected to a sustained challenge, and one of the few in which it was excluded. Many observers hoped that a blue-ribbon commission could replicate on a larger scale the success of the *Castro* experts in resolving their differences outside the confines of adversary litigation. This hope now seems naive; the most prominent panel to address scientific issues in DNA typing remained sharply divided by the issues it was convened to resolve.

The first major extrajudicial examination of forensic DNA typing was conducted by the congressional Office of Technology Assessment. Its 1990 report found the technology to be generally reliable, and it dismissed some of the objections to its forensic use as ''red herrings.'' Not surprisingly, the OTA report was dismissed by many critics of forensic typing as a whitewash. The National Research Council attempted to achieve a broader consensus by convening a panel that included leading critics as well as proponents of DNA typing. That panel, which met in 1991–2, vacillated between a highly qualified endorsement of forensic typing as then practiced and a call for a temporary moratorium on the presentation of match statistics. It finally opted for the former (so close to its reporting deadline that a *New York Times* headline story the previous day announced that it was going to opt for the latter). While the panel endorsed both the theory of forensic typing and many of the standard typing procedures, it also called for much stricter standards for certifying and testing laboratories, and it adopted the controversial ceiling principle discussed above.

In the seven years since the NRC report was released, its endorsement has had more impact than its qualifications. While crime laboratories have improved their performance and self-regulation, they remain a long way from the proficiency testing program the report called for. And, as discussed above, a second NRC panel (1996) rejected the ceiling principle, which had found only partial acceptance (and comprehension) in the courts (Kaye 1994).

DNA Typing and the Judicial Assessment of Scientific Evidence

The prominent role of extrajudicial panels in attempting to resolve controversies about DNA typing may have resulted in part from the premium that federal and much state law placed on expert consensus in the admission of scientific evidence. Under the *Frye* standard, which governed the admission of scientific evidence in federal and many state courts when DNA typing evidence was first introduced, judges were required to exclude scientific techniques and tests that did not have ''general acceptance'' in the relevant scientific community. The fact that DNA typing was

rarely excluded in the face of scientific controversy suggests that the courts focused on the general acceptance of its theory and standard methods, not on the sharp disagreement about its controls, quality assurance, and statistical interpretation. But it also suggests that *Frye* (1923) may have lost its hold well before the United States Supreme Court adopted new standards for the review of scientific evidence in 1993. The controversy over the admissibility of DNA typing results highlighted some of the tensions in *Frye*, and may have hastened its demise.

Frye can be seen as a reasonable if unsuccessful effort to preserve the authority of lay judges in reviewing scientific evidence. Rather than requiring the judge to educate herself in the relevant science, or to delegate her authority to a court-appointed expert, *Frye* let the judge resolve controversy by counting heads. In effect, it substituted a social for a scientific criterion: the existence of a consensus in the relevant scientific community.

There are obvious problems in deciding what the relevant scientific community is: the boundaries may be drawn more widely or narrowly, and it sometimes takes an expert to know one. The early controversies over forensic typing dramatized the problem: initially, there was far greater consensus about the reliability of typing among forensic scientists than among population geneticists. To decide that the relevant scientific community included the latter as well as the former was to reduce the odds of finding general acceptance. But how was a lay judge to decide what the relevant community was, without grasping some of the underlying science and technology? Such critical boundary determinations undermined the division of intellectual labor established by *Frye*.

The DNA typing controversies also provoked resistance to *Frye* by appearing to confer a ''dissenter's veto'' on mavericks and zealots within the scientific community. Under *Frye*, judges are not supposed to evaluate disagreement among experts, but merely to regard it as bearing on the issue of consensus. *Frye* thus appeared to give disproportionate weight to dissenters, allowing a small but persistent minority to block a finding of general acceptance. The fact that the articulate, persistent critics of DNA typing so rarely succeeded in doing so suggests that this fear may have been exaggerated. But it certainly influenced the climate of judicial opinion in the early 1990s, when the federal courts were re-examining the *Frye* standard.

In late 1993, the United States Supreme Court finally overruled *Frye*. In *Daubert* (1993), it required federal judges to assess the scientific validity of a test rather than canvass its acceptance. Although *Daubert* may have the effect of relaxing the standards for admitting scientific evidence, its intent was rather to increase the responsibility of judges for evaluating that evidence.

Daubert defined two roles for the trial court: first, to assess the threshold reliability of scientific evidence, based on such factors as its conformity to accepted research methods, its peer-review, and its replication; second, to assess the ''fit'' of scientific evidence to the case at hand. The latter role requires the judge to understand what is properly a scientific question and what is not – an understanding that has often been lacking, as we have seen, in the debate over the appropriate reference population for a DNA match. While a judge lacks the expertise to assess the extent of subpopulation differences or the adequacy of a population database, she is well equipped to assess how or whether the evidence in the case restricts the range of potential contributors

of the source DNA: whether the location, time, or other feature of the offense, or any other evidence in the case, limits potential contributors to certain subpopulations. *Daubert* affirms the competence and responsibility of trial judges to make such determinations of ''fit.''

