Science Fictions and Racial Fables: Navigating the Final Frontier of Genetic Interpretation

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Abstract

The meaning of "race" has been vigorously contested throughout history. Early theories of race assigned social, intellectual, moral and physical values to perceived physical differences among groups of people. The perception that race should be defined in terms of genetic and biological difference fuelled the "race science" of the eighteenth and nineteenth centuries, during which time geneticists, physiognomists, eugenicists, anthropologists and others purported to find scientific justification for denying equal treatment to non-white persons. Nazi Germany applied these understandings of race in a manner which shocked the world, and following World War II the concept of race increasingly came to be understood as a socio-political construction with no biological meaning. Modern theories thus understand race as a social grouping of persons necessary to preserve unbalanced relationships of power.

Nonetheless, there has been an increased willingness of late to understand race in terms of biological difference. In particular, federal and state courts in the United States have largely embraced the use of distinct racial DNA databases to form expert opinions on racial genomic probability. Race, however, remains a purely social construct. Scientific evidence that claims the ability to biologically discern race should therefore be rejected by courts as irrelevant, unreliable and unfairly prejudicial. This Article argues that the prevailing socio-political understanding of race is being threatened by an ascendance of modern "race science,"

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and advocates a conception of race that accounts for the teachings of modern genetics, while avoiding a biologically reductionist view of race.

INTRODUCTION

> So "natural," deep, and fixed did the differences between human races seem to scientists . . . that the scientists' view of human races served to structure the very reception they gave to novel scientific theories and to influence the interpretation they put upon new empirical data.[2]

> To the extent . . . that "DNA profiles are dependent on the construction of racial and ethnic subgroups that are conceptualized in purely biological terms," then in light of the "widespread agreement . . . that biologically distinct races do not exist," the profilers are unwittingly engaged in legendary "race science."[3]

Race is increasingly viewed as being reducible through genetic testing to a biological essence. A person's deoxyribonucleic acid ("DNA") may purportedly be analyzed to isolate one's "racial essence." DNA technology and genetic testing claim to be able to biologically discern a person's race, and DNA samples left at crime scenes have been analyzed to introduce probabilistic estimates that criminal defendants shared the same race as the perpetrators of the crimes. Intellectual and physical attributes are similarly being attributed to racial difference on the basis of DNA and genetic scientific discoveries.

The widespread legal acceptance of such scientific interpretations of race as relevant, reliable, and un-prejudicial evidence threatens to undermine modern conceptions of race as a socio-political construction. In its stead, the proliferation of racial DNA evidence promotes a biological view of race that hearkens back to nineteenth century "race science." From a doctrinal perspective, such evidence clearly fails to satisfy basic evidentiary requirements of relevance, reliability, and fairness under existing United States statutory law. From a normative perspective, the use of extant racial categories to interpret and give racial meaning to DNA and genetic evidence rests on a flawed understanding of race as biologically meaningful. This Article thus argues that the prevailing socio-political understanding of race is being threatened by legal acceptance of modern "race science," and proposes a conception of race that accounts for the teachings of modern DNA and genetic technology, while avoiding biological reductionism.

Race was once understood as a scientifically meaningful taxonomic structure for human society. Science—whether in the guise of taxonomy, biology, anthropology, anthropometrics, anatomy, medicine, eugenics, or physiognomy—was utilized to define racial boundaries and groupings, as well as to empirically demonstrate supposedly innate and immutable differences among the "races" in intelligence, sexuality, morality, and other

2. NANCY STEPAN, THE IDEA OF RACE IN SCIENCE: GREAT BRITAIN 1800-1960 xx (1982).
3. David S. Caudill, *Race, Science, History and Law*, 9 WASH. & LEE RACE & ETHNIC ANC. L.J. 1, 12 (2003).

physical and mental human characteristics. Unsurprisingly, science played a pivotal role in reinforcing and legitimizing folk beliefs of white superiority and non-white inferiority, thus maintaining a rigid system of racial oppression and hierarchy. The pseudo-scientific theories of white racial superiority became applied science during the racial eugenics movement in the United States and Germany. Following the horrific and coldly technical application of unsound scientific theories of race by Nazi Germany in World War II, the world flatly rejected biological conceptions of race and advocated a perception of race as a social and historical construction. Part I of this Article thus briefly reviews the role that science played in the historical development of the concept of race. This section will also analyze the American legal acceptance of scientific racial theories through time, noting that "race science" was once freely admissible in American courts, but was ultimately displaced by modern sociological theories of race.

