The Innocence Network: Analysis of 194 American DNA Exonerations

Greg Hampikian,1 Emily West,2 and Olga Akselrod2

1Department of Biology and Department of Criminal Justice, Boise State University, Boise, Idaho 83724; email: greghampikian@boisestate.edu
2The Innocence Project, New York, New York 10013

Keywords
STR, mitochondrial DNA, Y-STR, RFLP, DNA fingerprinting

Abstract
This new analysis of 194 DNA exonerations, representing 171 criminal events, examines the types of evidence and DNA testing that have been used to free the victims of wrongful conviction. In 43% of the exonerations, the true perpetrator of the crime was identified through postconviction testing. The types of DNA testing used to free the innocent parallels the growth of these techniques in forensic science. Short tandem repeat (STR) analysis now prevails (70%), though Y-STR analysis (16%) and mitochondrial testing (10%) are still used when STR analysis is not feasible, and the recently developed mini-STRs have been used for exonerations since 2008 (2.6%). The types of exculpatory evidence included intimate swabs (65%), clothing (53%), hair (13%), fingernail evidence (5%), cigarettes (3%), and other evidence. The most common factor associated with wrongful convictions was misidentification (75%), including misidentification by the victim (65%). False confessions (including admissions and pleas) were obtained in 30% of the cases, and snitch testimony (jailhouse and government informants) was used in 22% of the false convictions. Several types of invalid forensic science testimony were used to wrongfully convict in the 146 trials where transcripts or reliable forensic science data were available for analysis. Invalid testimony included serology (38%), hair comparison (22%), fingerprint comparison (2%), and bite mark comparison (3%).
BRIEF HISTORY OF DNA AND IDENTITY
The First Applications of DNA Fingerprinting

At the eighteenth International Symposium on Human Identity (2007) in Hollywood, California, Sir Alec Jeffreys, the father of forensic DNA typing, said, “The smartest thing I ever did was call it DNA fingerprinting.” That may be true, because other techniques he developed included more typically informative but less memorable names such as “minisatellite variant repeat mapping by PCR” (21). Although this technique was also a useful method of human identification, the title itself was not the stuff of tabloid headlines.

In 1985, three groundbreaking Nature papers by Jeffreys et al. demonstrated that tandemly repeated minisatellites in humans differed in related individuals (8), could distinguish a person from everyone but his or her identical twin (9), and could decide legal cases involving identity (10). The last of the three papers described a UK immigration case where Jeffreys’s remarkable probes showed that a UK mother was indeed related to the son whom immigration authorities had suspected was not her child. A single autoradiogram meant the difference between continued family life in England and a potential forced repatriation to Africa.

Jeffreys himself was surprised by the quick legal acceptance of his new technique (7), especially when this early immigration case soon led to the first criminal investigation to use DNA fingerprinting. The story of this rape and murder of two girls, three years apart, was well described in Joseph Wambaugh’s popular book The Blooding (19). The rapist left his biological calling card in the form of semen recovered from both victims. At the time of these investigations (1985–1988), serology was the only statistically based identification method available. Analysis of this evidence showed that whoever killed the girls was a secretor, a person whose blood type is expressed in all body fluids, including semen. Through traditional detective work, the police apprehended a primary suspect who matched the blood type (A) and secretor status associated with the semen. Only 10% of Englishmen share these characteristics, and during interrogation the 17-year-old suspect, Richard Buckland, confessed to the first killing. The only sticking point was that he stubbornly resisted confessing to the second, very similar, rape and murder. Jeffreys was given samples of the semen recovered from both victims and a reference sample from the suspect. With his new DNA fingerprinting probes, Jeffreys found that the semen samples indeed most likely came from the same man—however, that man was not the suspect. Once this result was independently confirmed by the Home Office, the suspect was released, and a massive voluntary DNA dragnet ensued; 4,582 local men gave samples to the police, and, as expected, 90% were eliminated by serology. The remaining samples were subjected to DNA fingerprinting, but no match to the semen was found. The final break in the case came from a woman who told investigators that she overheard a man, Ian Kelly, say that he had given a blood sample for his friend, the baker Colin Pitchfork. Pitchfork was then compelled to give a fresh sample, and is presently serving time for the crimes (19, 20).

This first DNA criminal case demonstrates several principal factors involved in DNA exonerations:

- In most cases, a true crime has been committed, and identity is at issue.
- The exonerating evidence is almost always collected during the original investigation; the preservation of that evidence is essential.
- An overreliance on human testimony, even confessions, can lead to false conclusions.
- Scientific matches (like the blood type evidence in this case) must be analyzed within a statistical framework, or else they can lead to false convictions.
- Investigators, like scientists, must be willing to reject a theory that contradicts the results of scientific testing.
Although DNA testing was able to exonerate Buckland before he was brought to trial and possibly convicted on the basis of the other evidence against him, DNA testing came too late for many others. To date, there have been 265 Americans who were wrongly convicted and whose convictions were later overturned based primarily on new DNA evidence that established their innocence. These cases teach us important lessons in the fallibility of the legal process and the kinds of evidence that lead to the conviction of innocents, including eyewitness misidentifications, false confessions, and forensic science that has not risen to the rigors of blind testing and statistical analysis.

This article reviews the history of DNA exonerations obtained by the Innocence Project and similar organizations in the United States, and presents new analysis based on an examination of each case with respect to the types of DNA testing used to exonerate and the types of evidence leading to exonerations. The authors of this article are all members of the Innocence Network: Emily West is research director at the Innocence Project, Olga Akselrod is a staff attorney at the Innocence Project, and Greg Hampikian is the volunteer director of the Idaho Innocence Project. The data on types of evidence and testing that led to exonerations most often came from official lab reports and/or motions to vacate the convictions, after DNA proved innocence. The Innocence Project obtained these documents from the lawyers representing the DNA exonerees during their exoneration process (for details, see Data Analysis and Methodology, below). The data present a contextual overview of these cases relating to type of crime, time served, whether the real perpetrator was identified, and the role of contributing causes of wrongful conviction, including misidentification, whether a false confession or plea was obtained, the role of snitch testimony, and the use of invalid or invalidated forensic science at the original trial.

These remarkable exonerations are the ultimate testimony of DNA's power—and more generally the power of science—to reduce errors in the justice system. It is worth noting, however, that even with the injection of science into the criminal process, freedom nevertheless depends on human laws and the very human administration of those laws. Sometimes science is ignored—or, worse, actively opposed. Even clear DNA results can be disregarded, as they were in the prosecution of one of the most famous crimes in New York City history, the 1990 Central Park Jogger case. Four of the five young suspects, ages 14–16, confessed to the rape of the jogger after long interrogations. However, the semen DNA recovered from the victim’s vagina, tights, and socks was consistent with a single donor, and did not match any of the suspects or the victim’s only consensual partner. Rather than allowing the suspects to retract their confessions and following up on the DNA evidence, the state crafted theories—without factual basis—to discount the DNA. These theories included, for example, that the hospital’s collection of the semen was less than ideal and they may have missed some of the DNA. The prosecution’s tactics are clearly recorded by former New York City prosecutor Harlan Levy in his book *And the Blood Cried Out* (14). However, in 2002, all of the Central Park Jogger convictions were vacated. A violent serial rapist and murderer confessed to the rape, described his solo attack on the victim, and matched all the DNA evidence. Coincidentally, the rapist who confessed to the Central Park Jogger attack, Matais Reyes, is also featured in Levy’s book in regard to a series of 1989 rapes and stabbings. Although science has the power to falsify a bad hypothesis, legal authorities must still be willing to reject a case theory when the scientific data show it to be false.

