

# BEHAVIORAL GENETICS RESEARCH AND CRIMINAL DNA DATABASES

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## I

### INTRODUCTION

DNA identification databases have made it possible to apprehend the perpetrators of crimes ranging from auto theft and petty burglary<sup>1</sup> to serial rapes and murders.<sup>2</sup> Yet the laws establishing these databases have been the subject of persistent litigation and repeated criticism. One recurrent refrain plays on the fear of research into genes and behavior. The public has been told that

There are no limits on who uses [the tissue sample]. Even if [a law enforcement agency] decides they're only going to use it for identification purposes, there's no restriction on their turning it over to somebody else who will use it to look for a crime gene . . . .<sup>3</sup>

Other advocacy groups and individuals have trumpeted the prospect of research seeking a "crime gene"<sup>4</sup> or have pointed to the sordid history of biological

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1. *E.g.*, Shaila K. Dewan, *As Police Extend Use of DNA, A Smudge Could Trap a Thief*, N.Y. TIMES, May 26, 2004, at A1; Alison Gendar, *DNA Test Buys Rob Busts*, N.Y. DAILY NEWS, Mar. 29, 2005, available at [http://www.nydailynews.com/news/crime\\_file/story/294437p-252113c.html](http://www.nydailynews.com/news/crime_file/story/294437p-252113c.html).

2. *See, e.g.*, ANN RULE, GREEN RIVER, RUNNING RED: THE REAL STORY OF THE GREEN RIVER KILLER—AMERICA'S DEADLIEST SERIAL MURDERER 343, 360 (2004).

3. Interview by Ira Flatow, NPR Talk of the Nation, with Nadine Strossen (May 25, 2001), available at [http://www.sciencefriday.com/pages/2001/May/hour1\\_052501.html](http://www.sciencefriday.com/pages/2001/May/hour1_052501.html); *see also* *Speeding DNA Evidence Processing: Hearing on H.R. 2810, H.R. 3087, and H.R. 3375 Before the Subcomm. on Crime of the H. Comm. on the Judiciary*, 106th Cong., 2000 WL 342540 (2000) (testimony of Barry Steinhardt, Associate Director, American Civil Liberties Union, Washington, D.C.) [hereinafter *Hearing*] (describing DNA samples as harboring our "most intimate secrets," possibly including "genetic markers for aggression, substance addiction, criminal tendencies and sexual orientation").

4. Benjamin Keehn, *Strands of Justice: Do DNA Databanks Infringe on Defendants' Rights?*, PBS NEWSHOUR ONLINE FORUM, July 17, 1998, [http://www.pbs.org/newshour/forum/july98/dna\\_databanks03.html](http://www.pbs.org/newshour/forum/july98/dna_databanks03.html) ("The hunt is already on for the 'crime gene' . . . [and] the process of searching for it may well be the path to totalitarianism."); *cf.* Jean E. McEwen, *Storing Genes to Solve Crimes: Legal, Ethical, and Public Policy Considerations*, in STORED TISSUE SAMPLES: ETHICAL, LEGAL, AND PUBLIC POLICY IMPLICATIONS 311, 323 (B.F. Weir ed., 1998) ("Banked samples from convicted offenders . . . could someday come to be seen as especially valuable resource for behavioral

theories of racial inferiority<sup>5</sup> as grounds for resisting or reversing DNA database initiatives.<sup>6</sup>

This article asks whether these concerns are valid objections to the DNA database laws now on the books. Part II considers the possible value of the databases for research. It concludes that talk of a “crime gene” is scientifically naive and that the databases themselves would be of little or no value in behavioral genetics research. The DNA information in these databases is limited to a small number of DNA base-pair variations that have been selected because they are useful for identification. These particular DNA variations are unlikely to reveal anything significant about any genes, let alone genes that might affect behavior. However, the DNA samples that are on file could be reanalyzed at more informative sites, and statistical studies of possible correlations between the new data and behavioral traits might be of some scientific interest. As such, the fears about the law-enforcement databases contributing to genetic research into crime cannot be so easily dismissed.

Part III surveys state and federal database legislation. It shows that several previous studies have overlooked or understated the restrictions on medical or behavioral genetics research with convicted-offender samples. Many of the pertinent statutes, although not drafted with precision, preclude such research. Nevertheless, even clear statutory provisions are subject to amendment through the legislative process. Inasmuch as the Constitution, as currently interpreted, offers rather weak protection for informational privacy, the policy question of allowing such behavioral genetics research with the samples in the law enforcement repositories must be confronted.

As to this final question, Part IV identifies and assesses some of the bioethical and social arguments against allowing such research. These include concerns about the possible misuse of or misunderstandings about the fruits of the research and the lack of consent on the part of the “donors” of DNA samples. This issue also raises the related policy issue of whether the DNA samples should be retained at all—as well as the question addressed in Part II of the research value of DNA databases and repositories. In these regards, the article concludes that an absolute prohibition on behavioral genetics research is not necessary. Instead, it proposes that if samples are to be retained (as they

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geneticists—such as those interested in studying the possibility of a genetic predisposition to violence, pedophilia, or alcoholism.”) (footnote omitted).

5. Nachama L. Wilker et al., *DNA Data Banking and the Public Interest*, in *DNA ON TRIAL: GENETIC INFORMATION AND CRIMINAL JUSTICE* 141, 147 (Paul R. Billings ed., 1992) (opposing research “designed to identify genes associated with criminal behavior” because it lacks scientific merit and “could be used as a new biological justification to bolster racist and ethnic prejudice”).

6. Michael Avery, *Landry v. Attorney General: DNA Databanks Hold a Mortgage on Privacy Rights*, 44 *BOSTON B.J.* 18, 18 (2000) (“Researchers are currently attempting to develop genetic profiles that would identify or predict homosexuality, aggression, criminality, mental illness, alcoholism, obesity and other conditions [and conducting] more than 200 clinical studies on the genetic basis of criminal behavior, [creating obvious] unfairness and potential for harm to individuals and families inherent in such social stereotyping.”).

currently are), then an independent body with appropriate expertise should evaluate proposals for research projects on a case-by-case basis.

## II

### THE SCIENTIFIC “IS”: OFFENDER DNA DATABASES AND REPOSITORIES AS A USEFUL SOURCE OF BEHAVIORAL GENETICS DATA

Is it true that geneticists, psychiatrists, or other biomedical researchers are itching to get their hands on the government’s information in order to discover a “crime gene”? Stated this baldly, the concern is more rhetorical than real.<sup>7</sup> However, the possibility that stored DNA samples collected from convicted-offender databases might be of interest to some researchers should not be summarily dismissed. Some observers describe convicted-offender samples as “tempting treasure troves”<sup>8</sup> or “a wealth of information for researchers interested in studying criminal behaviour”<sup>9</sup> and predict that “DNA repositories on convicted felons will eventually prove irresistible to behavioral geneticists who will seek to determine whether certain mutations that are correlated with behavioral problems are more prevalent than expected among such persons.”<sup>10</sup>

An evaluation of the scientific value of the records requires some appreciation of the nature of both the methods for ascertaining genetic influences on behavior and of the law-enforcement databases. This Part therefore describes several study designs that have been used to determine whether specific clusters of genes appear to have a significant impact on

7. *But see* Pallab Ghosh, *Behaviour Research Is ‘Overstated,’* BBC NEWS WORLD EDITION, Feb. 18, 2002, [http://news.bbc.co.uk/2/hi/in\\_depth/sci\\_tech/2002/boston\\_2002/1828387.stm](http://news.bbc.co.uk/2/hi/in_depth/sci_tech/2002/boston_2002/1828387.stm) (“The genes are really in the test tube waiting to be isolated now, and as soon as we get the gene for IQ or aggression, then it will be very easy to look at existing databanks to see whether those genes show up more in Africans than in whites, or in whites more than east Asians.”) (quoting Philip Rushton, a Canadian psychologist).

8. CATHERINE BAKER, AM. ASS’N FOR THE ADVANCEMENT OF SCI., *BEHAVIORAL GENETICS: AN INTRODUCTION TO HOW GENES AND ENVIRONMENTS INTERACT THROUGH DEVELOPMENT TO SHAPE DIFFERENCES IN MOOD, PERSONALITY, AND INTELLIGENCE* 89 (2004), *available at* <http://www.aaas.org/spp/bgenes/publications.shtml>.

9. KRISTINA STALEY, GENEWATCH UK, *THE POLICE NATIONAL DNA DATABASE: BALANCING CRIME DETECTION, HUMAN RIGHTS AND PRIVACY* 37 (2005), *available at* <http://www.genewatch.org/HumanGen/Publications/Reports/NationalDNADatabase.pdf>.

10. Avery, *supra* note 6, at 34 (quoting Philip Reilly); *see also* Jean E. McEwen, *DNA Sampling and Banking: Practices and Procedures in the United States*, in *HUMAN DNA: LAW AND POLICY, INTERNATIONAL AND COMPARATIVE PERSPECTIVES* 407, 410 (Bartha Maria Knoppers ed., 1997) (“[T]he unique composition of *forensic* DNA banks . . . will make those repositories a nearly irresistible source of samples for *behavioural* genetics research or testing . . . without the informed consent of those from whom the samples were taken.”) (footnote omitted); Eric T. Juengst, *I-DNA-fication, Personal Privacy, and Social Justice*, 75 CHI.-KENT L. REV. 61, 69 (1999) (“Collections of DNA samples from criminals or soldiers, for example, are likely to be perceived as particularly rich research resources by those interested in studying genetic factors involved in anti-social or aggressive behavior.”); National Commission on the Future of DNA Evidence, *Proceedings*, Sept. 26, 1999 (comment by Judge Ronald Reinstein), <http://www.ojp.usdoj.gov/nij/topics/forensics/events/dnamtgtrans7/trans-c.html> (“[T]here are people out there, it’s clear, that want these samples for research purposes [and at a conference,] the head of the Sexually Violent Person Program at the State Hospital in Arizona . . . asked me whether or not they could get the DNA samples for all the people in the SVP program and I said no.”).

behavior as well as some methods for ascertaining which genes might be involved. It explains why the outcry over “crime genes” is simplistic but nevertheless important. Finally, it indicates some research uses for the law-enforcement DNA samples that might have scientific merit.

#### A. Evidence for a Genetic Basis of Behavior

Evidence that genes play a role in specific behaviors comes from animal studies, family studies, twin studies, linkage analysis, and population studies. This is not the place for a detailed exposition of all these research designs, but a passing acquaintance with a few kinds of studies is helpful in assessing the possible value of law-enforcement databases for research into the genetics of behavior.

Some research designs are useful simply for revealing genetic influences on behavior. Controlled experimentation with animals certainly has demonstrated a genetic component to some behaviors in a variety of organisms. For example, one can selectively breed mice for fearfulness. In one of the largest and longest such studies, mice were selected for activity in a brightly lit box called an open field.<sup>11</sup> At the outset of the experiment, mice were placed in the box. Some would explore the field actively, while others would stay still, defecate, and urinate. The activity levels of the mice were monitored, and the most active animals were mated with other highly active mice. Likewise, the least active mice were segregated and mated. This process of selectively mating the apparently fearless mice and the seemingly fearful ones was repeated for thirty generations. The end result was a thirty-fold average difference in activity. “Mice from the high-active line now boldly run the equivalent total distance of the length of a football field during the six-minute test period, whereas the low-active mice quiver in the corners.”<sup>12</sup>

Such studies are powerful proof of causation to the extent that the experimenter manipulates the genotype while keeping the environment constant. But they do not directly prove anything about human behavior. Bridging the gap between mice, worms, fruit flies, or other experimental animals and humans takes a theory about their commonalities or more direct data on the human animal.<sup>13</sup> With observational studies of causation, one must make do with “natural experiments” that are prone to confounding variables. Twin studies illustrate one such approach. Monozygotic (MZ), or identical, twins develop from the same fertilized egg (zygote). Hence, their genotypes are almost identical.<sup>14</sup> Fraternal, or dizygotic (DZ) twins develop from two

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11. ROBERT PLOMIN ET AL., *BEHAVIORAL GENETICS* 61 (3d ed. 1997).

12. *Id.*

13. See generally NUFFIELD COUNCIL ON BIOETHICS, *GENETICS AND HUMAN BEHAVIOUR: THE ETHICAL CONTEXT* 61–63 (2002), available at <http://www.nuffieldbioethics.org/fileLibrary/pdf/nuffieldgeneticsrep.pdf> (describing the pitfalls in extrapolation about the effects of genes across species).

14. Developmental and epigenetic factors (those inducing heritable changes without altering the sequence of DNA base-pairs) affect the extent to which each twin's genes are expressed.

genetically distinct ova and spermatozoa. About one-quarter of their alleles are the same.<sup>15</sup> Since both pairs of twins are raised in very similar environments, something that is almost entirely under genetic control, such as the ridge pattern in fingerprints, will be far more similar in MZ twins than in DZ twins.<sup>16</sup> However, something that has nothing to do with genes should occur no more often among pairs of MZ twins than among DZ twins.

Naturally, many behavioral traits fall somewhere in between these extremes. Consider antisocial personality disorder, an extremely heterogenous disorder that includes a history of illegal or socially disapproved activity beginning before age fifteen and continuing into adulthood (for example, irresponsibility, irritability, aggressiveness, recklessness, and disregard for truth).<sup>17</sup> One study of more than 3,000 pairs of adult male twins found correlations of 0.47 for MZ twins and 0.27 for DZ twins.<sup>18</sup> Many twin studies of criminal behavior (self-reported as well as criminal convictions) show a similar pattern.<sup>19</sup>

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15. The expected genetic similarity in DZ twins depends on the parents' genotypes. Suppose both parents have the same version ("allele") of a particular gene. These individuals are said to be homozygous, and we can refer to the shared allele as A1. All their children will be (A1,A1). At the other (and more common) extreme, suppose both parents are heterozygous (they each have a pair of distinct alleles). For example, one parent might be type (A1,A2), and the other parent might be (A3,A4). Now there are four equally likely possibilities for the genotypes of the DZ-twin children: (A1,A3), (A1,A4), (A2,A3), and (A2,A4). Suppose one such twin has the genotype (A1,A3). The chance that the other does is 1 in 4. The same reasoning applies to the other three genotypes. Therefore, the chance that both twins have the same genotype (whichever one of the four it may be) is 1 in 4.

As for phenotypes (the external traits influenced by these underlying genotypes), suppose one twin with the heterozygous parents in our example is (A1,A3). The chance the other twin also has an A1 is 1 in 2 (since 2 of the 4 equally likely genotypes contain an A1). The same is true for A3. By similar reasoning for all the genotypes, it follows that the chance that both twins have at least one copy of the same allele is 1 in 2. If the genetic system involves a dominant Mendelian trait (meaning that one allele suffices to determine the phenotype without regard to the other allele), then some 50% of the DZ twins will have the same phenotype. If the trait is recessive (meaning that it takes not one, but two copies of the allele for the phenotype produced by that recessive allele to appear), then only about 25% will exhibit it.

16. The correlation in the ridge pattern for MZ twins has been found to be 0.96 compared to 0.47 for fraternal twins. D.S. FALCONER & T.F.C. MACKAY, INTRODUCTION TO QUANTITATIVE GENETICS 173 (4th ed. 1996).

17. PLOMIN ET AL., *supra* note 11, at 210. Affected individuals used to be denominated as sociopaths, and before that, psychopaths. *Id.*

18. M.J. Lyons et al., *Differential Heritability of Adult and Juvenile Antisocial Traits*, 52 ARCHIVES GEN. PSYCHIATRY 906, 910, Tbl.3 (1995). There was little difference when the adults were asked about antisocial traits—a correlation of 0.39 for the MZ twins and 0.33 for the DZ twins. *Id.* This is consistent with other findings that although antisocial personality disorder shows early roots, the vast majority of juvenile delinquents and children with conduct disorders do not develop antisocial personality disorder. PLOMIN ET AL., *supra* note 11, at 210. The correlation of adult and adolescent ASP symptoms is about 0.40, and it is thought that from adolescence to adulthood, the genetic influence on ASP symptoms increases. *Id.* at 211. More information on such studies is available in S.H. Rhee & I.D. Waldman, *Genetic and Environmental Influences on Antisocial Behavior: A Meta-analysis of Twin and Adoption Studies*, 128 PSYCH. BULL. 490, 495–97, 517 (2002).