Social Impact: Criminal Investigation and Adjudication

In contrast to the large body of scholarly writing on the reliability and interpretation of forensic DNA typing, little research has been done on its routine utilization and impact. Almost nothing is known about the vast majority of cases in which DNA typing is performed – cases where typing is employed in the investigatory or pretrial stage, but never introduced at trial. We know very little about how frequently DNA typing is being employed in cases where it is feasible and potentially useful; whether its utilization is limited by a lack of suitable material, budgetary constraints, or institutional inertia; or what role DNA evidence plays in the cases where it is employed.

This is a significant gap in our understanding. The 1992 National Research Council report on forensic DNA typing cautioned that ''the introduction of a powerful new technology is likely to set up unwarranted or unrealistic expectations.'' DNA typing is particularly likely to give rise to unwarranted expectations because of the way it establishes identity: through a person's genetic code. Public perception of DNA typing may be distorted by the same ''genetic essentialism'' that exaggerates the significance of genetic links in custody disputes and genetic predispositions in risk assessment (Dreyfuss and Nelkin 1992).

DNA typing may give rise to exaggerated expectations in two areas. One, which has already been discussed, is in the level of confidence it can provide about source identity. The second is in its impact on the resolution of criminal cases and the operation of the criminal justice system. Forensic typing greatly increases the discriminatory potential of biological residues, and permits a far wider range of biological residues to be analyzed, in far smaller quantities. But it can only make a difference in cases where (1) identity or the occurrence of physical acts is at issue and (2) biological material whose source is relevant to that issue is available for typing, and (3) other evidence bearing on identity is unavailable or inconclusive.

The research of Peterson and his associates suggests that identity is not at issue in most criminal cases, and is less likely to be at issue in cases where forensic evidence is available. Peterson et al. (1987) found, for example, that in about 60 percent of rape cases, the complainant had a prior relationship with the accused, making identity less likely to be an issue. In addition, Peterson et al. (1984) found more biological evidence collected in cases with more extensive victim-perpetrator interaction, which suggests that biological material is more likely to be available in cases where it is less likely to be needed for identification. (At the same time, a recent FBI survey found that DNA was submitted to crime laboratories in less than 10 percent of all rape cases and tested in only 6 percent (Weedn and Hicks 1998: 5). These figures certainly suggest that the potential of DNA typing to resolve identification issues has not been fully realized.) While DNA typing is relevant to other issues besides identity, these and

similar findings suggest that it may not be relevant to the disputed issues in a majority or large minority of criminal cases. Moreover, the impact of DNA typing on cases that do have relevant issues is uncertain. While anecdotal reports suggest that many cases rest heavily on DNA typing, an assessment of its marginal impact requires an appraisal of the other evidence that was available in the case, or could have been made available.[5]

The role of DNA typing on the investigation of criminal cases is virtually certain to increase with the advent of forensic data banking. By 1999, almost every state required DNA samples from convicted sexual or violent felony offenders for inclusion in a computerized database. As these databases become operational, law enforcement officials can check the residues in new or unsolved cases against the profiles of prior offenders. Prosecutions in several states have been initiated by such ''cold hits'' (Weedn and Hicks 1998: 5–6). The impact of forensic DNA data banking has been more immediate and dramatic in the United Kingdom, which allows profiles to be obtained from suspected as well as convicted offenders. In 1995, the year the British DNA database system went into operation, it had 360,000 profiles and was reported to have linked 28,000 people to crime scenes (though how many of those would have been linked by other evidence is not known). The system, eventually expected to include a third of all British males between the ages of 16 and 30, is already reported to have a 50 percent chance of yielding a ''hit'' on the first try (Wade 1998; Weedn and Hicks 1998).

The most striking effect of DNA typing, however, may be in exonerating suspects who would otherwise have been charged, arrested, or convicted. Of the more than 400 tests conducted by the FBI Crime Laboratory by early 1990, over a third excluded the suspect. These high rates of exclusion have persisted; a 1996 national telephone survey of crime laboratories conducted by the Justice Department, that included 13 state and local and 4 private laboratories, as well as the FBI and an armed forces laboratory, found an overall rate of exclusion of 23 percent, with 16 percent of tests inconclusive (Conners et al. 1996).

While some of these exclusions served to eliminate ''usual suspects'' and some may have limited exculpatory value, an unknown percentage vindicated suspects who would have been, or already were, charged or arrested. The most compelling evidence of the exculpatory potential of DNA typing comes from a 1996 Justice Department report. It identified 28 cases in which a convicted defendant was ultimately released as the result of a DNA test excluding him as the source of organic material found on the victim or at the crime scene. All 28 cases involved sexual assault; in 6, the victim was murdered (Connors et al. 1996).