Notwithstanding the scientific and heretofore legal understanding that race is strictly a social construct, there has been an increased willingness of late to understand race in terms of biological difference. Genetic ancestry testing is now widely available, purporting to trace an individual's genetic ancestry to geographic regions that serve as misleading proxies for race: Africa, Europe, Asia, and "Native America." Additionally, pharmaceutical companies have developed drugs designed for specific races and ethnicities,[4] while medicine increasingly views race as a valid biological entity for epidemiological study.[5]

The judiciary has similarly fallen victim to accepting unfounded scientific notions that race has a genetic basis. The forensic analysis of crime scene genetic samples—such as blood, hair, and bodily fluids—has long been a staple of law enforcement. Scientific advancements in the understanding of genetic differentiation and DNA analysis, however, have encouraged law enforcement to develop DNA profiles of criminal suspects that are racial in nature. The Federal Bureau of Investigation, for instance, maintains a large database of genetic profiles of DNA samples that are classified in part by race. During a criminal investigation, the crime scene sample of genetic material is compared with the suspect's DNA sample. The discovery of a match between the crime scene sample and the suspect's DNA means that suspect is a potential, but not the only possible, contributor of the genetic material found at the crime scene.

The next step in the DNA identification process involves the development of a probability estimate of the chance that someone other than the criminal suspect could have contributed the crime scene sample. A statistical estimate may be generated by comparing the tested samples with the DNA profiles present in the general population; for instance, an estimate that there is one-in-a-million chance that another person in the United States could have contributed the crime scene DNA sample. However,

4. *See generally* Pilar Ossorio & Troy Duster, *Race and Genetics: Controversies in Biomedical, Behavioral, and Forensic Sciences*, 60 AM. PSYCHOLOGIST 115, 115-16 (2005).
5. *See* Lorena Madrigal & Guido Barbujani, *Partitioning of Genetic Variation in Human Populations and the Concept of Race, in* ANTHROPOLOGICAL GENETICS: THEORY, METHODS, & APPLICATIONS 19, 28-30 (Michael Crawford ed., 2007).

criminal prosecutors are increasingly relying on expert comparisons of the tested DNA samples with the DNA profiles present in a specific racial group. It is now commonplace for courts to admit probabilistic estimates that, for instance, there is only a 1-in-41-million chance that another "Hispanic" person contributed the genetic material found at a crime scene.[6]

The second section of this Article will therefore briefly discuss the fundamentals of modern genetic science, while the third section will examine the field of population genetics and its role in forensic DNA analysis and racial DNA profiling. The fourth section of this Article examines the judiciary's acceptance of racial probabilistic interpretations of DNA samples as relevant and admissible evidence, and therefore its embrace of a biological concept of race.

A normative and doctrinal critique of the courts' embrace of "race science" is set forth in the fifth section of the Article, where I argue that such DNA racial evidence fails the standards for relevance, reliability, and fairness that guide the admissibility determination in United States courts. Race remains an arbitrary social construction, notwithstanding the implications and exclamations of certain sectors of the genetic science field. Authoritative scientific studies in genetics have affirmed that there is no valid basis for dividing humans into genetically defined racial groups. As such, analyses of DNA evidence that purport to scientifically identify persons by race are inadmissible.