19. PLOMIN ET AL., *supra* note 11, at 212 (reporting concordances such as 51% and 30% for MZ and DZ male twins, respectively). Again, there are indications that shared environmental influences make the major contribution to arrests and criminal behavior before age fifteen, and that genetic influences become more apparent later. *Id.*

In short, some genetic heterogeneities in the DZ twins seem to be at work in producing the different concordances of criminal conduct in pairs of DZ as opposed to MZ twins. However, establishing that sets of genes affect certain behaviors is much easier than identifying the specific genes that are interacting with one another and with environmental variables to influence behavior. Locating specific genes is important to understanding the link between genes and behavior—a link that could be far more complex than the notion of a gene “for” certain behavior.<sup>20</sup> In principle, experimental and observational studies can permit the identification of particular genes that play a role in human behavior. Controlled experiments with animals have elucidated specific genes that have been conserved over long periods of evolution and that clearly affect behavior.<sup>21</sup> Although one cannot automatically assume that the same gene operates in the same way in a mouse and a human,<sup>22</sup> animal studies can suggest loci and alleles that merit study in human populations.

In addition, one can collect observational data for indications of the alleles that might influence behavior. A traditional approach in medical genetics looks to individuals within the same families. Family members are likely to have been subject to more similar influences than members of a heterogeneous population, so observing a genetic difference between affected family members and unaffected ones may be significant. Classical “linkage” studies use genetic markers at known locations on the chromosomes. Researchers note how often the trait and alleles for the markers are inherited together.<sup>23</sup> Frequent co-inheritance suggests that the gene for the trait is located near the marker allele, and thus is “linked”. This technique works best for highly penetrant, single genes that cluster in some families.<sup>24</sup> For example, the gene that produces

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20. It cannot be assumed that there is a set of genes “for” a particular trait just because DZ twins are less concordant in a behavioral trait than MZ twins. For example, one could try to explain the greater concordance in ASP among identical twins as a reflection of the greater physical similarities of these twins. The physical appearance of an individual can affect how that person is treated by others, and that treatment, in turn, could affect whether the individual develops ASP or engages in crime.

21. The leading example is the gene dubbed “forager” (*for*). Fruit flies with one allele are “rovers,” while those with another allele are “sitters.” Rovers traverse a large area while feeding; sitters cover a small area. Marla B. Sokolowski, *Foraging Strategies of Drosophila Melanogaster: A Chromosomal Analysis*, 10 BEHAV. GENETICS 291, 291 (1980). The gene codes for a cell-signaling molecule (PKG), and the rover allele generates larger quantities of it. K.A. Osborne et al., *Natural Behavior Polymorphism Due to a cGMP-Dependent Protein Kinase of Drosophila*, 277 SCIENCE 834, 834 (1997); Marla B. Sokolowski, *Genes for Normal Behavioral Variation: Recent Clues from Flies and Worms*, 21 NEURON 463, 464 (1998). It also affects feeding behavior in honeybees and nematodes, and PKG genes have been found in nineteen species, from green algae to humans. Elizabeth Pennisi, *A Genomic View of Animal Behavior*, 307 SCIENCE 30, 30 (2005).

22. A strong statement of the dangers of extrapolation can be found in the AAAS REPORT. BAKER, *supra* note 8, at 54–55; cf. Garland Allen, *DNA and Human-Behavior Genetics: Implications for the Criminal Justice System*, in DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE 287, 291 (David Lazer ed., 2004) (“It is not possible to make predictions about behaviors in one species from analogies to a similar behavior in other species.”).

23. See, e.g., Neil J. Risch, *Searching for Genetic Determinants in the New Millennium*, 405 NATURE 847 (2000).

24. E.g., Joel N. Hirschhorn & Mark J. Daly, *Genome-Wide Association Studies for Common Diseases and Complex Traits*, 6 NATURE REV. GENETICS 95, 95–96 (2005).

Huntington's disease, a disease with noticeable behavioral effects,<sup>25</sup> was located by painstaking research of this type.<sup>26</sup>

The monoamine oxidase A (MAOA) gene on the X chromosome is an intriguing example of a gene associated with criminality on the basis of a study of a single family.<sup>27</sup> Over several generations, male members of a Dutch family had committed various criminal acts such as raping a sister, stabbing a man with a pitchfork, committing arson, and attempting to run over another man with a car. Other males in the family line had no such records. The aggressive males were found to have a complete absence of activity of the enzyme MAOA, which breaks down many of the brain's key neurotransmitters. Genetic analysis revealed that the affected men carried a mutation on the X chromosome in the gene that codes for MAOA.<sup>28</sup> The mutation stops the production of the enzyme in brain cells.<sup>29</sup> However, a total absence of MAOA activity is so unusual that "this finding seemed to be of limited import for a general understanding of genetic factors affecting violence . . . ."<sup>30</sup>

Subsequent work investigated the possibility that related, more common genes affecting MAOA activity could affect behavior,<sup>31</sup> and this investigation produced a more complex picture.<sup>32</sup> A sample of male children was followed from birth to adulthood to determine why some children who are maltreated grow up to develop antisocial behavior, whereas others do not.<sup>33</sup> The

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25. Mild psychotic and behavioral problems can appear some years before the onset of Huntington's disease. See Per Jensen et al., *Crime in Huntington's Disease: A Study of Registered Offences among Patients, Relatives, and Controls*, 65 J. NEUROLOGY, NEUROSURGERY & PSYCHIATRY 467, 470 (1998) (finding an increased prevalence of minor crimes in men with the genetic mutation that causes Huntington's disease and concluding this was linked to the personality changes often seen in people with the condition).

26. J.F. Gusella et al., *A Polymorphic DNA Marker Genetically Linked to Huntington's Disease*, 306 NATURE 234, 235 (1983); Nancy Wexler, *Clairvoyance and Caution: Repercussions from the Human Genome Project*, in THE CODE OF CODES: SCIENTIFIC AND SOCIAL ISSUES IN THE HUMAN GENOME PROJECT 211, 212-13 (Daniel J. Kevles & Leroy Hood eds., 1992).

27. See generally H.G. Brunner et al., *Abnormal Behavior Associated with a Point Mutation in the Structural Gene for Monoamine Oxidase A*, 262 SCIENCE 578 (1993).

28. *Id.* at 579.

29. J.C. Shih & R.F. Thompson, *Monoamine Oxidase in Neuropsychiatry and Behavior*, 65 AM. J. HUM. GENETICS 593, 593-94 (1999) ("Sequencing of the MAOA gene showed, at position 936, a C•T mutation that introduces a premature-termination codon and that creates a null allele in the gene.").

30. Paul S. Appelbaum, *Law & Psychiatry: Behavioral Genetics and the Punishment of Crime*, 56 PSYCHIATRIC SERVICES 25, 25 (2005). Nevertheless, "low levels of [MAOA] are correlated with mental retardation, . . . addiction, reduced inhibition, lack of self control, and aggression. Several studies have found a relationship between low [MAOA] levels and criminality. This has led to a theory that people who have low [MAOA] levels react more impulsively . . . and are therefore more likely to commit a crime." BAKER, *supra* note 8, at 84-85.

31. Because mutations that lead to an absence of MAOA activity were unlikely to be present, the researchers examined 442 males in the group for differences in the promoter region of the gene, which determines how strongly the gene is expressed (that is, how much MAOA is produced). Appelbaum, *supra* note 30, at 25.

32. Avshalom Caspi et al., *Role of Genotype in the Cycle of Violence in Maltreated Children*, 297 SCIENCE 851, 851-53 (2002).

33. The cohort consisted of 1,037 children in Dunedin, New Zealand. The participants had first been assessed at three years of age and had just completed their ninth follow-up at age twenty-six. *Id.* at 852.

researchers found that “[m]altreated children with a genotype conferring high levels of MAOA expression were less likely to develop antisocial problems.”<sup>34</sup> “These findings,” they suggested, “may partly explain why not all victims of maltreatment grow up to victimize others, and they provide epidemiological evidence that genotypes can moderate children’s sensitivity to environmental insults.”<sup>35</sup>

Some critics of human behavioral genetics seem willing to dismiss all such findings out of hand. Genewatch’s report on the United Kingdom’s database, for instance, summarily rejects “the overall approach” as flawed, stating “[a]ll research into behavioural genetics relies on an approach that has been subject to severe criticism. Most studies of this type seem to be good at producing correlations but rarely generate any robust or meaningful evidence.”<sup>36</sup>

However, this criticism is painted with too broad a brush. It is true that many if not most initial findings in linkage studies of specific loci and psychiatric disorders and behaviors have been thrown into doubt by subsequent studies,<sup>37</sup> but this may reflect the fact that linkage analysis, being limited by the size of the families studied, is not powerful enough to detect quantitative trait loci whose

34. *Id.* at 851. As Dr. Appelbaum explains,

Specifically, the researchers were interested in how experiences of maltreatment between the ages of three and 11 years affected the later antisocial propensities of participants with either a high or low MAOA activity.

Using four separate measures of antisocial behavior, including convictions for violent crime, the research team found that each measure was significantly increased in the group that had both low MAOA activity and a history of severe maltreatment. In contrast, for participants with high levels of MAOA, no significant increase was found in any of the antisocial measures, even when they had experienced the same level of maltreatment. The overall impact of this gene-environment interaction can be judged from the fact that the 12 percent of the cohort that had both low MAOA and maltreatment accounted for 44 percent of the cohort’s convictions for violent crime. Looked at somewhat differently, 85 percent of the males with both risk factors developed some form of antisocial behavior.

Paul S. Appelbaum, *supra* note 30, at 25.

35. Caspi et al., *supra* note 32, at 851. The jury is still out on whether the observed interaction is real. A recent study of self-reported conduct problems and criminal convictions among sibling pairs from the National Longitudinal Study of Adolescent Health found a trend in the predicted direction, but the result was not statistically significant. See B.C. Haberstick et al., *MAOA Genotype and Antisocial Behaviors in the Presence of Childhood and Adolescent Maltreatment*, 135B AM. J. HUM. GENETICS (Neuropsychiatric Genetics) 59 (2005).

36. STALEY, *supra* note 9, at 37 (citing P.R. Billings et al., *The Genetic Analysis of Human Behaviour: A New Era?*, 35 SOC. SCI. & MED. 227 (1992)); see also Wilker, *supra* note 5, at 147 (“[A]nother problem may arise if researchers try to use biological samples collected and stored in forensic contexts in experiments designed to identify genes associated with criminal behavior. . . . [S]uch research has no scientific merit or basis . . .”).

37. See, e.g., Steven O. Moldin, *Genetic Research on Mental Disorders*, in GENETICS AND CRIMINALITY: THE POTENTIAL MISUSE OF SCIENTIFIC INFORMATION IN COURT 115, 131 (Jeffrey R. Botkin et al. eds., 1999) (“Linkage analyses have so far failed to convincingly identify a well-demarcated chromosomal region as containing a susceptibility locus for any mental disorder. Given that there are likely multiple susceptibility loci of small relative effect, this is not surprising.”); H.J. Williams et al., *Detailed Analysis of PRODH and PsPRODH Reveals No Association with Schizophrenia*, 120B AM. J. MED. GENETICS 42 (2003); R. Segurado, *Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder*, 73 AM. J. HUM. GENETICS 49, 50 (2003).



individual effects are small.<sup>38</sup> The only criticism the Genewatch report supplies is a misrepresentation of the results of one study of adoptees<sup>39</sup> and a cartoon-like example of obvious confounding variables.<sup>40</sup> Nonetheless, other observers have offered a more systematic critique as the basis for the rejection of human behavioral genetics as a field of study. One thoughtful skeptic writes that in human studies, as opposed to work with other animals,

We cannot control environmental conditions rigorously in raising children, something that would be necessary to ascertain whatever interaction might be operative in determining, for example, a tendency toward violent or criminal behavior. As a result, human-behavior geneticists have been forced to adopt more indirect methods . . . such as reliance on twin and adoption studies, in which behavioral traits in adults are correlated with the degree of biological relatedness between parent and child or between collateral relatives (siblings, first cousins, etc.). These methods provide circumstantial evidence at best, primarily because they are unable to correct for, or even identify, the myriad factors involved in the development of a child from conception to maturity. . . . My assessment is that human-behavior genetics at present

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38. See, e.g., Hirschhorn & Daly, *supra* note, 24, at 96; E.S. Lander & N.J. Schork, *Genetic Dissection of Complex Traits*, 265 *SCIENCE* 2037, 2040 (1994).

39. To prove that all, or almost all, correlations are spurious, the report refers to a Danish study that supposedly found an association between the criminal records of adopted children and their biological parents with regard to the offense of house break-ins but not other crimes. The report does not cite the study itself but refers to Dorothy C. Wertz, *Crime Genes: The Danish Adoption Studies*, GENESAGE, Jan. 11, 1996. However, the correlation is not confined to house break-ins alone, but to property crimes more generally. See Sarnoff A. Mednick et al., *Genetic Influences in Criminal Convictions: Evidence from an Adoption Cohort*, 224 *SCIENCE* 891, 892 (1984) (the original study, reporting “a statistically significant relation for property crimes but not violent crimes”). This difference might mean that there is no true correlation with regard to any offense. E.g., Heathcote W. Wales, *Tilting at Crime: The Perils of Eclecticism*, 74 *GEO. L.J.* 481, 488 (1985) (reviewing JAMES Q. WILSON & RICHARD HERRNSTEIN, *CRIME AND HUMAN NATURE* (1985)). It also could reflect a measurement problem for crimes of violence. See NUFFIELD COUNCIL, *supra* note 13, at 93 (“[S]tudies of murderers reveal that approximately half have lengthy histories of repeated assaults, rapes, robberies and other offence types, but the other half have committed a single extreme act after a lifetime free from crime. This indicates that the most serious of violent offences, homicide, as a legally constructed status, captures individuals likely to be quite heterogeneous in their genetic dispositions. Low base rates and heterogeneous participants may explain why studies using conviction data have found no heritability for violence.”). The data also could indicate “that violent and property offenses may have different genetic antecedents,” not that adoption studies show no meaningful associations. John Monahan, *Slouching Toward Crime*, 95 *YALE L.J.* 1536, 1542 (1986) (reviewing JAMES Q. WILSON & RICHARD HERRNSTEIN, *CRIME AND HUMAN NATURE* (1985)).

40. The Genewatch report misconstrues the Danish example of a false positive as a manifestation of confounded variables:

This point is illustrated by the following hypothetical example. If research were carried out in the USA to find genetic links to criminal behaviour, the genes influencing skin colour would probably be found to be linked with crime. This is because the majority of prisoners in the USA are African-American. But it would be wrong to conclude that the genes that produce skin pigment cause criminal behaviour or for researchers to claim they had found a criminal gene. The results would demonstrate only a correlation that on its own would be pretty meaningless.

STALEY, *supra* note 9, at 37. For a variety of reasons that have nothing to do with genetics (denoted by Z), skin color is correlated with crime (more precisely, with apprehension and conviction (Y)). The melanocortin 1 receptor gene (X) is correlated with skin color. Therefore, the gene X also is correlated with criminal records Y. The XY correlation is real, but the correlation is driven by the unmeasured confounding variable Z, which is the true cause. Needless to say, geneticists are aware of this phenomenon. See, e.g., Lander & Schork, *supra* note 38, at 2041 (using the example of the HLA-A1 allele’s being misinterpreted as causing the use of chopsticks among San Francisco residents just because this HLA type is concentrated among Asians).

can contribute little or nothing of use in determining the causes of certain human social behaviors—like criminality . . . .<sup>41</sup>

The value of controlled experimentation in investigating causation cannot be gainsaid. Yet there are other fields of inquiry in which controlled experimentation with human beings is not feasible, and this does not mean that a combination of observational research on humans and experimentation with animals and tissues cannot supply meaningful causal theories. Multiple hypothesis testing, spurious correlations, and other threats to causal analysis are endemic to social and biomedical science. The risk of false alarms is a reason for raising the bar to publication, for caution in interpreting initial reports, for studying the mechanisms by which the loci in question act, and for demanding replication.<sup>42</sup> It is not a reason to conclude that real associations and interactions cannot be found or that exploratory studies should not be performed.<sup>43</sup>

### B. The Mythical “Crime Gene”

Technically speaking, the phrase “crime gene” is an oxymoron. In the words of one well known behavioral genetics researcher:

There are no genes for behavior just as there are no genes for beauty or athletic ability. Genes are chemical structures that can only code for amino acid sequences. These amino acid sequences interact with all of what we are and can thus indirectly affect endpoints as complex as behavior, but there is no gene for a particular behavior. For example, genetics appears to affect alcoholism but this does not mean there is a gene that makes us consume large quantities of alcohol. It may be that genetic factors influence our sensitivity to alcohol so that some of us need to drink more to get “high” and are for that reason at greater risk for alcoholism.<sup>44</sup>

Moreover, the chemicals associated with genes do not act in isolation, which makes unqualified statements of genetic causation problematic. One eminent neuroscientist, seeking to emphasize the complexities in this regard, wrote that:

Genes, of course, have plenty to do with behavior. By now, surely, everyone knows that they determine intelligence and personality. Certain genetic makeups cause criminality, alcoholism[,] and a proclivity toward misplacing car keys. And I’d better not go on in this vein with a straight face, or you won’t even bother to finish this paragraph: in truth, such bald statements about genes are a total crock. I find it inconceivable that anyone reading this magazine could believe in that kind of medieval genetic determinism. Genes don’t cause behaviors. Sometimes they influence them.