Forensic DNA typing may have a significant effect not only in vindicating particular defendants, where its impact will be limited to cases with preserved residues, but in increasing skepticism about other forms of identification evidence. Even a handful of well-publicized cases where DNA typing unambiguously exonerates a suspect implicated by eyewitness or other standard evidence may sensitize law-enforcement officials to the risk of mistaken accusations. The attention paid to DNA typing may also promote the more frequent and careful utilization of other forensic evidence. The accuracy of criminal adjudication might be greatly enhanced by placing less reliance on conventional forms of identification and greater reliance on forensic evidence.

Social impact: privacy

The threat to privacy from DNA typing arises from two sources: the ease with which DNA can be obtained and the amount of data it can yield. Usable DNA can be extracted not just from blood and semen, which may only be taken with probable cause and a court order, but from trace amounts of tissue and saliva. The courts have not yet resolved what constraints govern the ''search and seizure'' of such material by oral swab or hair sample, or whether people have any constitutionally protected expectation of privacy in such material once it leaves their bodies (see generally, Office of Technology Assessment 1988). Federal courts have, however, upheld the taking of DNA samples from all convicted felony offenders for use in forensic databases (Wade 1998).

More broadly, civil libertarians are concerned about the potential for abuse arising from the inclusion of increasingly large segments of that population in DNA data-banks. Now limited to profiles from convicted defendants, those data-banks may be augmented by DNA from other groups, such as military personnel and employees in high-security positions. It may soon be technically possible to screen a large portion of the population for involvement in any crime where testable body residues are found. Perhaps more worrisome, these data banks may also be augmented by other types of information, such as fingerprints, criminal records, and behavioral profiles.

The DNA molecule itself is becoming an increasingly rich source of personal information. Thousands of medical conditions have already been mapped to specific regions of the genome, and genetic ''markers'' are likely to be found for many physical traits and behavioral and psychiatric conditions. While most of the loci used in typing do not appear to have functional significance, the mapping of the human genome may place some of these loci in close proximity to the genes associated with significant traits. Access to personal data could be limited by storing only DNA profiles, but there are reasons for preserving DNA, such as the opportunity for reanalysis by an independent laboratory or with a new technique. As typing becomes more reliable and more standardized, however, preserving samples for reanalysis may become less of a concern.

Conclusion

Forensic DNA typing is unlikely to either revolutionize criminal investigation or radically undermine privacy. In the area of criminal prosecution where it has had its most visible impact, sexual assault, it may well effect an enduring increase in the frequency and accuracy of convictions. And its role in vindicating wrongfully convicted defendants has a moral significance that is not reflected in the small number of cases.

The most encouraging long-term effects of the DNA typing may lie in its contribution to more professional law enforcement, to a healthy skepticism about the standard types of evidence by which most convictions are obtained, and to closer collaboration among scientists, policy-makers, and lawyers in the review of scientific evidence.

Notes

1 Mitochondrial DNA, which is inherited from the mother, has also been used in recent years for identification purposes, although rarely in criminal cases. It can be recovered from residues where nuclear DNA cannot be found, is available in insufficient quantities, or is too degraded to analyze. But because only a small region of mitochondrial DNA is highly polymorphic, it lacks the discriminatory potential of nuclear DNA (Weedn 1996).

2 There is also the problem of considering siblings and other relatives as alternative suspects. The probability that the DNA sample came from an (untested) relative of the suspect may be far greater than the possibility that it came from someone picked at random from some larger population, and some commentators have argued that any match statistic presented to the fact finder must be qualified by this possibility, unless all relatives can be tested, or ruled out as suspects (see Lempert 1991; Symposium 1997: 454–61).

3 Actually, it proposed both an interim ceiling principle, for use until adequate subpopulation databases were developed, and a permanent ceiling principle once they were. Both principles have complexities that I have ignored in the text.

4 The few cases to exclude match results altogether did so because of doubts about the laboratory's performance, not about the underlying theory or the population statistics; in a larger number of cases, still a small minority, the match was admitted, but its statistical interpretation was excluded or restricted.

5 The only published study on the impact of forensic DNA typing (Purcell et al. 1994), a survey of the prosecutors in about a quarter of the first 200 recorded cases in which DNA evidence was introduced at trial, found that testimony from a DNA expert significantly increased the odds of conviction and the length of sentence. The prosecutors surveyed regarded DNA typing as important in winning cases involving stranger-crimes and cases involving older, employed defendants. In an ongoing study of the utilization and impact of forensic DNA typing in four Maryland jurisdictions, conducted by the author and several colleagues, preliminary analyses indicate that typing is more likely to be employed in stranger crimes, crimes without confessions, and crimes involving weapons, and that matches are associated (in one or more jurisdictions) with higher conviction rates and longer sentences (Wasserman et al. 1999).

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