I. SCIENCE, LAW, AND THE HISTORICAL DEVELOPMENT OF THE RACE CONCEPT

The idea of "race" as a tool of social categorization and control likely did not evolve until the late sixteenth and early seventeenth centuries.[7] Ever since the inception of the race concept, science has been instrumental in defining the contours of racial categories as well as in justifying unequal social and political treatment based on such classifications. One of the first racial taxonomies relied on biology in making scientific distinctions between groups of humans. Carolus Linnaeus, a Swedish biologist and taxonomist, published *Systema Naturae* in 1735 in an effort to classify what he deemed to be the three basic kingdoms of nature: the animal kingdom, the "kingdom of stones," and the plant kingdom.[8] Humans were, of course, described as occupying the animal kingdom of nature, and were separated into four separate biological categories associated with skin color and geographical ancestry: Europaeus (white), Africanus

6. *See, e.g.*, Virgin Islands v. Penn, 838 F. Supp. 1054, 1065 (D.V.I. 1993) (establishing the probability of a random match at one in 41 million).
7. *See* Christian B. Sundquist, *The Meaning of Race in the DNA Era: Science, History and the Law*, 27 TEMP. J. OF SCI. TECH. & ENVT'L LAW 231, 233-34 (2008) (noting that "[t]here is some merit to the contention that racial theories separating people into categories, and assigning positive and negative values to those categories, were prevalent by the end of the Middle Ages and during the Renaissance era in England").
8. CAROLUS LINNAEUS, SYSTEMA NATURAE (2d ed. 1758); *see* Uppsala Universitet, Systema Naturae- An Epoch-Making Book, http://www.linnaeus.uu.se/online/animal/1_1.html (last visited Sept. 4, 2008).

(black), Americanus (red), and Asiatic (yellow).[9] The taxonomy proposed by Linnaeus, surprisingly similar to modern racial classifications of African, Caucasian, Asian, and Native American, represents one of the earliest known racial classification schemes that purported to scientifically attribute negative and positive mental characteristics to race. Europeans were noted as being gentle, inventive, "keen-minded, and innovative," while Africans were described as relaxed, negligent, "lazy, and careless"; American Indians were believed to be stubborn and easily angered, while Asians were thought of as avaricious and easily distracted.[10] Perhaps unsurprisingly, "[t]he assumption [by Linnaeus] that mental and moral traits were associated with race was to inform many scientific investigations during the next two hundred years."[11]

The philosophies of empiricism and rationality espoused during the Enlightenment period undoubtedly facilitated further scientific investigation of racial difference. Against a backdrop of widespread belief in the Aristotelian notion of a "great chain of being,"[12] the development of independent scientific fields, such as biology and anthropology, encouraged precise description of racial categories and tabulation of human difference:

> Empiricism encouraged the tabulation of perceivable differences between peoples and from this it deduced their natural differences. Rationalism proposed initial innate distinctions (especially mental ones) to explain the perceived behavioural disparities. . . . The emergence of independent scientific domains of anthropology and biology in the Enlightenment defined a classificatory order of racial groupings – subspecies of Homo sapiens – along correlated physical and cultural matrixes.[13]

The focus on empiricism and rationality during the Enlightenment thus facilitated a shift from a pre-modern understanding of human difference in terms of religion and noble lineage to a "scientific" view of human difference rooted in race.[14]

Scientific investigation of racial difference after the Enlightenment increasingly came to be relied upon as a tool to validate folk notions of "white" racial superiority while preserving structures of racial hierarchy.

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9. WILLIAM H. TUCKER, THE SCIENCE AND POLITICS OF RACIAL RESEARCH 9 (1994).
10. CAROLUS LINNAEUS, SYSTEMA NATURAE 20-23 (2d ed. 1758).
11. *Id.* The racial taxonomy set forth by Linnaeus was relied on by other prominent scientists in their investigation of racial difference. For example, Johann Friedrich Blumenbach, a German physiologist, accepted Linnaeus' division of the world into four distinct racial categories, yet substituted the descriptors "Europaeus" and "Asiatic" in favor of the terms "Caucasian" and "Mongoloid," respectively.
12. The idea that there exists a "great chain of being" in this context refers broadly to the notion that some people are naturally inferior to other people. *See generally* ARTHUR O. LOVEJOY, THE GREAT CHAIN OF BEING (1960).
13. DAVID GOLDBERG, RACIST CULTURE: PHILOSOPHY AND THE POLITICS OF MEANING 28-29 (1993); *see also* GEORGE MOSSE, TOWARD THE FINAL SOLUTION: A HISTORY OF EUROPEAN RACISM 1, 3 (1978) (arguing that "Eighteenth Century Europe was the cradle of modern racism" due to the "preoccupation with a rational universe, nature and aesthetics" that characterized the Enlightenment philosophies).
14. GOLDBERG, *supra* note 13, at 24-29; *see also* MOSSE, *supra* note 13, at 3.