### Organizations Using DNA to Exonerate
Centurion Ministries was the first organization established to exonerate innocent prisoners. Founded in 1983 by James McCloskey, a lay minister and former Wall Street executive, this nonprofit organization takes on innocence claims in rape and murder cases with sentences of life or death.
The Innocence Project, created by Barry C. Scheck and Peter J. Neufeld, was established in 1992 as a nonprofit legal clinic affiliated with the Benjamin N. Cardozo School of Law at Yeshiva University. This litigation and policy organization is dedicated to freeing innocent prisoners through DNA testing and reforming the criminal justice system to prevent future injustices. Soon afterward, other innocence organizations and law clinics began to surface throughout the United States, and the Innocence Network formally established itself in 2005. This network is a group of affiliated organizations taking on claims of innocence from prisoners. To date, there are a total of 64 Innocence Network Projects—55 in the United States and 9 in other countries.1

Funding sources for the projects include university support (the largest source of funding for clinics located within law schools), private donations, and foundation support. The annual budgets are quite diverse—from less than $10,000 to over $6 million (at the Innocence Project) per year.

DESCRIPTION OF FORENSIC DNA TESTING METHODS

In 1987, Tommie Lee Andrews became the first American convicted by DNA evidence. This Florida conviction signaled a sea change in biological evidence collection and analysis, and was the impetus behind legislation creating DNA databases in several states. As with any new forensic technology, there were significant legal challenges to DNA evidence in the late 1980s and early 1990s, which led to refinements in both forensic DNA science and the law. One of the most significant court challenges occurred during the 1989 Castro case in New York City (14). This case is important not only because of its legal ramifications and the press attention it generated, but also because it thrust two former Legal Aid attorneys—Peter Neufeld and Barry Scheck—into the DNA spotlight. The Castro case also involved some of the finest minds in the emerging field of molecular genetics, and brought Neufeld and Scheck to James Watson’s Cold Spring Harbor laboratory. Two of the witnesses who were originally pitted against each other at a DNA admissibility hearing before the Castro trial were MacArthur “Genius” Award winner Eric Lander of MIT and future Nobel Prize winner Richard Roberts. In the end, the particular DNA autoradiogram in the Castro case was found inadmissible because it lacked an important control to assure that there was sufficient DNA to prevent band dropout. An image of the ethidium–bromide-stained gel (before Southern blotting) would have sufficed, but the company that performed the test, Life-codes, did not use this control at the time. Other significant problems in the nascent field of DNA fingerprinting were also exposed by the experts consulted in this case (13), which certainly helped improve laboratory practices. The press covered the story as a brewing controversy over DNA evidence in general, but the actual result was that a foundation for DNA admissibility was firmly laid, and the scientists all agreed that DNA held great promise for forensic science. Legal challenges to real and perceived abuses of DNA evidence will continue (15), but the preeminence of DNA as a method of identification is firmly established.

Restriction Fragment Length Polymorphisms

The science of DNA identification developed rapidly through the 1980s and 1990s (reviewed in 17). Jeffreys’s original DNA fingerprints used multilocus probes on Southern blots of total genomic DNA that had been digested with one restriction enzyme. Basically, genomic DNA was extracted from a small biological stain (approximately the size of a dime or larger), digested with a restriction enzyme, and blotted onto a membrane (nitrocellulose or nylon). In Europe the enzyme of choice was HinfI, but in the United States it was HaeIII. (This was the
beginning of what has become the great challenge of heterogeneous international methods and standards in DNA profiling.)

Within a few years, the multilocus probes were refined to single-locus probes that allowed each gel lane to be read as a simple one-band (homozygous) or two-band (heterozygous) pattern. These probes resulted in profiles with a high power of discrimination, to the point of identifying an individual, but required a significant amount of nondegraded genomic DNA, and were labor and time intensive—taking up to two months to develop a suitable autoradiogram. Profiles developed in this way were the first data to be stored in criminal DNA databases.

**DQ Alpha, Polymarker, and D1S80**

The polymerase chain reaction (PCR), invented by Kary Mullis in 1985, changed DNA analysis forever. This invention, which garnered him a Nobel Prize, was soon incorporated in forensic identification testing, allowing scientists to use a thousand times less DNA (0.5 ng) than they need for standard restriction fragment length polymorphisms (RFLPs). By the early 1990s, commercial PCR kits with conveniently bound probes were being used by law enforcement laboratories across the United States. These kits included membrane-bound, sequence-specific oligomers that discriminated between alleles differing by a single base. The DQ alpha test strips allowed for colorimetric detection of alleles from the HLA locus on chromosome 6, and the Polymarker test scored alleles from five other loci simultaneously: low-density lipoprotein receptor, glycophorin A gene, hemoglobin gamma globin, D7S8 (a noncoding region on chromosome 7), and GC (group-specific component). These tests were easy to perform, relatively quick, and sensitive (requiring a small amount of DNA); however, they had a low power of discrimination: approximately 1 in 2,000 people could be discriminated. The DQ alpha and Polymarker tests were sometimes combined with the PCR analysis of the D1S80 locus, which increased the power of discrimination of these combined profiles, but the statistical power still fell far short of RFLP’s ability to individuate (see 17).

**Short Tandem Repeats and Match Statistics**

Contemporary short tandem repeat (STR) kits have been the mainstay of forensic testing worldwide for more than a decade (2). STR profiles are the basis for the Combined DNA Index System (CODIS), a system of databases at the local, state, and national level that contain and compare the profiles of offenders and the profiles of unknown perpetrators developed from crime evidence and cold cases. Although different loci are used in different countries, since 1998 the U.S. Federal Bureau of Investigation (FBI) has required that labs contributing offender profiles to the U.S. National DNA Index System (NDIS) database upload alleles from at least the 13 core loci. A complete profile from these loci is always expected to have a random match probability far lower than 1 in a trillion. Although matches between siblings have been reported for 12 of 13 loci, no matches at 12 core loci for nonsiblings has been reported. Most labs will report a 13-locus match as confirmation that the evidentiary sample originated from the suspect or his or her identical sibling.

Some U.S. laboratories have also validated the use of mini-STRs. These tests amplify DNA from the standard STR loci, but use primers closer to the target tandem repeat region and thus produce shorter amplicons. Mini-STR primers work better than traditional STR primers on degraded samples that contain smaller (on average) fragments of DNA, because PCR requires intact DNA (between the primers) to amplify.