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41. Allen, *supra* note 22, at 294.

42. See Editorial, *Freely Associating*, 22 NATURE GENETICS 1, 2 (1999).

43. See, e.g., BAKER, *supra* note 8, at 56 (“[R]esearchers are increasing sample sizes and improving statistical methods. The astounding advances in microarray technology have allowed researchers to target ever-smaller regions of DNA while scanning ever-larger segments of the genome simultaneously; over time this should improve the yield for ‘gene hunters’, while reducing the number of false positives.”). Allen gives a further reason to act on “the assumption” that human behavioral genetics research is “useless”—“to proceed under any other assumption will certainly lead to a legal and ethical quagmire . . . .” Allen, *supra* note 22, at 294. I address this concern about the misuse of knowledge in Part IV.

44. ROBERT PLOMIN, NATURE AND NURTURE: AN INTRODUCTION TO HUMAN BEHAVIORAL GENETICS 20–21 (1990).

With that out of the way, we can flaunt our sophistication. Genes influence behavior, the environment influences behavior, and genes and the environment interact—that concept is one of the great scientific clichés of the latter part of the twentieth century. What it means is that the effects of a given gene on a plant or animal usually vary with changes in the environment, and the effects of the environment usually vary with changes in the genetic makeup of the organism.<sup>45</sup>

That genes always act in the context of the environment is not the only reason that “crime gene” talk is misleading. The notion of a *single* gene causing different behaviors is clearly too simplistic. Blood types, some simple metabolic processes, a few physical traits, and some rare diseases are monogenic—they are governed by single genes<sup>46</sup> that produce easily observed effects in a wide range of environments and that display patterns of simple dominant or recessive inheritance in family studies.<sup>47</sup> Other physical traits and conditions, such as height, blood pressure, weight, and digestive activity, vary on a continuous scale. Unlike a congenital condition such as Tay-Sachs disease that is either present or absent, these complex traits vary across a broad range of values. The corresponding “quantitative trait loci” (QTLs)<sup>48</sup> are the product of many additive or interacting genes,<sup>49</sup> and “[t]he same is true for all complex behaviors. Each is affected by multiple genes interacting with multiple environmental influences. For any given behavior, relevant genes and environmental factors number in the dozens, hundreds, or perhaps thousands.”<sup>50</sup> In these circumstances, the contribution of any particular gene to the behavior is small,<sup>51</sup> perhaps on the order of one percent.<sup>52</sup>

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45. Robert M. Sapolsky, *Genetic Hying*, THE SCIENCES, Mar.–Apr. 2000, at 12–13. Dr. Sapolsky adds,

I say *usually* because a powerful influence from one side of the interaction can overwhelm the other. In the realm of intellect, for instance, even the most salutary environment will not compensate for the catastrophic consequences of, say, the genetic makeup that leads to Tay-Sachs disease, a malady that causes severe brain damage. And conversely, some environmental influences can overwhelm the effects of genetics: having the innate mental capacities of an Einstein will scarcely matter if you are subjected to severe and prolonged protein malnutrition during childhood. But in less extreme cases, genes and environment achieve a balance.

*Id.* at 13.

46. BAKER, *supra* note 8, at 17 (“[C]ystic fibrosis, early onset Alzheimer’s, and Huntington’s disease have been tracked to one gene.”).

47. David Altshuler & Andrew G. Clark, *Harvesting Medical Information from the Human Family Tree*, 307 SCIENCE 1052, 1052 (2005) (reporting that “[a] central goal of human genetics is to identify and understand causal links between variant forms of genes and disease risk in patients. To date, most progress has been made studying rare, Mendelian diseases in which a mutation in a single gene acts strictly in a deterministic manner, that is, the mutation causes the disease.”); Risch, *supra* note 23.

48. A “locus” is a particular location on a specified chromosome.

49. *E.g.*, Risch, *supra* note 23.

50. BAKER, *supra* note 8, at 17; *see also* Katherine I. Morley & Wayne D. Hall, *Is There a Genetic Susceptibility to Engage in Criminal Acts?*, 263 AUSTRALIAN INSTITUTE OF CRIMINOLOGY: TRENDS AND ISSUES IN CRIMINAL JUSTICE 1, 3 (2003) (“ASPD and related disorders are not influenced by a single gene . . . . The consensus view is that these traits are influenced by the additive effects of many different gene variants that are widely distributed throughout the general population . . .”).

51. *E.g.*, Altshuler & Clark, *supra* note 47, at 1052. Moreover, as Neil Risch explains,

The gene mutations studied by Mendel, and those more recently discovered by positional cloning, are those with large effect and strong genotype–phenotype correlations. They are

And yet even if it is scientifically crude to resort to phrases like “crime genes,” more temperate terminology does not alter the basic concern. Certain DNA sequences (the genes) at multiple loci are “expressed” by the cellular machinery as proteins; differences in the sequences at these loci (different “alleles” of a gene) lead to the production of different proteins, or varying amounts of proteins;<sup>53</sup> and some of these differences can result in different physiological or behavioral outcomes under some (environmental) conditions. But this more sophisticated understanding of QTLs does not preclude the possibility that law enforcement databases would be useful for discovering loci that are at least weakly associated with some behavioral disorders that would be of interest to medical or social scientists. To assess this possibility more fully, the kind of data that law enforcement authorities could provide for research purposes and how those data might profitably be analyzed must be considered.

### C. Law Enforcement Databases and Repositories as a Source of Genetic Data

#### 1. The Nature of the Data Collected from Offenders

To construct a law enforcement database, samples of DNA must be collected, the samples analyzed, and the resulting data stored in such a way that it can be accessed efficiently. In the systems now in use, blood, saliva, or other tissue or fluid is collected, a portion is taken for analysis, and some of the remainder is preserved and stored. A minute portion of the genetic information in the sample is analyzed. The analysis generally is limited to thirteen short tandem repeat (STR) loci that yield patterns, or “genotypes,”<sup>54</sup> that approach

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effectively the “low-hanging fruit” that are easy to harvest. Now, however, we are left with the great majority of the fruit at the top of the tree with no obvious way to reach it. In genetics terms, these are the numerous genes of smaller effect that are likely to underlie most common, familial traits and diseases in humans—that is, the genes more closely related to the biometrical view of the world.

Risch, *supra* note 23, at 850.

52. See, e.g., Robert Plomin et al., *Behavioral Genomics*, in *BEHAVIORAL GENETICS IN THE POSTGENOMIC ERA* 531 (Robert Plomin et al. eds. 2003). Plomin writes:

[W]e do not know the distribution of effect sizes of QTLs for any complex trait in plant, animal, or human species. Not long ago, a 10% effect size was thought to be small, at least from the single-gene perspective in which the effect size was essentially 100%. However, for behavioral disorders and dimensions, a 10% effect size may turn out to be a very large effect. If QTLs account for 1% rather than 10% of the liability to disorders, this would explain why QTLs of smaller effect size, as in the case of associations between dopamine genes and hyperactivity, yield less consistent results than for apolipoprotein E and dementia where the QTL . . . accounts for more than 10% of the liability to dementia.

*Id.* at 535.

53. There is more to gene expression than this. Some “genes” do not code for RNA that is translated to proteins; instead, these transcriptional elements code for RNA that directly affects the expression of the protein-coding genes. See W. Wayt Gibbs, *Unseen Genome: Gems Among the Junk*, *SCI. AM.*, Nov. 2003, at 49–50; Rodrigo Yelin et al., *Widespread Occurrence of Antisense Transcription in the Human Genome*, 21 *NATURE BIOTECHNOLOGY* 379 (2003).

54. A DNA “allele” is a measurable variation (from person to person) in the structure of the DNA at a given locus. Thus, the collection of the DNA alleles at the thirteen loci is the person’s “genotype” (even though this “genotype” involves no genes). Forensic scientists often refer to such DNA genotypes with the nontechnical term “DNA profiles.”

the level of unique identification. Despite the connotation of “genotype,” the DNA sequences at these loci are *not* genes; these alleles are noncoding, nonregulatory DNA sequences.<sup>55</sup> In themselves, they reveal information no more intimate than the particular blood serum enzyme that an individual happens to have, the pattern of blood vessels in the retina of the eye, or the whorls and ridges in a fingerprint. In short, these alleles disclose nothing about the individual’s susceptibility to diseases, bodily structure, or mental functioning.<sup>56</sup>

The identifying genotypes, expressed as a set of numbers, are entered into state or local databases.<sup>57</sup> From the state level, they can be entered into a national database known as NDIS—the National DNA Index System—maintained by the Federal Bureau of Investigation (FBI). Police looking for the person who might have left blood, semen, or other biological trace evidence at crime scenes can search individual state databases or the national database to learn whether a known offender might be the source of the crime-scene DNA. The multilevel system of local, state, and national databases constitutes CODIS—the Combined DNA Index System.<sup>58</sup>

In short, there are databases that store digital data records, and there are tissue repositories, or biobanks, that preserve the original samples taken from offenders. All the database records can be searched by computer to determine whether any match the genotypes from the trace-evidence samples associated with the crime. Ordinarily, there is no reason to re-examine the sample on file.<sup>59</sup>

## 2. The Prospects for Case-Control Studies of Association

The databases themselves are of little or no value in behavioral genetics research. Being noncoding, nonregulatory sequences, the identification STRs cannot be QTLs, and it would be an extraordinary coincidence if they turned out to be adjacent to such loci (which could make them markers for QTLs). The DNA samples, however, are another story. Two types of research might be proposed for them. In one scenario, it can be imagined that scientists already have located genes that are plausible candidates for QTLs that would tend to increase (or decrease) the probability of commission of certain crimes. For instance, a number of studies suggest that longer alleles of the dopamine-D4 receptor gene (DRD4) lead to greater novelty-seeking behavior (in humans as

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55. D.H. Kaye, *Two Fallacies About DNA Databanks for Law Enforcement*, 67 BROOK. L. REV. 179, 182 (2001).

56. *See id.* at 188; D.H. Kaye, *Bioethics, Bench, and Bar: Selected Arguments in Landry v. Attorney General*, 40 JURIMETRICS J. 193, 198 (2000).

57. “Typically, the Local DNA Index System, or LDIS, is installed at crime laboratories operated by police departments or sheriff’s offices.” FBI, What’s the Difference Between NDIS and CODIS? (Oct. 8, 1998), [http://hope-dna.com/docs/difference\\_codis.htm](http://hope-dna.com/docs/difference_codis.htm).

58. *Id.*

59. If a match is found, further police work is required to establish a case against the suspect. If the full investigation suggests guilt and the case goes to trial, the prosecution should not rely on the database search to link the defendant to the crime. Rather, defendant’s genotypes should come from the analysis of a new confirmatory sample of the suspect’s DNA.

well as other animals), and a neurochemical explanation for this result can be constructed.<sup>60</sup> Since one might predict that the DRD4 7-repeat allele (the allele often said to be positively associated with novelty seeking) will be found at a higher level in the offender DNA samples than among the population not known to be involved in crime, the convicted-offender samples could have some conceivable research value. Similar examples of genes that are candidates for such case-control studies with subsets of the convicted-offender samples could come from animal and other studies on the genetics of drug dependence.<sup>61</sup>

In another scenario, it is also possible that the forensic DNA databanks might attract researchers interested in locating rather than confirming possible QTLs.<sup>62</sup> Once a pejorative term among statisticians, “data-mining” in large population groups has become a mainstream research strategy in medical genetics.<sup>63</sup> “Genome scans” for single-nucleotide polymorphism (SNP) markers<sup>64</sup> probably would show higher frequencies of certain markers in cases than controls, suggesting avenues (as well as blind alleys) for more definitive research.

In short, it is at least conceivable that associational studies with the DNA samples of convicted offenders would be of scientific interest. To be sure, the collections of DNA samples maintained by law enforcement authorities have serious limitations as research tools, but the possibility that researchers may

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60. See, e.g., Richard P. Ebstein et al., *Behavioral Genetics, Genomics, and Personality, in BEHAVIORAL GENETICS IN THE POSTGENOMIC ERA*, supra note 52, at 365, 368–69; Brien Riley, *Molecular Genetics and the Human Personality*, 191 J. NERVOUS & MENTAL DISEASE 482 (2003) (reviewing *MOLECULAR GENETICS AND THE HUMAN PERSONALITY* (J. Benjamin, et al. eds., 2002)). But other studies are less clear-cut or inconsistent with this theory. See generally A.N. Kluger et al., *A Meta-analysis of the Association between DRD4 Polymorphism and Novelty Seeking*, 7 MOLECULAR PSYCHIATRY 712 (2002); J.A. Schinka et al., *DRD4 and Novelty Seeking: Results of Meta-analyses*, 114 AM. J. MED. GENETICS 643, 643–48 (2002).

61. See, e.g., Andrew C. Heath et al., *Genetic and Environmental Risks of Dependence on Alcohol, Tobacco, and Other Drugs, in BEHAVIORAL GENETICS IN THE POSTGENOMIC ERA*, supra note 52, at 309, 328 (referring to “the somewhat chaotic literature on candidate gene associations with substance abuse disorders”).

62. It has been said that the repositories are not “particularly useful” for identifying loci of interest because they lack samples from family members needed for linkage analysis. McEwen, supra note 4, at 322. However, as previously indicated, studying linkage in families is not a method of choice here because it typically lacks the necessary statistical power to uncover QTLs with small effects.

63. See, e.g., Symposium, *Human Genetic Sampling: Ethical, Legal, and Social Considerations*, 45 JURIMETRICS J. 111 (2005); Symposium, *Regulation of Biobanks*, 33 J.L. MED. & ETHICS 7 (2005); Jocelyn Kaiser, *NIH Ponders Massive Biobank of Americans*, 304 SCIENCE 1425 (2004).

64. See, e.g., Ian W. Craig & Joseph McClay, *The Role of Molecular Genetics in the Postgenomic Era, in BEHAVIORAL GENETICS IN THE POSTGENOMIC ERA*, supra note 52, at 19, 36 (proposing scans of SNPs in coding regions (cSNPs) targeting “nonhousekeeping loci” expressed in the brain as “a feasible project for the high-throughput approaches”). Whether this particular strategy is optimal is debatable. See Hirschhorn & Daly, supra note 24, at 98 (“[T]he alleles that underlie complex traits have more subtle effects on disease risk and might be more likely to include non-coding regulatory variants with a modest impact on expression.”). In any event, a variety of promising techniques for studies with large populations rather than families is emerging. See, e.g., William Y. S. Wang et al., *Genome-wide Association Studies: Theoretical and Practical Concerns*, 6 NATURE REV. GENETICS 109 (2005).

want to open the vaults at criminal DNA databanks cannot be dismissed as a mere fantasy.<sup>65</sup>

### III

#### THE LEGAL "IS": PERMISSIBILITY OF RESEARCH ACCESS TO OFFENDER DATABASES

A common refrain sounded by critics of DNA databases for law enforcement is that laws allow, if not invite, genetic information collected to catch rapists, murderers, and other criminals to be used for genetic research into criminal conduct, as well as mental illness and other diseases. The following alarms are typical:

- (1) "In about fifteen of the fifty states, the statutes expressly permit that the databanks . . . can be used for research purposes in . . . medical research, humanitarian needs, and what have you."<sup>66</sup>
- (2) "Twenty-four states allow DNA samples that have been collected only for law enforcement identification to be used for a variety of other non-law enforcement purposes."<sup>67</sup>
- (3) "[T]wenty states allow law enforcement to use DNA samples to improve forensic techniques, 'which could mean searching . . . DNA samples for genetic predictors of recidivism, pedophilia or aggression'."<sup>68</sup>

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65. A practical problem is that the samples are scattered among the fifty states and the District of Columbia. Then, there are concerns about whether the samples are sufficiently representative. Genewatch has complained that "the DNA profiles and samples will not be representative of either the general or the 'criminal' population. Genetic research using the database is therefore likely to be misleading as well as controversial." STALEY, *supra* note 9, at 8. This criticism seems confused. First, research into the interactions of genes and environment on criminal behavior has been "controversial," particularly in America, but this fact is an argument against the research only if the objections to the research are well founded. Second, convicted offenders are not representative of the general population, but that is precisely what makes them of interest. Third, it is true that *convicted* offenders are not a representative sample of the "criminal population," which includes individuals who have never been convicted of crimes they committed, and a researcher who overlooks this fact could misconstrue genetic differences. However, this possibility hardly makes all research involving convicted offenders "misleading." For instance, burglars who evade detection may plan more carefully than those who are caught. A set of loci with alleles that differ as between the general population and convicted petty burglars might have more to do with impulsivity than with a putative genetic tendency to enter premises for criminal purposes. Research that is sensitive to this facet of the data would not be misleading. Here, the convicted offender samples might still be useful, in conjunction with other data, for studies of QTLs for impulsivity.