The chattel enslavement of Africans in the United States during the seventeenth, eighteenth, and early nineteenth centuries, for instance, spawned a regrettable expansion of "race science." While slavery in the United States was initially justified in terms of economic necessity and religious difference,[15] science was soon invoked to provide an irrebuttable defense of the "peculiar institution." Purportedly objective studies based in biology, anatomy, and anthropology—as well as in pseudo-disciplines such as phrenology and anthropometrics—maintained that Africans were biologically inferior to whites, and that slavery thus "improved blacks 'in body, mind, and morals.'"[16]

Even following the end of *de jure* slavery in America during the nineteenth century, many scientists believed that science continued to maintain an "obligation to settle the relative rank among . . . races."[17] Phrenologists such as Dr. Samuel Morton thus examined the cranial capacities of the races, finding that "Caucasians" had a significantly larger cranial capacity than "Ethiopians," and thus were naturally the more intelligent race.[18] Anthropometricists also took up the scientific call to arms by extensively examining the bodies of black people, and interpreting any purported anatomical differences between blacks and whites in racial terms. A "discovery" that black people had a smaller facial angle than whites, for example, would be perceived as scientific evidence of reduced intelligence.[19]

While the "pseudo-science" of the nineteenth century is rightly criticized as explicitly incorporating racial biases that resulted in empirically flawed and objectionable scientific conclusions,[20] some of the "race scientists" of that era were sincerely attempting to objectively study racial difference and variation and yet reached racist conclusions. For example, the noted Swiss naturalist Louis Agassiz, an outspoken supporter of the *objective* scientific investigation of race, eventually concluded that the "submissive . . . negro [demonstrated] a peculiar indifference to the advantages afforded by civilized society," and therefore that social treatment of blacks should be "guided by a full consciousness of the real difference existing between us and them."[21] Such scientists—supposedly scientifically examining race in an unbiased manner—were knowingly and unknowingly guided by their learned folk conceptions of race, white superiority, and black inferiority. In many cases, scientific "evidence, often sketchy and incomplete, was unconsciously manipulated to fit preconceived notions. As a result, an objective assessment about human

15. *See* Sundquist, *supra* note 7.

16. *See* TUCKER, *supra* note 9, at 14, 174-85 (quoting S. A. Cartwright, *Report on the Diseases and Physical Peculiarities of the Negro Race*, 7 NEW ORLEANS MEDICAL AND SURGICAL JOURNAL 691, 707-09 (1851)).

17. *Id.* at 18 (quoting Louis Agassiz, *The Diversity of Origin of the Human Races*, 49 CHRISTIAN EXAMINER 110, 142 (1850)).

18. *Id.*

19. *Id.* at 23.

20. *See, e.g.*, STEPHEN JAY GOULD, THE MISMEASURE OF MAN (1981).

21. *See* TUCKER, *supra* note 9, at 18 (quoting Agassiz, *supra* note 16, at 144).

variation was prevented by practices and procedures embedded in science itself."[22]

The race science of the nineteenth century was heavily influenced by Charles Darwin's theory of evolution. The concept of evolution theorized by Darwin was non-racial on its face, and Darwin took pains to explain that it should not be applied to interpret supposed racial differences:

> Although the existing races of man differ in many respects as in color, hair, shape of skull, proportions of the body, etc., yet if their whole structure be taken into consideration they are found to resemble each other closely in a multitude of points. Many of these are so unimportant or of so singular a nature that it is extremely improbable that they should have been independently acquired by aboriginally distinct species or races.[23]

The theory of evolution and its emphasis on gradual evolution pursuant to a process of natural selection, however, proved to be too tempting for race theorists to ignore. "Social Darwinists" sought to apply Darwin's evolutionary principles to interpret human difference and account for class and racial inequality in society. Assuming that different groups of people—whether organized by race or class—occupied different positions on the evolutionary ladder, social Darwinists believed that social welfare programs hindered evolutionary progress. Social Darwinists thus rallied against any efforts to reduce social inequality, including minimum wage legislation, free public education, and charitable aid to the needy.