It is usually a simple matter to include or exclude an individual as a possible contributor of DNA to a single-source, complete STR profile. An inclusion should always be accompanied by a relevant statistic, but in the case of an exclusion, no statistic is needed. An exclusion is absolute, and even a single locus can exclude a suspect. The analogy to a phone number illustrates this point. Imagine that investigators develop a partial telephone number for a cell phone found at
a crime scene. If they can only determine that the phone number starts with area code 208, then every phone registered outside of Idaho is excluded, and no statistic is needed to justify this exclusion. However, if the investigators have a suspect with a 208 area code and want to demonstrate the power of this inclusion, they need to determine how common the 208 area code is in the relevant population. If the relevant population is “phones in Idaho,” then this partial match is not very powerful; if, however, the phone was found in an isolated community in Australia, then it may be an important piece of evidence, and various statistical measures could be proposed to illustrate its significance.

The reliance on statistics sets DNA analysis apart from many other forensic science practices. In single-source DNA samples, the calculations are rather straightforward, but mixtures of three people or more can be remarkably difficult to deconvolute, and different laboratories have very different interpretation guidelines, often resulting in disagreement between experts in the analysis of complex mixtures. The Scientific Working Group on DNA Analysis Methods (SWGDAM), which meets under the guidance of the FBI, states in its 2010 interpretation guidelines that “the laboratory must perform statistical analysis in support of any inclusion that is determined to be relevant in the context of a case, irrespective of the number of alleles detected, and the quantitative value of the statistical analysis” (18). However, many U.S. crime labs do not yet report statistical analysis with all inclusions, particularly in cases where there are complex mixtures. Without statistical measures, statements such as “cannot exclude” do not comply with the 2010 SWGDAM guidelines, but are still being used by some crime labs.

**Y-Chromosome Short Tandem Repeats**

Y-chromosome markers are very helpful in cases where there is a lot of DNA from a female victim and little from a male perpetrator. Typical examples include sexual assault without ejaculation, sexual assault of a female by an azoospermic (vasectomized) male, male DNA under the fingernails of a female victim, and male “touch” DNA on the clothing or belongings of a female victim.

In cases where there is a sufficient male-to-female ratio of DNA (as determined by sex-specific quantification), traditional STR analysis is preferred, because profiles are individuating and can be uploaded to the NDIS database. Y-STR profiles have a low power of discrimination, cannot individuate, are identical in related males who share a Y chromosome, and cannot be used to search the NDIS database. However, a single Y-STR locus (or test) is sufficient for an exclusion, so Y-STRs are powerful tools for exoneration. Mini-Y-STRs (1, 3, 16), developed by several laboratories, are similar to the mini-STRs described above but are not currently used in forensic casework.

**Mitochondrial DNA Analysis**

Like Y-STRs, mitochondrial haplotypes have a low power of discrimination, cannot individuate, and cannot be used to search the NDIS offender and forensic sample database. They are, however, recorded for unidentified remains, and compared with the missing-persons reference database maintained by the CODIS for Missing Persons [CODIS(mp)].

Mitochondrial haplotypes are passed from mother to child through the oocyte, without any contribution by males. Mitochondrial analysis is typically used when DNA is too degraded for STR analysis, or when evidence consists of hair shafts without roots. The abundance and persistence of mitochondria (up to thousands per cell) is why they are often used in cases where evidence or remains were subjected to extreme conditions and/or great lengths of time. PCR is used to amplify the hypervariable regions of the mitochondria, which are then sequenced and compared with the revised Cambridge Reference Sequence (rCRS). Although the power of discrimination for mitochondrial profiles is low (comparable to Y-STRs), they are excellent for exclusions
in cases where hairs or degraded evidence is required to exclude an individual.

**DATA ANALYSIS AND METHODOLOGY**

**Background Data on Exonerees**

The information on DNA exoneree statistics presented in Table 1 (see Overview of DNA Exonerees’ Cases, below) comes from the database maintained by the Innocence Project. Each time a DNA exoneree is announced, information on the case is entered into this database based on information obtained by the postconviction lawyers and/or reliable media sources. In this review, all numbers and data represent exonerees and their cases (194), rather than the number of criminal events (171), which is a smaller number because some wrongful convictions involved multiple exonerees.

**Forensic Science Used at Trial**

The information presented on valid and invalid forensic science used at the exonerees’ trials comes from data on the first 220 DNA exonerees in Brandon Garrett & Peter Neufeld’s (6) article “Invalid Forensic Science Testimony and Wrongful Convictions.” Additional data were obtained from Garrett’s (5) book *Misjudging Innocence*, which updates the data presented in Garrett & Neufeld’s article to include the first 250 DNA exonerees.

The types of testimony that Garrett & Neufeld identified as invalid fell into six categories (see Appendix): nonprobative evidence presented as probative, exculpatory evidence discounted, inaccurate frequency or statistic presented, statistics provided without empirical support, nonnumerical statements provided without empirical support, and conclusions that evidence originated from the defendant.

**Types of Testing and Types of Evidence Used to Exonerate**

Information on type of DNA testing and type of evidence used to exonerate has never been

---

**Table 1 DNA statistics for 194 exonerees, representing 171 criminal events**

<table>
<thead>
<tr>
<th>Category</th>
<th>Count</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Race of exoneree</td>
<td></td>
<td></td>
</tr>
<tr>
<td>African American</td>
<td>112</td>
<td>58</td>
</tr>
<tr>
<td>White</td>
<td>62</td>
<td>32</td>
</tr>
<tr>
<td>Hispanic</td>
<td>15</td>
<td>8</td>
</tr>
<tr>
<td>Asian</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Cross-race crime</td>
<td>83</td>
<td>43</td>
</tr>
<tr>
<td>Major crime category</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rape or sexual assault without murder</td>
<td>130</td>
<td>67</td>
</tr>
<tr>
<td>Rape and murder</td>
<td>52</td>
<td>27</td>
</tr>
<tr>
<td>Murder without rape or sexual assault</td>
<td>9</td>
<td>5</td>
</tr>
<tr>
<td>Other (2 carjacks, 1 attempted murder)</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>Prison time</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Average number of years in prison</td>
<td>13.3</td>
<td>—</td>
</tr>
<tr>
<td>Cumulative number of years in prison</td>
<td>2,535</td>
<td>—</td>
</tr>
<tr>
<td>Real perpetrator</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Exonerees who had the real perpetrator</td>
<td>84</td>
<td>43</td>
</tr>
<tr>
<td>identified in their cases</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of additional violent crimes real</td>
<td>65</td>
<td>—</td>
</tr>
<tr>
<td>perpetrators were convicted of,</td>
<td></td>
<td></td>
</tr>
<tr>
<td>subsequent to the wrongful convictions</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Misidentification</td>
<td>145</td>
<td>75</td>
</tr>
<tr>
<td>Exoneree misidentified by victim</td>
<td>126</td>
<td>75</td>
</tr>
<tr>
<td>Guilty pleas, confessions, and admissions</td>
<td>57</td>
<td>30</td>
</tr>
<tr>
<td>Guilty plea with or without specific</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>confession or admission during interrogation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Guilty plea with no specific confession or</td>
<td>6</td>
<td>3</td>
</tr>
<tr>
<td>admission during interrogation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Confession by exoneree only</td>
<td>35</td>
<td>18</td>
</tr>
<tr>
<td>Confession by codefendant only</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>Confession by both exoneree and codefendant</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>Snitch testimony (including jailhouse and</td>
<td>42</td>
<td>22</td>
</tr>
<tr>
<td>government informants)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Death penalty</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>Part of a group exoneration</td>
<td>36</td>
<td>18</td>
</tr>
</tbody>
</table>

---

*aRace data was missing for 3 exonerees (2%).

bThe percentage of cross-race crime is probably higher than 43%, but we could not confirm victim race in 46 cases.