66. Peter Neufeld, Remarks at the Conference on DNA and the Criminal Justice System (Nov. 19–21, 2000), [http://www.ksg.harvard.edu/dna/transcribe\\_table\\_page.htm](http://www.ksg.harvard.edu/dna/transcribe_table_page.htm).

67. Barry Steinhardt, *Privacy and Forensic DNA Data Banks*, in DNA AND THE CRIMINAL JUSTICE SYSTEM, *supra* note 22, at 173, 176; cf. Jonathan Kimmelman, *The Promise and Perils of Criminal DNA Databanking*, 18 NATURE BIOTECHNOLOGY 695, 696 (2000) ("On the negative side, . . . 23 states (directly or indirectly) authorize release of samples or records for research uses that would assist law enforcement . . . . Retaining samples sustains the possibility that they will find ethically problematic uses in the future; authorizing research on samples, even if they are stripped of individual identifiers (as mandated by most laws) nearly delivers them to this unseemly fate.").

68. Jill C. Schaefer, Comment, *Profiling at the Cellular Level: The Future of the New York State DNA Databanks*, 14 ALB. L.J. SCI. & TECH. 559, 576 (2004) (citation omitted); see also Troy Duster,

- (4) “[M]any state statutes allow access to the samples for undefined law enforcement purposes and humanitarian identification purposes, or authorize the use of samples for assisting medical research.”<sup>69</sup>

Even the FBI has endorsed this view, conceding that in most states “there appear to be no protections against the dissemination of DNA samples.”<sup>70</sup> At the other pole, it has been said that “the fear that DNA information or samples in law enforcement databases will be turned over to medical researchers is largely unfounded” because no statutes allow DNA samples taken by compulsion from convicted offenders to be used for medical research.<sup>71</sup>

The explanation for these antipodal views lies, at least in part, in the expansive readings some commentators have given to certain phrases, or to the absence of direct mention of research uses for samples, in the statutes establishing offender databases. The disagreement, therefore, is one of statutory construction, and it can be illustrated and clarified by examining four statutes.

#### A. Federal Law

For years, the federal government did not take DNA from any convicted offenders. Instead, the FBI merely maintained the national database (NDIS), as part of the “Combined DNA Index System” (CODIS), composed of records derived from samples collected by participating states. When police were unable to find a match in the state or local databases, they could turn to CODIS to see if the source of the crime-scene sample might be an offender from another state. The DNA Analysis Backlog Elimination Act of 2000,<sup>72</sup> however, authorized the collection and analysis of samples from individuals convicted of violating a set of federal criminal laws and the inclusion of the identifying DNA genotype records in CODIS.<sup>73</sup> As of July 2005, CODIS contained DNA

*Selective Arrests, an Ever-expanding DNA Forensic Database, and the Specter of an Early-Twenty-First-Century Equivalent of Phrenology*, in *DNA AND THE CRIMINAL JUSTICE SYSTEM*, *supra* note 22, at 315, 328 (“Twenty states authorize the use of data banks for research on forensic techniques [that] could easily mean assaying genes or loci that contain predictive information.”).

69. Mark Rothstein & Sandra Carnahan, *Legal and Policy Issues in Expanding the Scope of Law Enforcement DNA Data Banks*, 67 *BROOK. L. REV.* 127, 156 (2001) (citations omitted).

70. Randall S. Murch & Bruce Budowle, *Are Developments in Forensic Applications of DNA Technology Consistent with Privacy Protections?*, in *GENETIC SECRETS: PROTECTING PRIVACY AND CONFIDENTIALITY IN THE GENETIC ERA* 212, 226 (Mark A. Rothstein ed., 1997).

71. Davina Dana Bressler, Note, *Criminal DNA Databank Statutes and Medical Research*, 43 *JURIMETRICS J.* 51, 54, 63–66 (2002); *cf.* Jonathan Kimmelman, *Risking Ethical Insolvency: A Survey of Trends in Criminal DNA Databanking*, 28 *J.L. MED. & ETHICS* 209, 212 (2000) (“[S]everal statutes brush perilously close to involuntary uses of banked DNA samples for research purposes . . . . Five states appear to authorize release of DNA samples for the support of ‘identification research and protocol development.’”).

72. 42 U.S.C. § 14135 (2000).

73. Under 42 U.S.C. § 14135a(a)(1), the Director of the Bureau of Prisons must “collect a DNA sample from each individual in the custody of the Bureau of Prisons who is, or has been, convicted of a qualifying Federal offense . . . .” Section 14135a(b) states that “[t]he Director of the Bureau of Prisons or the probation office responsible (as applicable) shall furnish each DNA sample collected under



identification profiles from more than two million convicted state, federal, and military offenders.<sup>74</sup>

Under federal law, for a state to participate in CODIS—as every state does—it must operate “pursuant to rules that allow disclosure of stored DNA samples and DNA analyses only” for the purposes enumerated in 42 U.S.C. § 14132(b):

- (A) to criminal justice agencies for law enforcement identification purposes;
- (B) in judicial proceedings, if otherwise admissible pursuant to applicable statutes or rules;
- (C) for criminal defense purposes, to a defendant, who shall have access to samples and analyses performed in connection with the case in which such defendant is charged; or
- (D) if personally identifiable information is removed, for a population statistics database, for identification research and protocol development purposes, or for quality control purposes.<sup>75</sup>

These limitations apply equally to the samples and records of federal offenders.<sup>76</sup>

The upshot of these restrictions is clear. Behavioral genetics researchers wanting to use the samples in CODIS (and in the state and local databases feeding CODIS) are excluded. Their research would not qualify under subsection (A) as undertaken “for law enforcement identification purposes” because the CODIS legislation was adopted to support and expand a well-defined system of identification—namely, an operational, computerized database of records of identifying DNA genotypes that would let investigators search for DNA matches between crime-scene samples and convicted-offender samples. In the abstract, checking people for genes that might bear some statistical association to antisocial behavior might be said to be a “law enforcement identification purpose,” but this ignores the fact that the statute refers to a system of using trace DNA to link individuals to completed crimes—not to “identify” people who might be predisposed to some behaviors. Prediction of possible behavior is not comparable to the retrospective, definitive system of “identification” authorized and funded by Congress.

This contextual reading of subsection (A) is confirmed by subsection (D), which defines the allowable scope of “research” with the samples. Subsection (D) allows only research designed to improve the paradigmatic use of DNA to match trace evidence to possible perpetrators. It permits research on

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subsection (a) of this section to the Director of the Federal Bureau of Investigation, who shall carry out a DNA analysis on each such DNA sample and include the results in CODIS.” Section 14135b contains analogous provisions for the DNA from individuals convicted for crimes in the District of Columbia, and 10 U.S.C. § 1565 establishes a similar regime for the military.

74. Federal Bureau of Investigation, NDIS Statistics, <http://www.fbi.gov/hq/lab/codis/clickmap.htm> (last visited Sept. 2, 2005) (reporting 2,599,959 convicted-offender samples).

75. 42 U.S.C. § 14132(b) (2000).

76. *Id.* § 14135e(b). “A person who knowingly—(1) discloses a sample or result described in subsection (a) of this section in any manner to any person not authorized to receive it; or (2) obtains, without authorization, a sample or result described in subsection (a) of this section, shall be fined not more than \$100,000.” *Id.* § 14135e(c).

anonymized—and only on anonymized—samples for only three purposes: “for a population statistics database, for identification research and protocol development purposes, or for quality control . . . .”

Population statistics databases are collections of data from various populations on the DNA alleles and genotypes used in forensic identification. They are used to estimate allele frequencies that are then combined according to population-genetics theory to ascertain the frequencies of the DNA genotypes used in criminal identification.<sup>77</sup> “Identification research and protocol development” refers to work that could enhance the efficacy of matching individuals to traces of DNA found at crime scenes. Developing or testing additional polymorphisms to assist in individualization or to investigate new methods for typing loci would fall into this category. Likewise, “quality control” research fits squarely into the approved identification paradigm, being nothing more than work intended to keep analytical or clerical errors to a minimum.

## B. Massachusetts Law

The Massachusetts statute merits attention because it frequently is held up as an example of a law that is shockingly devoid of constitutionally required safeguards against medical or behavioral research with DNA samples. The public has been told, for example, that “[t]he Massachusetts law set no limits on the purposes for which the samples could be used” and that “samples could be used for research, a practice prohibited by the Nuremberg Code.”<sup>78</sup> A similar argument was made to the Supreme Judicial Court of Massachusetts by outstanding law professors and students at several universities.<sup>79</sup> The argument is untenable.

The Massachusetts statute distinguishes between “DNA records” and “DNA samples.”<sup>80</sup> A sample is “biological evidence of any nature that is utilized to conduct DNA analysis.”<sup>81</sup> A record is “DNA information that is derived from a DNA sample and DNA analysis . . . .”<sup>82</sup> The statute specifies the

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77. See, e.g., IAN W. EVETT & BRUCE S. WEIR, *INTERPRETING DNA EVIDENCE: STATISTICAL GENETICS FOR FORENSIC SCIENTISTS* (1998); NATIONAL RESEARCH COUNCIL COMMITTEE ON DNA FORENSIC SCIENCE, *THE EVALUATION OF FORENSIC DNA EVIDENCE* 89–90 (1996); David H. Kaye, *DNA Evidence: Probability, Population Genetics, and the Courts*, 7 HARV. J. L. & TECH. 101 (1993); Neil J. Risch & B. Devlin, *On the Probability of Matching DNA Fingerprints*, 255 SCIENCE 717 (1992); B.S. Weir, *Independence of VNTR Alleles Defined as Fixed Bins*, 130 GENETICS 873 (1992); B. Devlin et al., *No Excess of Homozygosity at Loci Used for DNA Fingerprinting*, 249 SCIENCE 1416 (1990).

78. Paul R. Billings, Op-Ed, *DNA Data Banks Would Taint Justice*, BOSTON GLOBE, Jan. 14, 1999, at A19.

79. See Kaye, *supra* note 56 (analyzing the arguments in *amicus curiae* briefs filed by Lori Andrews, Harold Krent, and Michelle Hibbert (then at the Chicago-Kent School of Law) and by the Owen M. Kopperschmid Holocaust Human Rights Project of Boston College Law School and the Criminal Justice Clinic of Boston College Law School).

80. The discussion of the Massachusetts statute that follows is adapted from Kaye, *supra* note 56.

81. MASS. GEN. LAWS ANN. ch. 22E § 1 (LexisNexis 2003).

82. *Id.*

permissible uses for the records,<sup>83</sup> and it penalizes all unauthorized uses.<sup>84</sup> In particular, the statute gives the director of the state police laboratory discretion to

make DNA records available . . . for the limited purpose of (1) advancing DNA analysis methods and supporting statistical interpretation of DNA analysis, including development of population databases; provided, however, that personal identifying information shall be removed from DNA records . . . and (4) advancing other humanitarian purposes.<sup>85</sup>

However, the law contains no corresponding list of the authorized uses for samples and imposes no penalty for their misuse.<sup>86</sup> Should this lack of parallelism be interpreted to mean that state employees are free to use and disseminate the samples for any purpose, including medical research? Or does it mean exactly the opposite—that the legislature assumed the samples would not be used for any purpose except to produce the records and therefore deemed it unnecessary to develop a list of allowable uses for the samples?

The Supreme Judicial Court adopted the latter interpretation. It construed the authorization to disclose the records for certain purposes, combined with the omission of any such authorization for disclosure of the sample, as a prohibition on any release of the samples.<sup>87</sup> The court concluded,

the Act confines the use of the samples to a DNA analysis which generates only “numerical identification information.” In most cases, only the resulting “DNA record,” which contains the numerical identification information derived from the samples by the analysis, may be distributed. In addition, the Act limits the purposes for which the DNA records may be distributed, and does not permit dissemination of the DNA samples themselves. . . . The plaintiffs assert that [a section] of the Act, which compels disclosure of the records to comply with Federal statutory or grant obligations, and allows disclosure of records for various scientific or humanitarian purposes, may somehow lead to leakage of complete genetic profiles. Their speculation that data may be used wrongfully is contrary to the language of the Act . . . .<sup>88</sup>

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83. *Id.* § 10.

84. *See id.* §§ 12–13 (making it a crime punishable by a fine of not more than \$1,000 or imprisonment of up to six months for an official to disclose a record or a part of it to “any person or agency not authorized to receive such record” and making it a similar crime to obtain a record or part of it “without proper authorization”).

85. *Id.* § 10(d).

86. The director merely is instructed to “promulgate regulations governing the . . . storage and disposal of DNA samples.” *Id.* § 6.

87. *Landry v. Att’y Gen.*, 709 N.E.2d 1085, 1096 (Mass. 1999) (“[T]he Act limits the purposes for which the DNA records may be distributed, and does not permit dissemination of the DNA samples themselves.”). In addition, the court noted that under the regulations promulgated by the state crime laboratory, even the STR profiles could not be released for “humanitarian purposes.” *Id.* at 1089 n.5.

88. *Id.* at 1096 (citations omitted). In a footnote, the court remarked,

When promulgating final regulations for the Act, the director may want to provide more detail as to tests that may be performed on the DNA samples that are being collected and stored. While the Act only authorizes use of those portions of DNA samples that are relevant for identification purposes, the indefinite storage of the entire DNA sample, see 515 Code Mass. Regs. § 1.05(4), creates some concern that the samples could be misused at some point in the future to search for and disclose private genetic information.

*Id.* at 1096 n.20.

This result seems clearly correct. It is the samples, not the essentially random numbers contained in the databases, that pose a serious privacy question and that make DNA database systems more threatening than, say, fingerprint databases. The critics of DNA databases have made precisely this point in legislative hearings<sup>89</sup> and briefs.<sup>90</sup> It would be perverse to maintain that a law adopted in this setting makes the sensitive samples freely available while imposing strict confidentiality constraints on the purely identifying data that reveal no personally sensitive information. Yet, this view of the statute persists, at least among advocacy groups.<sup>91</sup>

### C. Nevada Law

Another statute that has been falsely portrayed as authorizing “a variety of non-law enforcement uses” for samples “collected only for law enforcement identification”<sup>92</sup> is Nevada’s DNA database law. But the Nevada law, like the Massachusetts statute, is silent on this score. It merely provides for the collection of “a biological specimen”<sup>93</sup> from certain categories of offenders<sup>94</sup> and for the analysis of “genetic markers”<sup>95</sup> by a “forensic laboratory.”<sup>96</sup> However, whereas the Massachusetts law imposes explicit limitations on the use of the bio-identification records, the Nevada statute makes no mention of any allowed uses. Should this omission be taken to mean that anything goes for records and samples alike?

In a brief discussion of this point, the Nevada Supreme Court rejected such an expansive construction of the law. In *Gaines v. State*,<sup>97</sup> the defendant entered a negotiated plea to the unlawful use of coins in a gaming machine, burglary, and forgery arising from a failed attempt to cash three fake \$100.00 Visa

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89. *E.g.*, *Hearing, supra* note 3 (testimony of Barry Steinhardt).