*Includes guilty pleas where no specific confession or admission was given during interrogation.
systematically collected for the DNA exonerees. For our study, lab reports and motions to vacate were the two most common sources used to obtain this information, although when neither of these documents were available, or when the motion to vacate did not provide enough detail, published news or legal articles and reports were used.

Many of the lab reports were obtained through the document archives now available via the Innocence Record Web site (http://www.innocencerecord.org), developed by the law firm Winston & Strawn in collaboration with the Innocence Project. This archive of documents is a result of years of gathering all available nonprivileged case documentation on DNA exonerees and having them scanned and uploaded into a searchable database. Although the data obtained from the available postconviction lab reports most likely represented the full picture of the types of evidence and testing that provided probative exculpatory results, it is possible that there were additional lab reports that were not made available and that may have also contained information relevant to our analysis.

This review examines only the specific types of testing and evidence that resulted in probative exclusionary findings—that is, evidence used to exonerate. Therefore, the results do not represent the entire scope of types of testing pursued and types of evidence tested. In many of the cases, additional testing was conducted that did not yield interpretable results or developed results that were not relevant to establishing the identity of the perpetrator. For example, a case may have involved STR and Y-STR testing on an intimate swab and clothing. If the swab yielded a foreign profile that exculpated the defendant, but the clothing yielded only a profile consistent with the victim’s boyfriend (and thus was not relevant to establishing the perpetrator’s identity), only the swab was included in the study. Likewise, if testing produced only a Y-STR profile on the swab and no male profile with STR testing, only the Y-STR testing was included in our data.

Complete data on types of testing and evidence used to exonerate were located for 194 of the first 255 DNA exonerees. Owing to a lack of testing and evidence data, the 61 exonerees excluded from this study were significantly more likely to have been exonerated in earlier years. For example, the average year of exoneration for cases in this study is 2003, but it is 2001 for the 61 exonerees who were excluded from this study. Therefore, because our analysis underrepresents earlier exonerations, when RFLP and DQ alpha testing were in use, the actual number and percentages of exonerations using those methods is greater than reported in this study. Table 2 provides a breakdown of missing cases by year exonerated.

**OVERVIEW OF DNA EXONEREES’ CASES**

**Summary of DNA Exoneree Statistics**

As Table 1 presents, approximately two-thirds of the DNA exonerees are nonwhite, and at least 43% of these cases involve cross-racial crimes. Nearly all of the DNA exonerees (94%) were convicted of crimes involving sexual assault, and nearly one-third were convicted of crimes involving homicide.

On average, DNA exonerees spent over 13 years in prison—ranging from less than 1 year to 35 years—for crimes they did not commit, while the real perpetrators remained unidentified. Eventually, just under half of these 194 exonerees had the real perpetrators identified in their cases. Among the real perpetrators identified in this sample, 34 were convicted of a total of 65 other violent crimes during the time that an innocent person served for their crime.

The known factors that contributed to these 194 wrongful convictions include eyewitness misidentification (75%), the use of invalid forensic science at trial (45%—discussed in the next section), guilty pleas and/or confessions or admissions of involvement in the crimes by exonerees (30%), and the state’s use of jailhouse or government informants (22%). Although other factors also contributed to some of these
wrongful convictions, including police and prosecutorial misconduct and ineffective assistance of counsel, they are more difficult to systematically quantify and were not considered for the present study.

**Forensic Evidence Used at Original Trial**

As mentioned earlier, data discussed in this section are pulled from Garrett & Neufeld’s (6) article “Invalid Forensic Science Testimony and Wrongful Convictions” and Garrett’s (5) book *Misjudging Innocence*. Data on forensic testimony used at trial were available for 146 of the 194 exonerees. In the remaining 48 cases, 12 pled guilty, and the rest either did not have transcripts or reliable data available on the relevant forensic science testimony, or had no indication that forensic science was presented at trial.

At least 45% of these 194 exonerees had forensic science expert testimony at their trials that was invalid or incorrect, or testimony in which analysts did not disclose exculpatory results. However, not all testimony was improper—approximately 40% of the cases had valid testimony at the original trials relating to the forensic evidence. The definition of valid testimony speaks only to whether the language used and the data presented by the experts at trial fit within what was appropriate given the standards of the time, not whether the conclusion or inferences were true. It is possible that valid testimony about a match of a suspect to an evidentiary stain (by blood type, for example) could later be undone by more
Table 3 Types of valid and invalid forensic science expert testimony used at original trial (n = 146 cases with available forensic science data)

<table>
<thead>
<tr>
<th>Type of testimony</th>
<th>Valid testimony given (n = 77); number in parentheses is testimony at trial that actually excluded the exoneree</th>
<th>Improper testimony or undisclosed exculpatory evidence (n = 88)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serology</td>
<td>32 (3)</td>
<td>56</td>
</tr>
<tr>
<td>Hair</td>
<td>39 (13)</td>
<td>32</td>
</tr>
<tr>
<td>Fingerprints</td>
<td>15 (13)</td>
<td>3</td>
</tr>
<tr>
<td>DNA</td>
<td>9 (9)</td>
<td>4</td>
</tr>
<tr>
<td>Bite marks</td>
<td>1 (0)</td>
<td>4</td>
</tr>
</tbody>
</table>

Discriminating DNA testing. Testimony categorized as invalid was invalid at the time it was given. Table 3 presents more details about the types of forensic science testimony used in these cases.

**Serology.** Serology (including analysis of blood, saliva, semen, and vaginal fluids) was the most common type of testimony given at trial, and nearly two-thirds of all serology testimony examined for this study was found to be improper. Most of the exoneration cases analyzed here involved sexual assaults, and the evidence collected in rape kits often contains mixed samples (cellular material from both the victim and the assailant). Because serology featured so prominently in many of the cases where biological evidence was available for postconviction testing, the errors in this type of testimony have particularly come to light through the DNA exonerations. Garrett & Neufeld’s (6) article describes, the strongest conclusion an analyst can properly draw from visual hair comparisons is that the hair is “consistent with” or “could have come from” the defendant. However, some analysts went well beyond this conclusion, using words such as “identical,” “more likely than not [that it originated from the defendant],” and “match” to describe their findings.

**Fingerprints.** Only 3 of the 18 cases involving fingerprint testimony were found to be invalid or improper. In the other 15 cases, the analyst properly testified that the fingerprints excluded the exoneree (13 cases), were unidentifiable (1 case), or were nonprobative (1 case). In the 3 cases that were found to be problematic, the analyst in 1 case reported that the fingerprint was unidentifiable when in fact there was a clear print (later discovered and analyzed); in the 2 other cases, police officers who testified did not disclose the fact that there were fingerprints that excluded the exonerees.

**Hair.** Hair microscopy testimony was the second most common type of testimony given at trial, and just under half of all testimony relating to hair was deemed improper. Hair microscopy involves visually comparing characteristics of evidentiary hair, with reference hair(s) collected from a defendant and victim(s). One common type of invalid testimony involved improper statistics. Hair microscopy has never been systematically studied to determine the frequency with which certain characteristics of hairs are found within certain populations. As a result, analysts cannot legitimately discuss probabilities that a certain hair came from a particular individual. A few analysts ignored these fundamentals and made up their own frequencies and probabilities based on their own unfounded estimates. Additionally, some analysts improperly exaggerated the probative value of hairs. As Garrett & Neufeld’s (6) article describes, the strongest conclusion an analyst can properly draw from visual hair comparisons is that the hair is “consistent with” or “could have come from” the defendant. However, some analysts went well beyond this conclusion, using words such as “identical,” “more likely than not [that it originated from the defendant],” and “match” to describe their findings.
courtroom, there were at least 15 cases where DNA was tested prior to conviction. Of these 15, 13 had transcripts or other accurate information on the DNA results available. The majority of these cases included proper testimony, with DNA results that excluded the exoneree (9 of the 13 cases). These exclusions were explained away by the state in various ways—perhaps the defendant had an unknown codefendant, the DNA could have come from a consensual sex partner, etc. In 4 cases, however, the testimony regarding DNA was not proper.

In 5 of the 13 cases, DQ alpha tests included the exonerees as possible contributors. In 4 of these 5 cases, however, more discriminating tests performed postconviction excluded the exonerees. In the remaining case, a second round of DQ alpha testing exonerated the defendant after it was discovered that the original lab analysis was incorrect.

There were four cases where improper DNA testimony was given at trial. In one, the analyst testified about a match based on DQ alpha testing; however, the analyst did not disclose that it was only a partial match. In another case, the analyst did not provide the proper statistic for the population included by the results of DQ alpha testing. In a third case, the analyst testified that the DNA matched the exoneree, but failed to disclose an additional exclusionary DNA result. In the final case, the analyst misinterpreted the results of the testing (which was performed incorrectly—failing to separate the male and female DNA during differential extraction), falsely including the exoneree as a source of the DNA when in fact he should have been excluded.

**Bite marks.** Bite mark testimony was introduced in five of the exonerees’ trials. One reason that this type of forensic analysis is controversial is that it assumes that every person’s bite mark impression is unique, but the field lacks the statistical basis for this assumption (6). In four of the five cases with bite mark expert testimony, the testimony was deemed improper, with analysts suggesting a definite or near-certain match to the defendant.

### TYPES OF DNA TESTING USED TO EXONERATE

**Overview of Types of Testing**

**Figure 1** presents the distribution of types of DNA tests used to exonerate the wrongfully convicted in this sample. As described above, this review examines only types of testing and evidence that provided probative exclusionary results, rather than all tests performed and evidence tested. Also, as mentioned in Data Analysis and Methodology (above), the exonerees
that were not included in this sample were more likely to have been exonerated earlier; therefore, this sample underrepresents the numbers for RFLP and DQ alpha testing.

The most common type of testing leading to exoneration was STR. This method was used to exonerate 135 exonerees (70%)—97 from STR testing alone, and 38 through STR and another type of testing (nearly all types of testing that relied on more than one type of test included STR as one type). DQ alpha (which is no longer used) was the second most common test, leading to exonerations in 40 cases (21%). The third most common type of test used to exonerate was Y-STR (32%–16%), either alone or in combination with another method—all but one being STR. Mitochondrial DNA testing aided in 19 exonerations. Five cases relied, at least in part, on RFLP testing, which is also no longer used. Finally, five of the more recent cases involved exclusionary mini-STR results.

**Trends in Types of Testing Over Time**

Figure 2 presents the types of testing used to exonerate the wrongfully convicted over time. Complete data were not available on the year that testing was performed; therefore, the year of exoneration is used here as a proxy. The average time from testing to exoneration (for those with information on both) was approximately one year. However, there are some cases where testing was performed much earlier than the actual exoneration. For example, Ryan Matthews and Travis Hayes were convicted of a murder in 1998 and 1999 after being misidentified by several witnesses. This case also involved a confession by Hayes, who told police after a lengthy interrogation that he was the getaway driver and Matthews the shooter. DNA evidence (DQ alpha and STR) was presented at their trials and excluded both of them as the source of DNA found on the ski mask worn by the perpetrator. Despite this, they were convicted. Years later, the defendants’ attorneys learned of an alternate suspect, and his DNA was found to match the DQ alpha and STR profiles on the ski mask. Based on these results and additional STR testing that excluded the defendants as sources of DNA on other clothing from the perpetrator, Matthews and Hayes were exonerated (in 2004 and 2007, respectively). Therefore, although Figure 2 shows a DQ-alpha-related exoneration as late as 2007, all of the DQ alpha tests were actually performed in the 1990s.

During the 1990s, 44 innocent men in this sample were exonerated based on DNA testing. For that decade, DQ alpha testing was the
most common type of testing, resulting in 34 exonerations (77% of all exonerations that occurred in the 1990s). RFLP was the second most common type of test used in early 1990 exonerations. However, STR testing was introduced in the mid-1990s, and by the end of that decade a total of 10 exonerations had resulted from STR testing. The rapid evolution of DNA testing methods during the 1990s is evident in Figure 2, which shows that by 1997, RFLP testing was no longer used to exonerate the wrongfully convicted.

By 2000, STR testing had become the standard, far exceeding any other testing method resulting in exonerations. From 2000 to 2005, STR testing was used to exonerate individuals in 70 cases, representing 86% of all exonerations during this time. Mitochondrial testing was the next most common type of test leading to exonerations during 2000–2005 (16 cases), and DQ alpha testing and Y-STR testing were the next most common (each representing 5 cases).

During the second half of this decade (2006–2010), STR testing continued to dominate the type of testing used to exonerate. However, Y-STR became more common, resulting in 27 exonerations. During this time period, 1 exonerations relied in part on DQ alpha testing; however, the testing actually took place in 1997, as explained above. Finally, mini-STR testing also began during this time, resulting in 5 exonerations from 2008 to 2010. Although no mitochondrial testing led to exonerations after 2008 in this sample, this method is still used today, and is anticipated to remain an important part of exonerative DNA testing.

Types of Evidence by Type of Crime

Figure 3 shows the type of exonerative testing performed along with the crime for which the exoneree was wrongly convicted. The types of testing for rape and rape-murder cases were quite similar, although crimes involving both rape and murder relied slightly more often on STR and Y-STR testing (the difference was not significant). Crimes involving murders (with or without sexual assaults) were significantly more likely than sex-related crimes to rely on Y-STR and mitochondrial testing to exonerate. Mini-STR testing (not shown in Figure 2 owing to the small number of cases) was used to reverse three rape cases, one rape-murder case, and one murder case.

Types of Exculpatory Testing Contributing to the Identification of the Real Perpetrators

Wrongful convictions are not only harmful to the exonerees and the crime victims (and their loved ones), but also to society in general, because the real perpetrators remain free and
Figure 4
Types of testing that contributed to the identification of real perpetrators (n = 84). Numbers above each bar indicate the number of perpetrators identified. Type of hit (cold or not cold) was missing for 2 cases involving STR testing.

often go on to commit other violent offenses. As mentioned earlier, 84 of the 194 exonerees had the real perpetrator identified in their cases.