90. *E.g.*, Brief of Electronic Privacy Information Center as Amici Curiae Supporting Appellant at 7–9, *United States v. Kincade*, 379 F.3d 813 (9th Cir. 2004) (en banc) (No. 02-50380), available at [http://www.epic.org/privacy/genetic/kincade\\_amicus.pdf](http://www.epic.org/privacy/genetic/kincade_amicus.pdf).

91. Notwithstanding the structure of the statute and the state’s highest court’s interpretation of it, the Director of the ACLU’s Program on Technology and Liberty continues to cite the Massachusetts statute as a prime example of a database law that permits unbounded circulation of “both the forensic DNA profiled and the raw biological sample that contains DNA.” Steinhardt, *supra* note 67, at 176; see also *id.* at 185 (“[T]he law the Massachusetts legislature passed allows virtually unlimited use of DNA”).

92. *Id.* at 176; see also Kimmelman, *supra* note 71, at 212 (suggesting only eight states (not including Nevada) “prohibit any meaningful use of banked tissues for genetic research”).

93. NEV. REV. STAT. § 176.0913(1)(b) (2003).

94. *Id.* § 176.0913(4).

95. *Id.* § 176.0913(1)(b).

96. *Id.* § 176.0913(2). Although the law does not define the term “genetic markers,” it is plain from the manner in which the term is used (not to mention the background of the law) that these encompass only those “genetic markers” that are useful for forensic identification. See *id.* §§ 176.0918(1), 176.0918(6)(a) (creating procedures under which “[a] person convicted of a crime and under sentence of death” may obtain “a genetic marker analysis of evidence” if “[a] reasonable possibility exists that the petitioner would not have been prosecuted or convicted if exculpatory results had been obtained through a genetic marker analysis of the evidence” and other conditions relating to a traditional forensic identification analysis are satisfied).

97. 998 P.2d 166, 168 (Nev. 2000).

travelers' checks at a Las Vegas casino, and another burglary charge stemming from a check forgery at a Las Vegas bank. The district court sentenced Gaines and ordered him to undergo "DNA genetic marker testing"; Gaines appealed.<sup>98</sup> In a shotgun attack on the constitutionality of the DNA database statute, Gaines maintained that the law was unconstitutional due to "overbreadth."<sup>99</sup> In particular,

Gaines argues that NRS 176.0913 [the Nevada DNA database statute] is overbroad because there are no restrictions on the amount of blood drawn, the testing of the blood, the time period for keeping the test results, and no requirement that the State dispose of the remaining portions of blood not used in the DNA testing. Essentially, Gaines is concerned that the State will use the DNA test results for a discriminatory or invasive purpose, such as determining a convict's predisposition to physical or mental disease.<sup>100</sup>

The court deemed these concerns speculative and conjectural<sup>101</sup> and dismissed them as inconsistent with "[t]he plain language of [the statute, which] limits the purpose of testing to identification."<sup>102</sup>

Taken together, *Landry* and *Gaines* indicate a judicial tendency to construe the scope of allowable uses for the law enforcement DNA records and samples narrowly, if only to blunt the force of constitutional attacks on the database laws. They also stand for the proposition that the meaning of statutory terms should not be divorced from historical context and statutory purpose. If other states follow the same approach, the number of statutes that allow non-law-enforcement research with offender DNA samples approaches zero.

#### D. Alabama Law

Alabama's statute is noteworthy because it has been depicted as authorizing every imaginable type of biomedical research with offender DNA samples.<sup>103</sup>

98. *Id.* at 169.

99. The "constitutional attacks on NRS 176.0913 [include] claims that the statute is overbroad and that it violates his right to be free from unreasonable search and seizure, right to equal protection, right to due process, and right to be free from cruel and unusual punishment." *Id.* at 171.

100. *Id.* at 175.

101. The court wrote:

Gaines' contentions concerning abuse of the genetic marker data are merely speculation and conjecture, as he has provided this court with no evidence regarding such abuse. Finally, we note that the Supreme Court of the United States has rejected an analogous argument: "While this procedure [collection of blood and urine for mandatory drug testing] permits the Government to learn certain private medical facts that an employee might prefer not to disclose, there is no indication that the Government does not treat this information as confidential, or that it uses the information for any other purpose."

*Id.* at 175 (quoting *Skinner v. Ry. Labor Executives' Ass'n*, 489 U.S. 602, 626 n.7 (1989)).

102. The only "plain language" the court identified was subsection 1(b) of NRS 176.0913 that "mandat[es] the samples be used for 'determin[ing] the genetic markers of the blood.'" *Id.*

103. See Gaia Bernstein, *Accommodating Technological Innovation: Identity, Genetic Testing and the Internet*, 57 VAND. L. REV. 965, 1009 (2004) (stating that the Alabama statute "expressly provides for use of the samples for research related to genetic disease"); Juengst, *supra* note 10, at 68–69 (suggesting that the sole limitation on research with these samples is that they be anonymized, which is not "technically possible"); Jean E. McEwen, *DNA Data Banks, in GENETIC SECRETS, supra* note 70, at 231, 238 ("[The Alabama] data banking law specifically authorizes the use of samples collected for its

Again, the truth is much less alarming. In its declaration of the statute's purpose, the legislature found that forensic DNA matching had become "generally accepted in the relevant scientific community"<sup>104</sup> and declared that

the Alabama Department of Forensic Sciences should be authorized and empowered to analyze, type and record any and all genetic markers contained in or derived from DNA and to create a statewide DNA database system for collection, storage and maintenance of genetic identification information as the same may pertain to the identification of criminal suspects.<sup>105</sup>

The legislature's purpose in "creat[ing] and establish[ing] a statewide DNA database" was to implement "the most reasonable and certain method or means to rapidly identify repeat or habitually dangerous criminals."<sup>106</sup> But the legislature recognized that the database might also "serve an array of humanitarian purposes, including . . . the identification of human remains from natural or mass disasters or the identification of missing, deceased or unidentified persons."<sup>107</sup> Moreover, "through the development of a population statistical database which does not include therein individual personal identification information an important research mechanism is obtained for the causation, detection and prevention of disease."<sup>108</sup>

These legislative findings have a common and circumscribing theme—using molecular biology to establish the origin of two or more DNA samples. The last declaration, though, expresses the hope that the frequencies of the alleles used in this type of forensic work would be valuable in medical research as well. While this belief does not seem to be true for the CODIS STR loci that dominate law enforcement work today, it was more plausible for some of the loci used in earlier years.<sup>109</sup> In any event, the DNA database system authorized in Alabama adheres to the trace-evidence paradigm of matching DNA samples, not to the dubious theory that "identification" includes prediction of what someone might someday do.<sup>110</sup>

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data bank for 'educational research or medical research or development'—an authorization that would presumably encompass behavioral research into, for example, genetic predispositions to violence."); Schaefer, *supra* note 68, at 576.

104. *Id.* § 36-18-20(e).

105. *Id.* § 36-18-20(h).

106. ALA. CODE § 36-18-20(g) (LexisNexis 2001).

107. *Id.* § 36-18-20(i).

108. *Id.* § 36-18-20(j). The statute defines a "DNA population statistical database" as "[t]hat system established by the Director of the Alabama Department of Forensic Sciences for collecting, storing, and maintaining genetic information relating to DNA population frequencies." *Id.* § 36-18-21(h).

109. See, e.g., M.A. Pani et al., *Vitamin D Receptor Allele Combinations Influence Genetic Susceptibility to Type 1 Diabetes in Germans*, 49 DIABETES 504 (2000); Matthias Wjst, *Variants in the Vitamin D Receptor Gene and Asthma*, 6 BIOMED. CENT. GENETICS 2 (2005).

110. The statute lists these sole purposes for the database:

- (a) Assisting federal, state, county, municipal, or local criminal justice and law enforcement officers or agencies in the putative identification, detection, or exclusion of persons who are the subjects of investigations or prosecutions of sex related crimes, other violent crimes or other crimes in which biological evidence is received or recovered.
- (b) Supporting identification research and protocol development of DNA forensic methods.

In particular, the Alabama law includes no express provision for using *samples* in medical research, and such use would exceed the scope of disclosure allowed for the operational “records.”<sup>111</sup> Only the “DNA population statistical database which shall not include therein individually identifiable information”<sup>112</sup> can be utilized to “provide data relative to the causation, detection and prevention of disease or disability” or “to assist in other humanitarian endeavors including, but not limited to, educational research or medical research or development.”<sup>113</sup> One can debate the merits of giving away, for any bona fide scientific or educational purpose, a database listing all observed forensic DNA types, and the notion that they have much medical value is far-fetched. However, it should be remembered that defendants in criminal cases often demanded the release of the population databases and sometimes argued that evidence of a DNA match was not admissible unless the databases from which the estimates of genotype probabilities were drawn were made available to the scientific community. Publicly accessible research databases are generally desirable, and researchers who refuse to make their data available to their colleagues often are viewed with suspicion.

In sum, it is literally true but potentially quite misleading to say “the authorized uses of DNA databases extend beyond criminal identification purposes into the realm of humanitarian and statistical research purposes” or to refer to “the use of their DNA database for genetic research” without clarifying the nature of the database and the genetic research.<sup>114</sup> The “databases” are

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- (c) Creating and maintaining DNA quality control standards.
  - (d) Assisting in the recovery or identification of human remains from natural or mass disasters.
  - (e) Assisting in other humanitarian purposes including the identification of missing, deceased or unidentified persons.

ALA. CODE § 36-18-24 (LexisNexis 2001).

111. Alabama Code § 36-18-27 specifies:

DNA records collected and maintained for the purpose of the identification of criminal suspects or offenders shall be disclosed only:

- (a) To criminal justice agencies for law enforcement identification purposes.
- (b) In judicial proceedings, if otherwise admissible.
- (c) For criminal defense purposes, to a defendant, who shall have access to samples and analyses performed in connection with the case in which such defendant is charged.

*Id.* § 36-18-27.

112. *Id.* § 36-18-31(a).

113. *Id.* § 36-18-31(b).

114. Seth Axelrad, American Society of Law, Medicine, and Ethics, Survey of State DNA Database Statutes (Jan. 12, 2005), [http://www.aslme.org/dna\\_04/grid/guide.pdf](http://www.aslme.org/dna_04/grid/guide.pdf). This publication of the American Society of Law, Medicine, and Ethics wisely cautions that

[s]tatutes provide an informative yet limited picture of each state’s DNA database system. Administrative rules and regulations, as well as the policies and procedures of individual forensic laboratories, play a large role in defining the real-world operation of these databases. Furthermore, statutes are subject to various interpretations, and the impact of any DNA database statute depends in large part on the interpretations and actions of law enforcement agencies and courts.

*Id.* In addition, it correctly notes that

electronic data on identification loci that constitute an infinitesimal fraction of the genome and that are no more stigmatizing than a passport number. They are not “future diar[ies],”<sup>115</sup> “a chapter in the book of life,”<sup>116</sup> “a glimpse into a person’s most intimate self,”<sup>117</sup> or any of the other exaggerated characterizations of the human genome that have reinforced a false sense of genetic determinism or essentialism.

Even the full set of human chromosomes does not match these metaphors, although it assuredly contains personal and sensitive information. As a result, laws like Alabama’s distinguish between the identifying records and the physical samples. Even in Alabama, whose law is most favorable to genetics research outside of the trace-evidence paradigm, only the anonymized forensic records—and not the underlying samples—can be released. Behavioral genetics researchers who come knocking on the doors of state or federal administrators for the DNA of convicted offenders will find them locked, and the key cannot be located within the disclosure and usage provisions of the current database laws.

However, the case law is thin, and it may be a mistake to think that courts will continue to reject extravagant and noncontextual constructions of the database laws. Moreover, inasmuch as statutes are subject to change,<sup>118</sup> it is important to ask what the legal regime *should* be.

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[b]ecause the terms used in the statutes are often vague or undefined, one cannot predict with certainty the scope of the databases’ authorized uses; examples include “law enforcement purposes” and “other humanitarian purposes.” The construction of each statute may provide clues as to whether these terms will be interpreted broadly or narrowly.

*Id.*

115. See George J. Annas, *Privacy Rules for DNA Databanks: Protecting Coded ‘Future Diaries,’* 270 J. AM. MED. ASS’N 2346, 2348 (1993).

116. See Nicholas Wade, *Life Is Pared to Basics; Complex Issues Arise*, N.Y. TIMES, Dec. 14, 1999, at F3 (“[A] medical ethicist . . . noted when biologists sequenced the first human chromosome last month, they called it ‘the first chapter in the book of life, as if life is chromosomes.’”).

117. LORI ANDREWS, *FUTURE PERFECT: CONFRONTING DECISIONS ABOUT GENETICS* 31 (2001).

118. *E.g.*, BAKER, *supra* note 8, at 89 (“Under current law, the tissue samples from which DNA is profiled (such as blood or saliva) are off limits to researchers, but . . . the law is subject to change.”); Kimmelman, *supra* note 71, at 212. In considering the likelihood of changes at the state level, it should be remembered that states that wish to participate in CODIS, as all do, would still need to comply with the DNA Identification Act of 1994. 42 U.S.C. §§ 14131-34 (2000). In addition, it could be argued that an expansive interpretation of existing laws or a revision to allow identified DNA samples to be used to search for genes that might influence behavior would violate constitutional protections of liberty or privacy or the right to be free from unreasonable searches and seizures. Under existing doctrine, however, such claims are unlikely to succeed. See generally Edward J. Imwinkelreid, *Can We Rely on the Alleged Constitutional Right to Informational Privacy to Secure Genetic Privacy in the Courtroom?*, 31 SETON HALL L. REV. 926 (2001); D.H. Kaye, *The Constitutionality of DNA Sampling on Arrest*, 10 CORNELL J. L. & PUB. POL’Y 455 (2001).



## IV

THE SOCIAL “OUGHT”: SHOULD THE CRIMINAL  
DATABANKS BE AVAILABLE FOR BEHAVIORAL RESEARCH?

The millions of DNA samples collected for investigating crime involving biological trace evidence could prove useful in research into genes and behavior. Although the notion of “crime genes” is simplistic, offender DNA repositories might be of some value in confirming reports of loci influencing behaviors such as novelty seeking or impulsiveness or even in identifying previously unsuspected QTLs in polygenetic systems influencing behavior. Although it is hard to know the range of practical applications of such knowledge, a clearer picture of what leads to extreme behaviors could be of benefit both inside and outside of the criminal justice system.<sup>119</sup> If this assessment is accurate and the research cannot be summarily dismissed as worthless, it becomes important to consider the dangers that research with these samples might pose and the human rights that the research might infringe.<sup>120</sup>

## A. Popular Misunderstanding of Research Results

One danger of behavioral genetics research (and other areas of genetics research) is public misunderstanding. The first report of an association may receive considerable publicity even though later efforts at replication fail. Even if an association is real, it may be spurious (the result of a third variable) or not especially predictive of any behaviors. In short, “while behavioral genetic studies do not provide any justification for simplistic talk about ‘a gene for starting to smoke’ or ‘a gene for divorce,’ people sometimes talk like that anyway.”<sup>121</sup>

Now, public misunderstanding is not always a major evil. The Big Bang theory is routinely misunderstood,<sup>122</sup> but the universe goes on. Normally, the antidote to public misunderstanding of research is public discourse and a free flow of scientific information. On issues ranging from transcendental meditation to homeopathy to fluoridated water, scholars, publicists, and journalists promulgate pernicious or unvalidated theories, thinly or thickly garbed in the dress of science.<sup>123</sup> The research can be, and often is, initially

119. See, e.g., Kimmelman, *supra* note 67, at 696 (“One needn’t be a behavioral geneticist to appreciate the promise offered by offender DNA repositories for those interested in the genetics of violence, sexual deviance, or recidivism. . . . [M]any potential benefits of such research can be envisioned (e.g., determining suitable treatment regimens for particular prisoners) . . .”).

120. As I have argued elsewhere, “biometric research” designed to validate or improve the use of DNA analysis as a means of *post hoc* identification in the criminal justice system should be permissible without the consent of the individuals whose DNA has been obtained involuntarily but lawfully. See Kaye, *supra* note 56, at 215–16. Research that is unrelated to the use for which the samples were collected is more problematic.