At least 34 of these real perpetrators were convicted of other violent crimes after the crime for which an innocent person went to prison. The number of subsequent violent crimes that might have been prevented had the real perpetrator originally been identified includes 45 rapes, 12 murders, and 8 other types of violent crimes. Of course, these violent crimes represent only the convictions—not the actual number of crimes—committed by those who escaped judgment while others served for their crimes.

Figure 4 presents the types of testing that contributed to the identification of the real perpetrator, and whether the identification resulted from an STR cold hit (a search through the CODIS database system) or from DNA comparison with a previously developed alternate suspect. The overwhelming majority of cases where the real perpetrator was identified relied at least in part on STR testing (71 of 84 exonerees—85%). In these STR cases, 42 perpetrators were identified through cold hits, and 29 were identified through DNA comparisons with previously developed suspects (with missing type of hit status on 2 STR cases). In the other 13% of cases where the real perpetrator was caught (none through cold hits), DQ alpha testing was used most frequently (8 cases), followed by Y-STR testing (2 cases) and mitochondrial testing (1 case).

TYPES OF PROBATIVE EXCULPATORY EVIDENCE USED TO EXONERATE

Overview of Types of Exculpatory Evidence

Because the overwhelming majority of the DNA exonerations involved wrongful convictions of sex crimes, it is not surprising that intimate swab and clothing evidence were the most common types of evidence resulting in probative exclusions. The intimate swabs category includes evidence collected from oral, anal, and vaginal swabs; the clothing category includes mostly clothing with semen stains (such as underwear, robes, pants, and shirts), although it also includes some clothing with other types of stains (such as the perpetrator’s saliva or blood).

Nearly two-thirds of the 194 exonerations included intimate swab evidence that resulted in probative exclusions (see Figure 5). Clothing evidence provided exclusionary results in approximately half of these cases—often in conjunction with exculpatory results on intimate swab evidence from the rape kit.

Other pieces of evidence that led to probative exclusions were used to exonerate (in 17 cases) were grouped together in an “other” category. Of these 17 cases, 9 involved semen samples collected from the floor, carpet, or couch; others involved DNA from bloodstains on nonclothing items (9 cases), DNA from a glass or bottle (2 cases), DNA on a gun or ligature (2 cases), or saliva from a bite mark (1 case).
Figure 5
Types of exculpatory evidence used to exonerate (n = 194).

Types of Evidence by Type of Crime

Figure 6 presents data on types of exculpatory evidence by type of crime. Rape-murder exoneration cases were significantly more likely to rely on intimate swab evidence than rape cases without murders (85% versus 63%). Rape cases without murders were significantly more likely to rely on clothing evidence to exonerate than were rape-murder cases (56% versus 38%). However, murders without sexual assault overwhelmingly relied on clothing to exonerate the wrongfully convicted (78%—7 of 9). Murder cases (with or without sexual assaults) were significantly more likely to rely on hair and fingernail evidence to exonerate than were nonmurder cases.

There were 14 cases in our sample that involved types of exclusionary evidence not indicated in Figure 6. Of these, 9 were rape-murder cases (mainly bloodstains on nonclothing items), 3 were rape cases, and 2 were homicide cases.

Types of Testing Performed on Specific Types of Evidence

Figures 7–12 present data on types of testing yielding exculpatory results on the evidence.
**Intimate swabs.** Figure 7 presents types of testing producing exculpatory results on intimate swab evidence. The most common type of testing performed on intimate swabs leading to exonerations was the STR method (89 of 126 swabs—71%), followed by DQ alpha testing (24 of 126—19%) and Y-STR testing (23 of 126—18%). Mini-STR testing provided exclusionary results on intimate swabs in 3 cases.

**Clothing.** Figure 8 presents types of testing methods used on clothing evidence that led to exonerations. Here, approximately two-thirds of these cases relied on STR testing, and another quarter (23%) relied on DQ alpha testing. Y-STR testing was performed in 19% of cases involving probative exclusionary clothing evidence, and less commonly used testing methods that led to exonerations included RFLP (5 cases) and mini-STR (2 cases). Clothing evidence that relied on more than one type of test to exonerate always included STR as one of the types.

**Hair.** Figure 9 shows that exclusionary hair evidence was most often analyzed using mitochondrial DNA testing (19 cases), followed by STR testing (6 cases). In 3 cases, DQ alpha was used on hair evidence producing probative exclusionary results. Only 2 of these hair cases relied on multiple types of tests to exonerate (these 2 cases involved DQ alpha and STR testing in 1 case and mitochondrial and STR testing in the other). Mitochondrial testing is the only mechanism that can be used when the hair being analyzed lacks a root.

---

**Figure 7**
Type of testing on intimate swabs yielding exculpatory results ($n = 126$).

**Figure 8**
Type of testing on clothing yielding exculpatory results ($n = 102$).

---

8.16 Hampikian • West • Akselrod
Bedsheets. Of the 13 cases where bedsheet evidence was used to exonerate, most relied on STR testing (9 cases), while 3 used DQ alpha and 1 used RFLP (see Figure 10).

Fingernail evidence. Figure 11 presents the types of testing leading to exculpatory results on fingernail evidence, indicating that most of these cases relied on STR testing (6 of 9 cases). Y-STR testing was performed in 2 cases, and DQ alpha testing was performed in 1 case.

Cigarettes. Figure 12 demonstrates that 4 of the 5 cases where cigarette butts provided probative exclusionary results relied on STR testing, and 1 relied on Y-STR testing.

Other evidence. All of the other types of evidence (semen collected from the floor, carpet, or couch; DNA from bloodstains or nonclothing items; DNA on a gun or ligature; or saliva from a bite mark) relied on STR alone (10 cases) or a combination of STR and Y-STR testing (7 cases).

CASE STUDIES
Ken Wyniemko

Contributing causes: misidentification, jailhouse informant testimony
Exonerating tests and evidence: STR testing with exculpatory results on cigarette butts, fingernail scrapings, and clothing

On April 30, 1994, a woman was robbed and repeatedly raped by a man who broke into her home in Clinton Township, Michigan. The attacker wore a mask through much of the incident, and the victim was never able to see him well, but police nevertheless asked the victim to assist them with creating a composite sketch. Two and a half months later, Ken Wyniemko (Figure 13) was arrested on an unrelated misdemeanor charge, and police determined that he resembled the composite sketch. As a result, Mr. Wyniemko was placed in a lineup viewed by the victim. She initially failed to identify him, but ultimately picked him out. Based largely on this identification and the testimony of a cellmate that Wyniemko confessed to him, Wyniemko was convicted of criminal sexual conduct, breaking and entering, and armed robbery. The cellmate received a generous deal on his own case, while Wyniemko was sentenced to 40–60 years in prison.
Wyniemko had maintained his innocence throughout his incarceration. In 2003, through the assistance of pro bono counsel Gail Pamukov and the Innocence Project at the Thomas M. Cooley Law School in Michigan, Wyniemko was able to obtain postconviction DNA testing on numerous items of evidence. At trial, analysts had discovered semen on the victim’s bedsheets, and the ABO blood antigens detected in the semen excluded both the victim and Wyniemko. But the antigens were consistent with the victim’s husband, and the prosecutors argued that the semen was likely from the husband, and thus that Wyniemko’s exclusion based on the semen was irrelevant. Using STR testing in 2003, the State Police Forensic Science Division found that the victim’s husband was indeed the contributor of semen on the victim’s bedding. However, the lab also discovered a consistent male DNA profile in saliva on a cigarette butt collected from the scene, in scrapings from under the victim’s fingernails, and on nylons used by the perpetrator to gag the victim. Such a redundant profile—meaning a profile from a single source on multiple items—can be critical in DNA investigations because obtaining the same profile on multiple probative items increases the likelihood that the DNA was deposited by the perpetrator, as opposed to an unrelated source at an earlier time. Neither the victim’s husband nor Wyniemko was the source of that redundant profile. Based on these results, Wyniemko was exonerated and released after spending nine years in prison.

The redundant DNA profile developed from the evidence was entered into the CODIS database, and it took another five years for the identity of the source to be revealed. In 2008, the profile produced a cold hit to Craig Gonser, a person whose profile had been entered into the DNA data bank earlier that year because of a domestic violence charge. Gonser could not be tried for the 1994 rape because the statute of limitations had expired. However, in April 2010, Gonser was convicted of an unrelated sex crime and sentenced to 10–25 years.

**Roy Brown**

**Contributing causes:** Improper forensic science, jailhouse informant testimony

**Exonerating tests and evidence:** STR testing with exculpatory results on saliva on nightgown

On May 23, 1991, a social service worker was found beaten, strangled, and stabbed to death near the upstate New York farmhouse where she lived. The victim had been bitten numerous times, and had been dragged from her home. The victim’s bloodied nightshirt contained at least seven separate saliva stains, consistent with the assailant having bitten
Police also swabbed the victim's skin in the location of the bite marks in the hope of collecting the perpetrator's saliva. Roy Brown (Figure 14) became a suspect because he had made threatening phone calls to the director of the social services agency where the victim worked, after the agency had placed Mr. Brown's daughter into a residential care facility, though the victim herself had not been involved with that situation.

At trial, the prosecution relied heavily on the testimony of a bite mark analyst who stated that the bite marks on the victim's body were “entirely consistent” with Brown. The defense contested that claim and presented the testimony of their own expert, who concluded that six of the bite marks were not sufficiently detailed for comparison, and that the seventh actually excluded Brown because it was made by six upper teeth—Brown had only four upper teeth. The prosecution failed to disclose until the time of trial that it had previously engaged another expert to examine the bite marks and that the prior expert's conclusions were consistent with those of the defense expert. The prosecution also presented the testimony of Brown's two ex-wives, who claimed that Brown had angrily bit them (one of the ex-wives ultimately recanted), and the testimony of a jailhouse informant that Brown had confessed to him. Brown was convicted and sentenced to 25 years to life.

Brown fought for years to prove his innocence from behind bars. In 1994 and 1995, courts denied Brown’s requests for DNA testing. Years later, through a Freedom of Information Law request to the Sheriff’s Department, Brown obtained police reports that had not previously been disclosed to the defense implicating another man, Barry Bench, in the murder. In 2003, Brown wrote to Bench, telling him that DNA would implicate him when Brown finally got testing. Bench committed suicide by throwing himself in front of a train five days after the letter was mailed.

In 2005, the Innocence Project took on Brown’s case and secured testing on the saliva stains remaining on the nightshirt. That testing revealed that all of the saliva stains contained DNA from a single male source, and excluded Brown. Some remaining portions of the bite mark swabs were also located, but the testing laboratory was unable to obtain a DNA profile. The Innocence Project then located Bench’s daughter, who gave a sample of her DNA. Half of her DNA matched the saliva on the shirt, consistent with her being the daughter of the source of the saliva. A judge finally ordered Bench’s body to be exhumed, and it confirmed that the saliva was consistent with Bench.

On January 23, 2007, after 15 years of incarceration, Brown was finally released from prison. The prosecution formally dropped all charges on March 5, 2007.

Charles Chatman

**Contributing causes:** Misidentification  
**Exonerating tests and evidence:** Y-STR testing with exculpatory results on rape kit

Charles Chatman (Figure 15) was convicted in 1981 of raping a woman in her Dallas apartment and was sentenced to 99 years in prison. The victim identified Mr. Chatman from a photo lineup and at a subsequent live lineup. The identification bore indications of a misidentification: the victim, a white female, only had a brief opportunity to see her attacker.
a black male, from the nose up. She had not told police that she had ever seen her attacker before, but ultimately identified Chatman, a neighbor who she sometimes saw on her street. Unconscious transference is one of the causes of mistaken identifications, whereby a witness may recognize a person in a lineup as a result of having previously seen them in casual passing and misattribute that recognition to their memory of the perpetrator. In addition to the victim’s identification, the state presented serological testimony that a semen stain recovered from the victim’s sheet was ABO blood type O, and that Chatman was a type O secretor. Forty percent of the black male population are type O secretors.

Chatman served nearly three decades in prison and endured multiple rounds of testing before DNA finally proved his innocence. STR testing conducted in 2002 was unable to develop any profile from the semen deposited in the rape. In 2007, Chatman’s appointed attorney, Michelle Moore (who was cocounsel with the Innocence Project of Texas on the case), asked that the evidence be tested again using Y-STR testing. With this technological advancement, the lab was able to develop a profile from the sperm that excluded Chatman as the source. Based on these results, Chatman was released from prison and exonerated in early 2008.

**Chris Ochoa**

**Contributing causes:** False confession

**Exonerating tests and evidence:** STR and mitochondrial testing with exculpatory results on rape kit (STR) and pubic hair (mitochondrial)

Nancy DePriest was raped and murdered in a Pizza Hut in Austin, Texas, in 1988. Chris Ochoa (Figure 16), a 22-year-old who had never previously been in police custody, was interrogated for two days in connection with the crime and was threatened with the death penalty if he did not cooperate. Although he initially denied any involvement in the killing, Mr. Ochoa ultimately confessed to the murder and implicated his friend, Richard Danziger, as a participant. Those of us who have never found themselves in Mr. Ochoa’s position may find it hard to understand how he confessed to a crime that he did not commit. However, many studies have shown that some innocent people who are falsely arrested, held by police, interrogated for
hours, and threatened with years in prison (or death) do in fact confess to crimes they did not commit, and the DNA exonerations reviewed here show that such false confessions are not uncommon. While it may be hard to imagine how one can become so vulnerable, there is a large body of research documenting the causes of false confessions, which include certain tactics used by police during interrogation (persuasion, deception, or coercion), individual traits that may make some people more vulnerable to the pressures used in interrogations (low IQ or being a juvenile), and suspects’ naïve mental states regarding their innocence (4, 11, 12).

Semen was found on a swabbing from the victim’s vagina, and DQ alpha testing was conducted. The testing excluded the victim’s husband and Mr. Danziger as the source, but could not exclude Ochoa. The DQ alpha profile detected in the semen could be found in approximately 8% of the Caucasian population, 10% of the black population, and 16% of the Mexican American population. A forensic expert also determined that a pubic hair found at the scene was microscopically consistent with Danziger’s pubic hair. In exchange for a life sentence, Ochoa pled guilty and testified against Danziger, who was convicted of rape and sentenced to life.