121. BAKER, *supra* note 8, at 18.

122. See Charles H. Lineweaver & Tamara M. Davis, *Misconceptions about the Big Bang*, SCI. AM., Mar. 2005, at 36.

123. The most recent and surprisingly popular propaganda effort is the “documentary,” *What the Bleep Do We Know!?*, featuring a cast of scientists, actors, and mystics. *What the Bleep Do We*

misleading, but we tolerate it, trusting the “marketplace of ideas” to separate fact from fiction, science from pseudo-science.

However, this does not mean that government resources must support the research. If the public cannot be trusted to get it right, and if there are immediate and significant harms from getting it wrong, discouraging the research itself could be defended. The unfortunate fact is that there are harms that might flow from false beliefs in genetic behavioral determinism. These fall into three categories: discrimination based on an individual’s actual genotypes, discrimination based on an individual’s membership in a genetically related group, and misguided public policy choices.

### 1. Discrimination Against Individuals with Known Genotypes

The bearers of “bad” alleles may be unjustly stigmatized.<sup>124</sup> For example, when the effects of particular mutations are exaggerated, the individuals who are known to have them could be misjudged and disadvantaged in having access to education, employment, or health insurance.<sup>125</sup> Moreover, they could be shunned and treated as pariahs in personal relationships.

There are several responses to this possible stigmatization, short of policies to discourage the acquisition of knowledge.<sup>126</sup> A barrage of laws to foster “genetic privacy” or to prevent “genetic discrimination” in the workplace and in health insurance already have been enacted.<sup>127</sup> In addition, as knowledge of human genetics matures, a more realistic appraisal of the limitations of behavioral predictions may come to permeate the public consciousness. Even so, laws against any kind of discrimination can only reduce, and not eliminate, the objectionable conduct, and at the interpersonal level, genetic features can

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Know!?” (Lord of the Wind Films 2004). See also James Clark, *A Chemical Conspiracy?*, 434 NATURE 275 (2005) (reviewing CHRISTOPHER BRYSON, *THE FLOURIDE DECEPTION* (2004)) (“[T]o group all flourine chemicals together as ‘bad’ is wrong. The book is peppered with similar absurdities, which will be annoying to those who know their chemistry but dangerously misleading to those who don’t.”).

124. See, e.g., 1 NATIONAL BIOETHICS ADVISORY COMMISSION, *RESEARCH INVOLVING HUMAN BIOLOGICAL MATERIALS: ETHICAL ISSUES AND POLICY GUIDANCE* 44–46 (1999), available at <http://www.georgetown.edu/research/nrcbl/nbac/hbm.pdf>.

125. A classic example is the exclusion of carriers of the sickle-cell anemia from the Air Force Academy in the 1970s. See, e.g., TROY DUSTER, *BACKDOOR TO EUGENICS* 24–27 (1990); DANIEL J. KEVLES, *IN THE NAME OF EUGENICS* 277–79 (1995).

126. In this context, “discourage” may be too strong a term. The issue is whether to facilitate research by making a public resource (a DNA repository) available.

127. See, e.g., Lawrence O. Gostin & James G. Hodge, Jr., *Genetic Privacy and the Law: An End to Genetics Exceptionalism*, 40 JURIMETRICS J. 21, 46–47 (1999). Indeed, “in one year in the late ‘90s, more bills were introduced into the nation’s state legislatures about the regulation of genetic information than any other single topic.” *Life Sciences, Technology, and the Law Symposium Transcript*, 10 MICH. TELECOMM. & TECH. L. REV. 175, 180 (2003) (address by Philip Reilly). Of course, the practical value of the laws is open to question, but so is the extent of genetic discrimination. See NATIONAL BIOETHICS ADVISORY COMMISSION, *supra* note 124, at 5 (“[T]o date there is little empirical evidence documenting extensive employment or insurance discrimination based on genetic status.”); Philip R. Reilly, *Genetic Discrimination*, in *GENETIC TESTING AND THE USE OF INFORMATION* 106, 106–07 (Clarisa Long ed., 1999). But see Karen H. Rothenberg & Sharon F. Terry, *Before It’s Too Late—Addressing Fear of Genetic Information*, 297 SCIENCE 196, 197 (2002) (explaining how there could be “widespread cases of genetic discrimination” even though they have not been observed).

join with cultural ones in defining social hierarchies that privilege some groups at the expense of others.

## 2. Attitudes Toward Racial and Ethnic Groups

A second mode of stigmatization might arise if people were led to believe that undesirable alleles are more prevalent in some racial, ethnic, or socio-economic groups.<sup>128</sup> Because linking behavioral traits and capacities with race-related genes has a particularly ugly history, research that could rekindle such racial stereotyping deserves special scrutiny. “For a variety of complex factors, the population of those arrested and convicted is disproportionately male, minority, and poor.”<sup>129</sup> Hence,

The possibility exists that a researcher conducting genome scans on samples collected for a criminal database might find an allele that occurs more than randomly and claim (or be misreported in the media as claiming) to have found a “gene for” criminal behavior. What the researcher might actually have found is an allele that is more common among, say, poor whites from the Bayou who couldn’t afford good lawyers, Mexicans caught up by immigration violations, or African Americans who faced racist juries. Such a claim could lead to discriminatory actions against others of the same demographic group who share the allele.<sup>130</sup>

There seem to be two somewhat poorly knitted threads to this argument. The first concerns the statistical problem of confounding variables—of thinking that one variable causes a result when a third variable (correlated with the first) is the true cause. The threat of confounding, as previously noted, is a pervasive issue in observational studies.<sup>131</sup> Suppose that there is an allele *S* that is more common in African Americans than in Caucasians.<sup>132</sup> Because African Americans comprise a greater proportion of the convicted-offender database

128. See, e.g., Lori B. Andrews, *Harnessing the Benefits of Biobanks*, 33 J. L. MED. & ETHICS 22, 24 (2005) (“If research on samples in a biobank shows that a particular ethnic group has a higher incidence of a certain illness or a genetic predisposition to a disfavored behavior, individuals from that ethnic group may face stigmatization and discrimination.”); Wilker, *supra* note 5, at 147 (“[Research with] biological samples collected and stored in forensic contexts in experiments designed to identify genes associated with criminal behavior . . . could be used a new biological justification to bolster racist and ethnic prejudice.”).

129. BAKER, *supra* note 8, at 89.

130. *Id.* The AAAS Report provides another variation on this theme:

Another consequence of genetic research that relies on arrest or conviction as synonyms for the criminal phenotype is that it will disproportionately focus on those who have committed “blue collar” crimes (assaults, property theft, petty drug offenses, etc.) compared to subjects who have committed “white collar” crimes (tax evasion, information theft, large-scale drug dealing, etc.). This is because those committing the latter type of crime are caught less often. Such research would inevitably reinforce the stereotype that the working class is more deviant than the professional class.

*Id.* at 89–90.

131. See *supra* text accompanying notes 40–42.

132. For example, *S* could be the sickle cell allele, which “has an allele frequency of 0.10–0.20 in Africans, compared with less than .001 in U.S. Whites . . .” Daniel C. Rowe, *Under the Skin: On the Impartial Treatment of Genetic and Environmental Hypotheses of Racial Differences*, 60 AM. PSYCHOL. 60, 61 (2005).

than of the general population,<sup>133</sup> the relative frequency of *S* will be larger in the convicted-offender database than in the overall population—even though it does not change the probability that an individual will engage in criminal conduct. This kind of confounding, however, is easily detected. To avoid mistaking *S* for an allele that influences behavior, one can compare the DNA samples from convicted African Americans with samples collected from African American controls in the general population.<sup>134</sup> Since the presence or absence of *S* is uncorrelated with the existence of a criminal conviction of an African American, there will be no significant difference.<sup>135</sup> In short, confounding due to racial or ethnic differences may not be an intractable problem.

But even research reports—and media reports about the research—that avoid confusing correlation with causation are not free from the risk of prompting discrimination on the basis of a group's genotype. Suppose, for the sake of argument, that certain alleles do affect behavior in a manner that makes it more likely that someone will be convicted of a crime *and* that these alleles are much more prevalent in African Americans (or some other group) than in Caucasians. The discovery of both these hypothetical facts could promote the belief that African Americans are “racially inferior” and prone to crime. In this situation, there is a genetic difference between two groups, and it is used stereotypically to disparage an entire group.<sup>136</sup>

But it may be unrealistic to posit the discovery of alleles that are both strongly related to crime and substantially more prevalent in one race than another.<sup>137</sup> And even if such a phenomenon were to be discovered, the social consequences are unclear. Women are biologically and genetically different from men in many ways—including some clear differences in the functioning and maturation of parts of the brain—but this knowledge does not seem likely to lead to a new wave of discrimination against women or to retard efforts to

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133. In 2002, there were 586,700 blacks out of 1,291,326 (45%) sentenced state and federal prisoners. PAIGE M. HARRISON & ALLEN J. BECK, BUREAU OF JUSTICE STATISTICS, PRISONERS IN 2002 9, Tbl.13 (2003). The 2000 census calculated a total population of 281.4 million, of which 34.7 million people, or 12%, reported only Black, while “an additional 1.8 million people reported Black and at least one other race”). JESSE MCKINNON, U.S. CENSUS BUREAU, THE BLACK POPULATION: 2002 (2001).

134. This type of statistical control is the norm in association studies in genetic epidemiology. See Stephen P. Daiger, *Was the Human Genome Project Worth the Effort?*, 308 SCIENCE 362, 362–63 (2005) (“[C]ase-control association studies look for differences in the frequencies of common genetic variants between *ethnically matched* cases and controls to find variants that are strongly associated with the disease.”) (emphasis added).

135. Cf. PLOMIN ET AL., *supra* note 11, at 214 (noting that researchers verified an association of the length of D4DR alleles with novelty-seeking *within families* to control for ethnic differences).

136. This is rather different than the concern expressed in the AAAS report over “discriminatory actions against others of the same demographic group *who share the allele*.” BAKER, *supra* note 8, at 89. The group-discrimination problem arises when members of the demographic group *who do not share the allele* are treated as if they do by virtue of their membership in the group.

137. Cf. Morley & Hall, *supra* note 50, at 5 (“The polygenic nature of antisocial behaviour also means that even if a susceptibility allele is found at a high frequency in a particular ethnic group, it is likely that a different susceptibility allele will be found at a similarly high frequency in another ethnic group.”). Of course, if such discoveries come, they will not emerge simultaneously.

achieve gender equality.<sup>138</sup> The vector sum of the social forces that encourage racism and sexism and those that moderate these attitudes may not be significantly affected by finding that a few alleles are more common in some groups than others—at least not when the alleles are found in all racial groups and when they do not ineluctably determine anyone’s behavior.

### 3. Misguided Public Policies

A third harm that has been attributed to behavioral genetics research relates to the impact of knowledge on governmental action. Thus, it has been said that

like the old eugenic studies and the new MAOA studies, genetic studies tend to misdirect attention from the overwhelming social causes of the behaviors they purport to explain by encouraging a determinism that suggests that efforts at social reform are ultimately futile. Where this misdirection reinforces existing social policy inequities, it is likely to have an even more pronounced effect.<sup>139</sup>

Not only is it said that social progress might be forestalled, but the identification of genes that affect behavior could be seen as “legitimizing draconian ‘medical’ responses to the targeted behavior, like eugenic sterilization.”<sup>140</sup> In fact, one eminent historian of biology predicts that “to proceed under [the] assumption” that human behavioral genetics research could generate useful knowledge “will certainly lead to a legal and ethical quagmire equivalent to that encountered by the eugenics movement of 1910–1940 and its push towards massive sterilization, and eventually, euthanasia, of the so-called unfit.”<sup>141</sup>

To the extent that these are warnings that the dissemination of new research results will promote repressive laws or thwart enlightened policies of reform, they pose a fundamental question about democratic self-government. Is it right for the state to withhold resources that might advance knowledge not because the information causes direct and immediate harm to individuals, but because it might lead the electorate or its representatives to follow misconceived or misguided policies? The proposition that government should not advance knowledge because the electorate or the elected representatives might misuse that knowledge in the political process is surely problematic.

Even assuming that the government can be justified in failing to support the acquisition of information it believes would promote the “wrong” laws, the question arises of how high the probability of this democratically endorsed “harm” must be for the knowledge to be officially discouraged. In this instance, the theory apparently is that if researchers refer to specific alleles as weakly associated with criminal conduct, then the public and the politicians will

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138. See, e.g., Natalie Angier & Kenneth Chang, *Gray Matter and the Sexes: Still A Gray Area Scientifically*, N.Y. TIMES, Jan. 24, 2005, at A1. Indeed, understanding these differences could lead to strategies better calculated to enhance the development of, say, mathematical ability in women. See Amanda Ripley, *Who Says a Woman Can't Be Einstein?*, TIME, Mar. 7, 2005, at 50.

139. Juengst, *supra* note 10, at 70.

140. *Id.*

141. Allen, *supra* note 22, at 294–95.

abandon or forego efforts to rehabilitate offenders or to reduce crime by improving the economic and social conditions that breed crime.

These possibilities cannot be excluded. Yet it seems equally possible that the people who believe that rehabilitation is impossible will adhere to this pessimism regardless of news about genetics, while those who are inclined to hope for reformation and redemption will continue to regard individual behavior as a malleable function of both genetic endowment and life history.<sup>142</sup> It is far from obvious that criminals as a group will come to be more stigmatized than they already are by the identification of individual genes having indirect and small influences on criminality. Similarly, the further diminution of social welfare programs is all too possible, but the role of genetic findings due to access to offender databases in this political process is likely to be marginal at best. As for the more dire predictions of a resurrection of eugenics laws, contemporary legal and public attitudes toward compulsory sterilization are quite different than they were in the days of *Buck v. Bell*,<sup>143</sup> and it is hard to conceive of discoveries about QTLs that would lead legislatures to enact<sup>144</sup>—and courts to sustain<sup>145</sup>—laws resembling the one upheld in *Buck*.

In many ways the objections to research into crime and genetics track the arguments made against research into intelligence and race. For example, when Arthur Jensen, a psychologist at the University of California at Berkeley, published a paper in 1969 asserting that it was “not an unreasonable hypothesis

142. Indeed, well designed studies of behavior can help reveal the effect of environmental variables, suggesting possible interventions rather than the abandonment of hope. Thus, it has been suggested that “genetic research is more likely to refine social policies by better specification of environmental risk factors than to divert funds from environmental crime prevention strategies.” Morley & Hall, *supra* note 50, at 5.

143. 274 U.S. 200, 206 (1927) (upholding a state law allowing compulsory sterilization of certain individuals on the ground that “experience has shown that heredity plays an important part in the transmission of insanity, imbecility, &c [sic].”).

144. See Daniel J. Kevles & Leroy Hood, *Reflections*, in THE CODE OF CODES 300, 318, *supra* note 26:

Eugenics profits from authoritarianism—indeed, almost requires it. The institutions of political democracy may not have been robust enough to resist altogether the violations of civil liberties characteristic of the early eugenics movement, but they did contest them effectively in many places. The British government refused to pass eugenic sterilization laws. So did many American states, and where eugenic laws were enacted, they were often unenforced. It is far-fetched to expect a Nazi-like eugenic program to develop in the contemporary United States so long as political democracy and the Bill of Rights continue in force. If a Nazi-like eugenic program becomes a threatening reality, the country will have a good deal more to be worried about politically than just eugenics.