In 1996, after an apparent religious conversion while serving time in prison on other convictions, a person by the name of Achim Marino wrote letters to the police and the district attorney’s office claiming sole responsibility for the crime. Marino’s letters contained detailed descriptions of the crime, and led police to the location of items that he had stolen from the Pizza Hut. An extensive investigation revealed that there was no link between Marino and either Ochoa or Danziger.

New DNA tests were conducted on the semen from the vaginal swabs, this time using the more discriminating method of STR testing. The new testing conclusively excluded Ochoa and Danziger as sources, and determined that the semen was wholly consistent with the DNA of Marino. Mitochondrial DNA testing was conducted on the hair that was purportedly consistent with that of Danziger, and the DNA proved that the hair did not come from Danziger. With the help of the Wisconsin Innocence Project, Ochoa and Danziger were exonerated in 2002.

**Jeffrey Todd Pierce**

**Contributing causes:** Misidentification, improper forensic science

**Exonerating tests and evidence:** STR testing with exculpatory results on rape kit and robe

Jeffrey Todd Pierce (Figure 17) was convicted in 1986 of raping and robbing an Oklahoma City woman in her apartment. Mr. Pierce was part of a landscaping crew that was working around the apartment complex on the day the victim was raped. Police spotted Pierce working near the complex when they responded to the scene, but when they pointed him out to the victim, she stated that he was not her attacker. The initial description of the perpetrator also did not match Pierce. Approximately 10 months after the rape, Pierce’s photo was included in a photo array, and the victim identified him as the rapist.

At trial, the prosecution relied on the testimony of forensic expert, Joyce Gilchrist. Gilchrist testified that 31 hairs collected from the victim and the crime scene were microscopically consistent with Pierce’s hair, and that the two shared “unique characteristics”; she stated that in her experience, she had never seen two
different individuals with microscopically consistent hair.

She also testified that she conducted serological analysis on semen collected from the victim after the rape and determined that it was consistent with the defendant’s ABO blood type. In particular, Gilchrist testified that the semen was deposited either by a person with ABO blood type O or by a person who is a nonsecretor, meaning someone who does not secrete their antigens in bodily fluids other than blood. At one point in her testimony, she went further and stated that she believed the perpetrator was in fact a nonsecretor. Pierce has ABO blood type AB and is a nonsecretor. According to scientific principles that were well established at the time, this testimony was improper because the only antigens detected in Gilchrist’s testing were consistent with the victim herself. Forensic samples collected after a rape are often a mixture of the victim’s own bodily fluids and those deposited by the perpetrator, and if a sample contains a proportionately greater amount of the victim’s own fluids than that of the perpetrator, the victim’s bodily fluids can mask any antigens that may be present from the perpetrator. Gilchrist did not conduct any analysis of the semen fraction in the sample. Because the only antigens detected were consistent with the victim, the only conclusion that she should have made was that the semen could have been deposited by any male in the population. Gilchrist also failed to mention in her testimony that Pierce had a particular enzyme type that did not appear in the semen sample. Because secretor status has no bearing on the presence of this enzyme in bodily fluids, the absence of Pierce’s enzyme type exculpated Pierce (if there was a sufficient concentration of semen in the sample). Based on Gilchrist’s forensic testimony and the victim’s identification, Pierce was convicted and sentenced to 54 years in prison.

Over the years, numerous criticisms were raised about Gilchrist’s work in Pierce’s case as well as many others. In 2001, the FBI reviewed eight separate Gilchrist cases, including that of Pierce, and found that in six of those cases, Gilchrist gave testimony that went beyond the limits of acceptable forensic science. With respect to Pierce’s case in particular, the FBI visually reanalyzed the hairs from the case and reported that Pierce’s hairs were clearly microscopically inconsistent with the hairs collected from the crime. In May 2001, Pierce was released from prison after STR testing conducted on semen from the crime conclusively excluded him as the source, and identified the true perpetrator through the DNA database. Pierce had been incarcerated for 15 years. Gilchrist was fired, and an investigation was launched into all of the cases she handled. To date, two other people have been proven innocent via DNA testing in cases in which Gilchrist’s testimony helped to obtain their convictions. No charges have been filed against Gilchrist.

CONCLUSIONS

The remarkable ability of DNA to correct historical error has been demonstrated in 265 U.S. exonerations. This study of 194 of these cases shows that the science of DNA exonerations continues to evolve. With each new method of testing and every new type of evidence used to free the wrongfully convicted, there is a new avenue of escape from the nightmare of false conviction. The United States has clearly led the way in postconviction DNA testing, but the movement begun by the Innocence Project is now spreading to other countries.

Although we cannot be certain about future methods of analytical science, the paramount importance of evidence preservation is clear: There would be no DNA exonerations without evidence preservation. At the time of this publication, 33 states have statutes requiring the preservation of DNA evidence in cases involving rape and murder. However, in several states, there is no controlling state law, and local jurisdictions vary tremendously in their storage practices. Simply finding the evidence to test can be a key hurdle in overcoming an incorrect verdict.
This study demonstrates that we can expect to see DNA exonerations continue as new methods of testing become available. With every new technique will come validation studies, legal challenges, and cost-benefit analysis—often played out in the popular press. There is current controversy surrounding methods associated with the terms touch DNA, low-template DNA, low-copy-number DNA, and familial searching—but all of these methods are just variations on available profiling techniques. More exciting and untested vistas are promised by next-generation sequencing, proteomics, and transcriptomics—none of which have penetrated the realm of forensic science. It may not be long before these methods allow us to deconvolute complex mixtures, identify individual bodily fluids and tissue types, and analyze forensic samples with single-molecule resolution.

APPENDIX
Definitions of Garrett & Neufeld’s six categories of invalid forensic testimony (for complete definitions and examples, see Reference 6):

1. Nonprobative evidence presented as probative: Empirical population data is used inaccurately to implicate a defendant.
2. Exculpatory evidence discounted: Evidence that clears the defendant is improperly dismissed as nonprobative or inculpatory.
3. Inaccurate frequency or statistic presented: Analyst testifies against defendant using inaccurate statistics that implicate the defendant.
4. Statistics provided without empirical support: Analyst offers statistical testimony when no statistical study has been performed.
5. Nonnumerical statements provided without empirical support: Expert testimony includes qualitative statements without quantitative definition.
6. Conclusions that evidence originated from the defendant: Analyst testifies that evidence did in fact come from the defendant and was unique to the defendant, without any empirical data permitting such conclusion.

DISCLOSURE STATEMENT
The authors of this article are all members of the Innocence Network: G.H. is the volunteer director of the Idaho Innocence Project, E.W. is the research director at the Innocence Project, and O.A. is a staff attorney at the Innocence Project. G.H. also assists other organizations with postconviction DNA analysis.

ACKNOWLEDGMENTS
The authors wish to thank Michael Davis for his help in manuscript preparation and Darren Veracruz for his research assistance.

LITERATURE CITED