145. See *Skinner v. Oklahoma*, 316 U.S. 535, 536 (1942) (striking down a sterilization law for certain criminals on Equal Protection grounds and describing “the right to have offspring” as “basic”); *id.* at 546 (Jackson, J., concurring) (“There are limits to the extent to which a legislatively represented majority may conduct biological experiments at the expense of the dignity and personality and natural powers of a minority—even those who have been guilty of what the majority define as crimes.”); JANET L. DOLGIN & LOIS L. SHEPERD, *BIOETHICS AND THE LAW* 359 (2005) (“The *Skinner* Court did not overrule *Buck v. Bell*. However, the Court’s categorization of procreation as a fundamental right and its later application of the most stringent review to statutes that interfered with that right left little room for future courts to invoke Justice Holmes’ 1927 decision in *Buck v. Bell* as precedent for the state’s right to compulsorily sterilize members of social groups deemed marginal by the state.”).

that genetic factors are strongly implicated in the average Negro-white intelligence difference,”<sup>146</sup> and suggesting that efforts to enhance educational opportunities could not remove the racial divide in occupational achievement, the immediate result was “a national furor”:<sup>147</sup>

Many of Jensen’s academic colleagues attacked his thesis on methodological grounds, but others criticized the nature of the inquiry itself. . . . The Society for the Psychological Study of Social Issues, an organization of social and behavioral scientists, expressed concern that hereditarian statements could be seriously misinterpreted, and used to justify repressive social policies. Elizabeth Alfert, a colleague of Jensen at Berkeley, wrote that many persons read and quoted Jensen’s work but failed to notice the many qualifiers it contained. Bernard Diamond, professor of law and psychiatry at Berkeley, found that race-IQ studies risked “social denigration” of the groups singled out and urged that researchers be required to obtain the consent of parents who might not wish their children to participate in studies aimed at discovering ethnic differences.<sup>148</sup>

These themes—the public will be misled, social progress will be retarded, and groups will be stigmatized by the research<sup>149</sup>—are precisely those that are sounded once again.<sup>150</sup> And they should be, for they are important and valid concerns. Yet they sound suspiciously like calls for content-based suppression of inquiry. Is it better to avoid “inopportune” knowledge altogether or to subject it to scientific scrutiny and public debate?<sup>151</sup> American society has taken the latter approach in response to the theories and studies of Jensen and others.<sup>152</sup> It is the bumpier road, but the historical record does not demonstrate that these publications have had a lasting, or even a measurable impact on public policy. The same appears to be true of reports of a link between XYY trisomy and criminality.<sup>153</sup> Although the social response to the early reports

146. Arthur Jensen, *How Much Can We Boost IQ and Scholastic Achievement?*, 39 HARV. EDUC. REV. 1, 82 (1969).

147. Richard Delgado et al., *Can Science Be Inopportune? Constitutional Validity of Governmental Restrictions on Race-IQ Research*, 31 UCLA L. REV. 128, 137 (1983).

148. *Id.* at 140.

149. One geneticist editorialized: “It perhaps is impossible to exaggerate the importance of the Jensen disgrace, for which we must all now share responsibility. It has permeated both science and the universities, and hoodwinked large segments of government and society. Like Vietnam and Watergate, it is a contemporary symptom of serious affliction.” Jerry Hirsch, *Jensenism: The Bankruptcy of “Science” Without Scholarship*, 25 EDUC. THEORY 3, 3–4 (1975).

150. Indeed, sometimes the old social science and IQ data are simply repackaged as if they were modern “genetic research.” See ANDREWS, *supra* note 117, at 94 (describing the *The Bell Curve* as a contemporary case of “genetic research . . . being used to ‘demonstrate’ the genetic inferiority of people of color”).

151. *Cf.* Delgado et al., *supra* note 147, at 153–225 (discussing First Amendment limitations on government responses to research that might show, or purport to show, racial inferiority).

152. Officially, there may be no constraints on research, but it can be severely inhibited by unofficial funding policies and sanctions for research on certain topics. See, e.g., Lila Guterman, *Scientists Censor What They Study to Avoid Controversy and ‘Lunatic-Proof’ Their Lives, Researchers Find*, CHRON. HIGHER EDUC., Feb. 11, 2005, available at <http://chronicle.com/daily/2005/02/2005021104n.htm>.

153. See Patricia A. Jacobs et al., *Aggressive Behaviour, Mental Sub-normality and the XYY Male*, 208 NATURE 1351, 1352 (1965) (“[T]he finding that 3.5 percent of the population [of institutionalized men] were XYY males must represent a marked increase in frequency by comparison with the frequency of such males at birth.”); Herman A. Witkin et al., *Criminality in XYY and XXY Men*, 193

often is cited as a modern example of genetic discrimination,<sup>154</sup> the scientific criticism of the reports (or, rather, the more sensational interpretations of them) was extensive,<sup>155</sup> no repressive legislation emerged, no American courts accepted the condition as a defense to criminal conduct,<sup>156</sup> and no instances of actual discrimination have been documented.<sup>157</sup> “Learning from history is indispensable,” but “[g]enetics today is not the same as eugenics and racial hygiene in the 1930s,”<sup>158</sup> and superficially respectable arguments for eugenics or sterilization laws are no longer at hand.<sup>159</sup>

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SCIENCE 547, 553–54 (1976) (reporting that XYY males showed evidence of a higher rate of criminality although they displayed no disproportionate tendency toward violence).

154. *E.g.*, Paul A. Lombardo, *Genetic Confidentiality: What's the Big Secret?*, 3 U. CHI. L. SCH. ROUNDTABLE 589, 596 (1996) (claiming that “[t]he more recent history of genetic discrimination is exemplified by the XYY controversy screening programs to deter criminality were proposed” but pointing to no instances of discriminatory acts against men with this karyotype).

155. *See, e.g.*, Digamber S. Borgaonkar & Saleem A. Shah, *The XYY Chromosome Male—Or Syndrome?*, in PROGRESS IN MEDICAL GENETICS 135, 202 (Arthur G. Steinburgh & Alexander G. Bearn eds., 1974) (“Because of the relatively small numbers, the absence of matched controls and of blind assessment procedures, and the inconsistent findings, there are relatively few psychologic, psychiatric, and behavioral characteristics which clearly and consistently distinguish the XYY males from comparable controls. . . . the few which do appear tend to refute the notion that XYY males are predisposed toward aggressive and violent behavior.”); Greogy Carey, *Genetics and Violence*, in 2 NATIONAL RESEARCH COUNCIL, UNDERSTANDING AND PREVENTING VIOLENCE: BIOBEHAVIORAL INFLUENCES 21, 26 (Albert J. Reiss, Jr. et al. eds., 1994) (“[P]rospective [studies] dispel the myth of the XYY as a ‘hyperaggressive, supermasculine sociopath’ and, in its place, portray a group of individuals within the normal range but with an array of relatively nonspecific behavioral differences in attention and cognition, motoric skills, and personality.”); NUFFIELD COUNCIL, *supra* note 13, at 160 (“[A 1976 study concluded] XYY males were more likely to be imprisoned, but that this was due to their low intelligence and low socioeconomic status[,] which placed them at higher risk of being caught.”).

156. *See* Deborah W. Denno, Comment, *Human Biology and Criminal Responsibility: Free Will or Free Ride?*, 137 U. PA. L. REV. 615, 620–21 (1988).

157. There are suggestions that some individuals have aborted XYY fetuses, but the basis for these statements is not apparent. *E.g.*, Virginia Morell, *Evidence Found for a Possible ‘Aggression Gene’*, 260 SCIENCE 1722, 1723 (1993) (“[Jonathan Beckwith cautioned]; It would be a disaster if people suddenly decided to begin screening babies for monoamine oxidase deficiencies – as some did for the XYY defect.”). It also has been claimed that “genetic test results” for the XYY karyotype conducted on “6,000 young men . . . were routinely passed to courts to use however they chose.” ANDREWS, *supra* note 117, at 94. The basis for this claim is a story in the now defunct news magazine, *Emerge*. Harriet A. Washington, *Human Guinea Pigs*, EMERGE, Oct. 1994, at 24. However, the *Emerge* article merely states that “[a]ccording to the *Washington Daily News* [another defunct publication], the children’s confidentiality was not protected and the blood tests results were passed to the courts to use as they saw fit.” *Id.* Years ago, the principal investigator of the NIMH study noted that the stories published in the *Washington Daily News* amounted to “inaccurate publicity” with “erroneous accusations.” Digamber S. Borgaonkar, *Cytogenetic Screening of Community-Dwelling Males*, in GENETIC ISSUES IN PUBLIC HEALTH AND MEDICINE 215, 218 (Bernice H. Cohen et al. eds., 1978). The consent form promised that “the results will be used only by our medical researchers for scientific study and will not be disclosed to any other person or agency.” *Id.* at 230. The researchers realized that it would not then have been possible to maintain this confidentiality in the face of a court subpoena, but they reported that, fortunately, no court ever requested the information, and the “results have been disclosed only to parents” of the juveniles. *Id.* at 227. In sum, the claim that XYY findings were routinely passed to courts appears to be another urban myth.

158. Manfred D. Laubichler, *Frankenstein in the Land of Dichter and Denker*, 286 SCIENCE 1859, 1860 (1999).

159. *See* Kevles & Hood, *supra* note 144, at 318 (“Awareness of the barbarities and cruelties of state-sponsored eugenics in the past has tended to set most geneticists and the public at large against such programs. Geneticists today know better than their early-twentieth-century predecessors that ideas concerning what is ‘good for the gene pool’ are highly problematic.”).



This is not to say that the worst could never happen. Human beings have a remarkable capacity for self-deception and credulity. If eternal vigilance is the price of liberty, it also is the price of avoiding the mistakes of the past. In the end, how much harm actually would flow from discoveries about genes, environment, and crime as a result of discoveries aided by the criminal-offender DNA repositories is an open question.

#### B. The “Right to Informed Consent”

Harms to individuals are not the only line of argument against permitting behavioral genetics research with law enforcement DNA repositories. A second line of argument involves an asserted “right to informed consent,” which builds on the assumption that individuals should choose how their samples are used. Invocations of some version of this right pepper the literature on the research uses of the databases and databanks. But it is not enough to assert, in the broadest possible terms, that “[t]he right to consent or refuse to take part in research is an important right for individuals and for society.”<sup>160</sup> A demonstration that a particular use of the tissue samples violates an “important right” requires explicating the boundaries of this right, and that task cannot be accomplished without a theory of the reasons for insisting on informed consent in medical research.

In this regard, there is no plausible moral right “to informed consent” as a prerequisite for any and all scientific research into human behavior, physiology, or anatomy. Rather, consent serves to waive other individual rights that stand between the subject and the research. These include the rights to be free from intentional bodily harm, from offensive touching or intrusion, from unnecessary confinement and physical restraint, and from serious and reasonable emotional distress. Thus, physicians are not at liberty to perform experimental (or even clinically accepted) surgery on their patients even when the surgery is the only hope for the patient.<sup>161</sup> Social psychologists cannot freely conduct experiments that might produce psychological harm or stress (although they may deceive subjects about some aspects of the study when this deception is essential and the risk of harm from the deception is *de minimis*).<sup>162</sup>

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160. STALEY, *supra* note 9, at 8; *see also id.* at 46 (“Seeking informed consent protects the freedoms, rights and dignity of the people who take part. . . . Consent should have to be obtained from the individuals on the database before genetic research is allowed to go ahead.”).

161. *See, e.g.,* Chambers v. Nottebaum, 96 So. 2d 716, 718 (Fla. Dist. Ct. App. 1957) (“The rule is well established which prevents a doctor from operating on a patient without his express or implied consent.”); Schloendorff v. Soc’y of New York Hosp., 105 N.E. 92, 93 (N.Y. 1914) (“Every human being of adult years and sound mind has a right to determine what shall be done with his own body; and a surgeon who performs an operation without his patient’s consent commits an assault, for which he is liable in damages.”). On the ethical constraints on human experimentation, *see, for example,* INSTITUTE OF MEDICINE, NATIONAL RESEARCH COUNCIL, RESPONSIBLE RESEARCH: A SYSTEMS APPROACH TO PROTECTING RESEARCH PARTICIPANTS (2002), *available at* <http://www.iom.edu/Object.File/Master/4/157/0.pdf>.

162. *E.g.,* PANEL ON INSTITUTIONAL REVIEW BOARDS, SURVEYS, AND SOCIAL SCIENCE RESEARCH, NATIONAL RESEARCH COUNCIL, PROTECTING PARTICIPANTS AND FACILITATING SOCIAL AND BEHAVIORAL SCIENCES RESEARCH 25 (Constance F. Citro et al. eds. 2003), *available at*

A counterargument to the thesis that research that infringes no independent, protected interests is morally permissible without prior consent builds on the Kantian perspective that a research subject is an autonomous agent who must not be used as a means to the researcher's ends, no matter how beneficent those ends may be. But this pronouncement is too glib. It knows no bounds and does not accord with historical and contemporary practices. Consider the following case: Traffic engineers want to study the effect of altering the timing of stoplights at the entrance ramps to certain freeways. Would this study infringe the freeway drivers' dignitary interest unless they first gave their informed consent to be observed?

A dedicated adherent to the no-research-without-consent rule might concede the validity of the counterexample but seek to rescue the broad rule by admitting the narrowest of exceptions. This reformulated thesis would hold that informed consent is required for all research except in those cases in which the research consists of observations of public behavior visible to any bystander.

Even with this amendment, however, the modified principle is too broad. Consider a data set consisting of records of blood or breath alcohol concentrations taken from drivers suspected of driving while intoxicated. Most of these data, let us assume, have not been obtained with the voluntary consent of the drivers (especially if they were, in fact, intoxicated at the time), but rather under threat of having one's driving license suspended as provided for in the jurisdiction's "implied consent law." Would it be unethical for the sheriff's office to make these records available to a researcher to analyze the distribution of alcohol levels in the sample?

Such counterexamples<sup>163</sup> suggest that no absolute requirement of obtaining consent can pertain to all "research" seeking information on human subjects.<sup>164</sup> Rather, the proposed research must entail some invasion of the subject's interests that would create a duty on the part of the researcher to the subject. That duty, moreover, does not arise simply because the words "medical" or "controversial" are placed in front of "research"<sup>165</sup> or because the Nuremberg

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<http://www.nap.edu/books/0309088526/html/>. Historians and other scholars have chafed at the rigid application of human subjects protections to their work. See, e.g., Jeffrey Brainard, *The Wrong Rules for Social Science?*, CHRON. HIGHER EDUC., Mar. 9, 2001, at A21.

163. See also 45 C.F.R. § 46.116(c) (2004) (allowing federally funded or conducted researchers evaluating public benefit or service programs to dispense with informed consent); Kaye, *supra* note 56.

164. Cf. 45 C.F.R. § 46.101(I) (2004) (permitting waiver for unspecified reasons of the consent requirement in federally funded or federally conducted research on human subjects); 45 C.F.R. § 46.116(d) (2004) (permitting waiver of the consent requirement in cases of "minimal risk").

165. For examples of this phrasing, see STALEY, *supra* note 9, at 37 ("Using the [U.K.'s national DNA database] for research would violate the right of research participants to opt out of potentially controversial studies."); Kimmelman, *supra* note 67, at 696 ("Although many potential benefits of such research can be envisioned (for example, determining suitable treatment regimens for particular prisoners), transferring databanked DNA for research protocols would violate the right of research subjects to opt out of participating in potentially controversial medical research . . .").

Dr. Kimmelman also noted that research use of convicted-offender samples "would also run counter to the guidelines on handling genetic materials proposed by several commentators . . ." Kimmelman, *supra* note 67, at 696. However, even if the tissue-banking guidelines of other

Code is invoked.<sup>166</sup> Inasmuch as the theory that “research can risk harming the individuals who are being studied”<sup>167</sup> supports the general rule that people should not be forced to participate in research unless they have given their informed consent, one must then ask whether the research threatens to cause personal harms before one can conclude that the general rule should apply.<sup>168</sup>

Research with tissue samples certainly could fall into this category. Concrete harms, already noted, might flow from the revelation to potential employers or insurers of certain genotypes. In addition, an individual has an autonomy interest in not knowing that he has particular alleles. For example, individuals should not be forced to undergo genetic testing to discover whether they carry the allele for Huntington’s disease. Some individuals with a family history that puts them at risk may prefer a life with ambiguity to one in which they know that they are destined for an early death. This personal choice as to how to live one’s life should be respected.<sup>169</sup>

Beyond the potentially harmful or autonomy-threatening consequences of possible “data leakage” lies a distinct and, as yet, ill-defined and inchoate concept of “genetic privacy”—a widely shared feeling that one’s genome should not be on display to any and all interested parties, that this information is part of one’s private sphere, and that this realm is wrongly invaded even if no one

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commentators are generally desirable, it is not obvious how they should be applied to law-enforcement databases and databanks. Unlike many tissue repositories of samples created in the context of a trust relationship between medical providers and patients, the law-enforcement repositories are not part of a consent-based regime. See Kaye, *supra* note 56.

166. For an instance of this polemic, see *supra* Part III.B (citing statements of Paul Billings, Lori Andrews, and others). The applicability of the Nuremberg Code to research on archival tissue samples is discussed in Kaye, *supra* note 56.

167. Ellen Wright Clayton et al., *Informed Consent for Genetic Research on Stored Tissue Samples*, 274 JAMA 1786, 1786 (1995) (explaining the position of several participants who advocated demanding more rigorous standards for consent in a 1994 workshop “to develop recommendations for securing appropriate informed consent when collecting tissue samples for possible use in genetic research and for defining indications for additional consent if samples in hand are to be used for genetic studies”).

168. The “rule” I am speaking of is one of morality, not law. It might be argued that behavioral genetics research with DNA samples, particularly those from prisoners, would violate the “Common Rule” that applies to federally funded or federally conducted research. See 45 C.F.R. pt. 46 (2004). For present purposes, let us assume that these administrative regulations, as they are interpreted by the Department of Health and Human Services’ Office for Human Research Protections, would not allow the research with the law enforcement samples to be funded or conducted. *But see* Henry T. Greely, *Breaking the Stalemate: A Prospective Regulatory Framework for Unforeseen Research Uses of Human Tissue Samples and Health Information*, 34 WAKE FOREST L. REV. 737 (1999) (discussing the generous interpretation of the Common Rule recommended by the National Bioethics Advisory Commission); Daniel S. Strouse, *Informed Consent to Research on Banked Human Tissue*, 45 JURIMETRICS J. 135, 150–52 (2005) (discussing ambiguities in the Common Rule and mechanisms for dispensing with informed consent). Although these regulations are intended to reflect the ethical norms of the research community, when one is asking what is morally justified, it is not enough that government regulations come out one way or the other. The rules are at most indicative of a descriptive morality, of the practices considered ethical in the research community. They are not a final answer in a critical morality, which asks whether these practices are justified.

169. Of course, it could be argued that if precautions are taken to render the possibility of data leakage (both to the research subject and to third parties) extremely remote, then the hypothetical possibility of these harms is not enough to trigger a duty to obtain consent. Federal regulations for the protection of research subjects have never imposed a blanket requirement of obtaining informed consent in this situation.

learns of the invasion. It is one thing to photograph a neighbor as she is walking in the corridor on the way to her high-rise apartment. It is another to photograph her naked body in her bedroom from the building across the way. Regardless of the woman's awareness of his conduct, the "peeping Tom" might have a duty not to look.

This analogy, however, is inapposite. The source of the duty not to peep does not arise because of the sensitivity of the "information." It is part of a comprehensive set of protections to assure people that, for a time, they can be alone and unobserved. Exactly where the protective line should be drawn is open to debate—perhaps the burden should be on the apartment-dweller to draw the blinds—but if there is a justification for according similarly stringent privacy protections to DNA samples, it rests on some other personal interest that has yet to be articulated. At this point, therefore, the rubric of "genetic privacy" seems inadequate as a specification of a personal interest that would give rise to a duty to seek consent.

Even assuming that individuals have a right to preclude others from studying their DNA because they might be harmed by data leakage, the resulting requirement to obtain informed consent before examining the samples could still be avoided—by anonymizing the samples. If the researchers have no realistic chance of discovering which sample goes with which offender, there is no real possibility of harmful data leakage.<sup>170</sup>

Even with anonymized samples, however, a further objection to the research might be raised. An individual might worry that the results of the study will stigmatize a group of which he is a member. Native Americans, for instance, may wish to block a genetic study for alcoholism on a reservation for fear that it

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170. Of course, with some research designs, it will be possible to infer the identities of the participants in the study. See National Commission on the Future of DNA Evidence, Proceedings, Privacy Considerations and Database Sample Retention Discussion (July 26, 1999) (statement of Philip Reilly), <http://www.ojp.usdoj.gov/nij/topics/forensics/events/dnamt/trans6/trans-h.html>:

[Y]ou cannot tell me that the statutes include currently an absolute guarantee of a pure anonymous and anonymity function in the research. . . . [B]ecause they will be a very limited sample of people, and a very limited sample of questions, . . . it will be possible to reconstruct . . . in a small cohort who were the subjects of the research . . . . Let's imagine that in the State of Massachusetts, I want to do research on 400 convicted pedophiles, and I want to ask whether an allele has a certain frequency that has a relative risk much higher in that group than the general population; and I find out that that is, in fact, true. . . . [I]t would be possible . . . to find out who was [in] the set of convicted pedophiles during those years.

However, knowing that an individual's DNA was included in a study does not imply that the individual has the allele for which the "relative risk [of pedophilia is] much higher." As in the general population, most of the study population will not have that allele. The knowledge about the individual Dr. Reilly described is no different than the knowledge that an individual is a member of a group that has an elevated risk factor. This fact is not a breach of anonymity, but it might be the basis for an argument that group harm warrants requiring informed consent. This line of argument is considered below.

Another puzzling argument is that because DNA is unique to individuals (and monozygotic twins), "samples cannot ever be truly anonymized." Andrews, *supra* note 128, at 24; cf. Juengst, *supra* note 10, at 68–69 (suggesting that anonymization of DNA samples is not "technically possible"). These ethicists do not explain how the researchers will obtain access to the data in CODIS (or elsewhere) that would permit the names of individuals to be linked to the DNA samples. If personal identification is not feasible, then the "technical" possibility is of no practical concern.

will reinforce the image of the “drunken Indian.” Genetic research on “Jewish diseases” like Tay-Sachs raises similar concern in Jewish communities. Do these concerns create a duty for the researcher to obtain consent from the “donors”? The donors are not the community, although they are a part of it. If the duty runs to the community, who speaks for that group, and why are their views about whether the risk of harm is justified privileged over those of everyone else?

As these questions reveal, the group harm argument fits awkwardly into the doctrine of informed consent. The harms that are supposed to trigger a duty on the part of the researcher extend to all members of the group who might be harmed, not just to the individuals whose DNA samples are on file. Their interest lies in not being misjudged by other people who do not appreciate the limitations or implications of the research. The view that researchers owe a duty to acquire the consent of everyone who might be affected by new knowledge is a recipe for frustrating all research about human beings.

A more plausible view is that if this possible change in status is the only harm to individuals—particularly to individuals who are not contributing to the research by any voluntary action—no obligation to obtain their permission arises. No man, to be trite, is an island. We are all members of intersecting, overlapping, and interacting groups. All research on humans can affect one or more of these groups.

This connectedness is not a reason to ignore the possibility of harm in deciding whether the research is, on balance, justified. In appropriate cases, “community consultation” may be valuable in designing or implementing the research as well as in deciding whether the possible benefits justify the research itself. But the possibility of group harm does not give the group veto power over the research. In other words, it does not create a right to informed consent that resides in the group as a whole. Instead, it simply constitutes a harm-based argument based on false beliefs in genetic determinism.<sup>171</sup> Depending on the circumstances, this argument may be compelling or it may be flimsy, but it is not sufficient warrant for the claim that it is the group that has the right to decide whether the research can proceed.

Consider, for example, a geographically defined community. Researchers doing contract research for the local police enter the area and go to barber shops in different neighborhoods to gather hair off the floor for drug testing. This testing reveals that some locales are drug-infested, while others are not. Did the researchers have an obligation to obtain the informed consent of the residents of each neighborhood before collecting the convenient samples of hairs?

The situation differs from the usual medical research context, in which the system seeks to foster trust between researchers and patients or subjects and in which legitimate acquisition of biological samples in the first instance depends

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171. *See supra* Part A.

on informed consent. It is closer to the convicted offender biobanks that house samples legitimately acquired without consent. As to these tissue repositories, the justification for demanding informed consent from the involuntary “donors” must be that the potential harms to these individuals are sufficiently palpable to require the “donors” to make the decision as to whether this research should proceed with their samples. The immediacy, probability, and severity of the harms, like the possible harms to individuals or racial or ethnic groups with known genotypes,<sup>172</sup> are far from clear.<sup>173</sup>

### C. Sample Retention and Research

Recognizing that repositories of individually labeled DNA samples create at least a theoretical possibility that personally sensitive information will be extracted, many commentators have questioned the need to retain the samples in the first place.<sup>174</sup> The National Commission on the Future of DNA Evidence debated this issue without success. Unable to reach a consensus, it recommended that another commission address the issue within five years.<sup>175</sup> In arguing before the commission, the FBI adduced four reasons for sample retention. First, it indicated that “[o]nly one state requires the destruction of samples after analysis.”<sup>176</sup> That a parochial practice<sup>177</sup> (or even a universal one) exists, however, is not a reason to perpetuate it.

Second, the FBI pointed to the “tremendous difficulty in regenerating or retyping databases after the samples have been destroyed.”<sup>178</sup> Throwing the samples away could lock the system into the thirteen STR loci now in place, which might be unfortunate if a superior typing technology were to emerge.

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172. *See supra* Part A.

173. With regard to research with offender samples, the group potentially stigmatized is not an extended family or a racial or ethnic minority that is evident in advance, but rather the group of potential or convicted criminals. This class already is about as stigmatized as any group could be. Admittedly, finding that some alleles occur more frequently among convicted criminals than among the rest of the population might reinforce perceptions of “natural born killers.” Yet, whether killers are born or made (or, more accurately, both born and made), their social and legal status is not likely to change dramatically as a result of these kinds of studies.

174. *E.g.*, Rothstein & Carnahan, *supra* note 69, at 156; Steinhardt, *supra* note 67, at 190.

175. *See* National Commission on the Future of DNA Evidence, Proceedings, Commission Discussion on Continued Tracking of Forensic DNA Issues: As Technology Expands, How Should Legal, Privacy, Funding and Research Issues be Addressed in the Future? (Apr. 10, 2000) (statement of Michael Smith), <http://www.ojp.usdoj.gov/nij/topics/forensics/events/dnamt/trans9/trans-n.html> (“[At a previous meeting] what we said was something like in no more than five years a body should be assembled which is not the creature of the labs or the law enforcement interests to revisit the question whether or not it’s necessary or desirable to retain samples.”).

176. National Commission on the Future of DNA Evidence, *supra* note 10 (statement of Tom Callaghan).

177. At least four countries—Belgium, Germany, Netherlands, and Norway—“destroy reference samples so as to remove any possibility or perception that government be able to perform any other inappropriate or illegal testing on the sample.” Christopher H. Asplen, *International Perspectives on Forensic DNA Testing*, paper presented at the International Society for the Reform of Criminal Law Conference, Aug. 24–28, 2003, at 4–5.

178. National Commission on the Future of DNA Evidence, *supra* note 10 (statement of Tom Callaghan).

Nonetheless, it would seem that the STR loci are satisfactory and could continue to be used in parallel with a new system.<sup>179</sup>

Third, the FBI maintained that “destruction of samples would affect the quality assurance of the DNA database.”<sup>180</sup> In particular, the Bureau noted that “mistakes can happen” and that “going back to the original sample and retyping that sample and confirming the accuracy of the identity of the individual prior to the name being released to law enforcement would identify mistakes” and spare individuals from the trauma of false accusations.<sup>181</sup>

Finally, the FBI suggested that there was no real problem that warranted the destruction of potentially useful samples. “DNA databasing,” it noted, “has occurred for ten years, and there has been no record of misuse of any sample in a DNA analysis database.”<sup>182</sup> Of course, this fact is not an affirmative reason to retain the samples.

Neither these arguments nor the additional value of the samples to behavioral genetics research provide compelling reasons to retain samples indefinitely. If a strong case for indefinite retention cannot be made, then eliminating the stockpile of samples might be a politically appealing strategy because it would assure the public that misuse of samples cannot occur.<sup>183</sup> Such a change in current policy would, of course, foreclose the use of the samples for behavioral or medical research, but this might be a small price to pay for enhanced public trust.

#### D. Independent Review of Research Proposals and Protocols

Even if the existing sample retention policy is continued, and even if arguments for a categorical ban on behavioral genetics research with law enforcement databanks or for requiring consent from all criminal “donors” are rejected, it does not follow that researchers should have unchecked discretion

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179. However, Dr. Callaghan, Program Manager of the Federal Convicted Offender Database, pointed to one subtlety in this regard:

One of the difficulties in current DNA analysis is resolving mixtures. When mixtures cannot be resolved, the entire mixture profile would be searched against the database, generating a lot of hits that would have to be further investigated. There may be markers in the future that are discovered that are far more discriminating and therefore mixtures would be much easier, much easier to resolve and to profile, not associated or only associated with one individual could be put in the DNA database and searched.

*Id.*

180. *Id.*

181. *Id.*

182. *Id.*

183. Professors Rothstein and Carnahan make this pragmatic argument when they observe that [t]he retention of samples, however, even under conditions of stringent security, raises concerns among the public that the samples could be re-analyzed for purposes other than identification. Therefore, samples should be destroyed immediately after analysis.

Rothstein & Carnahan, *supra* note 69, at 163. See also D.H. Kaye & Michael E. Smith, *DNA Identification Databases: Legality, Legitimacy, and the Case for Population-wide Coverage*, 2003 WIS. L. REV. 413, 438 (proposing a population-wide identification database in which “[l]aw enforcement agencies would not need—and should not be permitted—to handle, much less retain, the samples.”).

to proceed with studies of human behavior. Some research may be ill-conceived or may not be likely to achieve adequate anonymization of samples (where that is necessary). Therefore, procedures should be implemented to ensure that the merits of the particular research justify the risks it creates.

The usual procedural mechanism for avoiding excesses on the part of individual researchers in federally funded or directed research is an institutional review board (IRB) that is charged with verifying that the research is not unduly harmful.<sup>184</sup> IRBs are no panacea,<sup>185</sup> but they are better than nothing.<sup>186</sup> If tissue samples in law enforcement databanks are to be made available for biomedical or behavioral (rather than biometric) research, then the proposed research should be reviewed by an independent board with expertise in this type of research. This review could help ensure that the specific research has sufficient merit to justify the risks of stigmatization or discrimination. IRB approval already is required for researchers seeking federal grants for projects that would make use of law enforcement biobanks. It would be reasonable to add this same layer of review to private or state projects that fall outside this regulatory framework.

## V

### CONCLUSION

Behavioral geneticists are not yet massing at the gates of law enforcement DNA databanks preparing to breach these citadels in the search for “crime genes.” Nevertheless, concerns that DNA samples collected from convicted offenders for the construction of DNA identification databases also might be used in behavioral genetics research are legitimate. For better or worse, not all such research can be dismissed as devoid of scientific merit, making it necessary to decide whether the samples should be available for studies of alleles that might be linked to behavioral traits such as impulsiveness, novelty-seeking, or aggressiveness.

Existing legislation in the United States seems to preclude these uses of the samples, but one could argue that this limitation is squandering a useful resource for genetic research. Conversely, it can be argued that this research should be discouraged and that the samples should not be used for any purpose

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184. On the nature and role of IRBs, see 1 NAT'L BIOETHICS ADVISORY COMM'N, ETHICAL AND POLICY ISSUES IN RESEARCH INVOLVING HUMAN PARTICIPANTS: REPORT

185. See, e.g., James F. Childress, *The National Bioethics Advisory Commission: Bridging the Gap in Human Subjects Research Protection*, 1 J. HEALTH CARE L. & POL'Y 105, 113-14 (1998); Jay Katz, *Human Experimentation and Human Rights*, 38 ST. LOUIS U. L.J. 7, 9 (1993); Anne Wood et al., *The Crisis in Human Participants Research: Identifying the Problems and Proposing Solutions* (2002), <http://bioethics.gov/background/emanuelpaper.html>.

186. Recent discussions include: INSTITUTE OF MEDICINE, *supra* note 161; Carl H. Coleman, *Rationalizing Risk Assessment in Human Subject Research*, 46 ARIZ. L. REV. 1 (2004); Sharona Hoffman, *Continued Concern: Human Subject Protection, the Institutional Review Board, and Continuing Review*, 68 TENN. L. REV. 725 (2001); Lars Noah, *Deputizing Institutional Review Boards to Police (Audit?) Biomedical Research*, 25 J. LEGAL MED. 267 (2004).



other than biometric identification. These competing arguments produce no clear winners. On the one hand, the risks of psychosocial harms, informational privacy, and the protection of human subjects may not justify banning all behavioral genetics research with the samples. On the other hand, the research need for these samples may not be pressing. But even if the existing categorical rule against using the samples is thought to be unwarranted, the doors to the law enforcement biobanks should not be thrown wide open. Some studies will be better designed to uncover interesting discoveries and to respect the privacy interests of the “donors” of the samples than others. With ordinary biomedical research involving human subjects, the peer review process for grant requests by academic investigators offers some assurance that the study design is appropriate, and review by IRBs offers further protection for the interests of “donors.” Comparable review should be required before releasing law enforcement samples for behavioral genetics or other biomedical research.