The Social Darwinists believed that class and racial conflict could only be resolved by the gradual extermination of biologically inferior groups from the gene pool. The eventual elimination of inferior non-white races was viewed as an inescapable evolutionary fact:

> If [blacks] were the highest form of human life . . . we might be concerned . . . [but] to the clear, cold eye of science, the plight of these backward peoples appears practically hopeless. They have neither part nor parcel in the future history of man.[24]

Social Darwinists were not simply engaged in the theoretical application of evolutionary principles to society, but rather sought to practically apply their scientific beliefs by subtly guiding the evolutionary process. Thus the social Darwinism movement "evolved" into the eugenics movement, as more and more scientists during this era became interested in the scientific promotion of superior genetic traits, and the concomitant inhibition of inferior genetic traits. The eugenicists of this era embraced the dominant racial ideology and its assumption that evidence of white superiority could be gleaned through science. As such, eugenicists were

22. NANCY STEPAN, *supra* note 2, at xv (1982).
23. CHARLES DARWIN, DESCENT OF MAN: AND SELECTION IN RELATION TO SEX 152 (Barnes & Noble Publishing, Inc. 2004) (1871).
24. *See* TUCKER, *supra* note 9, at 31 (quoting WILLIAM BENJAMIN SMITH, THE COLOR LINE 192 (Negro Universities Press 1969) (1905)).

influential in the passage of anti-miscegenation laws, immigration restrictions, and policies of forced sterilization in the United States.[25]

Eugenicists also sought to validate their claims that heredity determined genetic potential by developing intelligence tests and other statistical measures of intellectual ability. Francis Galton, a cousin of Charles Darwin and widely considered to be one of the founding fathers of eugenics, created such an intelligence test and purported to scientifically determine that "blacks" scored two grades lower than "whites," thus providing evidence that blacks were "half-witted" and biologically inferior to whites.[26] The mental tests developed by eugenicists and psychologists, as well as the interpretation of their results, were undoubtedly skewed by the cultural expectations of the scientists:

> Even before data from the new mental tests had been gathered, many social scientists had already made up their mind about the intelligence of blacks and immigrants. . . . Indeed, had the data conflicted with already received opinion, the new instruments would probably have been invalidated as measures of intelligence and discarded; some earlier tests of ability had already suffered such a fate when they failed to yield the expected racial ordering.[27]

The eugenics movement had substantially gained in popularity by the end of World War I. Eugenicists from both America and Europe were calling for national eugenics policies prior to the beginning of World War II, generally warning that "[*w*]*e must at any price keep the quality of the* [white] *race at a high level*. . . . If strong measures in race hygiene are not taken in time, the [superior white] race will meet with dissolution and extinction."[28]

Germany, in particular, came to blame its economic decline following the First World War on the country's purported racial denigration. The post-war Weimar government thereafter adopted a popular policy of *rassenhygiene* (race hygiene) and established scientific centers to monitor the country's racial health.[29] Proposals for sterilization and anti-miscegenation programs (modeled after those in the United States) that were merely advocated by the Weimar government were soon put into practice by the successor Nazi government led by Adolf Hitler. Race theory further transformed into applied science as the Nazi government sought to hasten the elimination of racial "impurities" by coldly implementing euthanasia programs. These programs initially targeted the physically and mentally handicapped before expanding to target all supposed genetically inferior non-Aryan persons, including Jews, Romas and Slavs. Nazi Germany's "Final Solution" was specifically aimed at annihilating the Jewish population, which was regarded as a "parasitic race" that threatened the racial purity of the nation. The resulting holocaust

25. *Id.* at 59-61. It is estimated that over forty-five thousand persons were sterilized in thirty states pursuant to state statutes aimed at "socially inadequate" persons.
26. *Id.* at 43-44.
27. *Id.* at 74-75.
28. Herman Lundborg, *Race Biological Perspectives,* 9 SOCIAL FORCES 397, 400 (1931).
29. TUCKER, *supra* note 9, at 111.

claimed the lives of over six million Jews in one of the starkest examples of the dangers of subscribing to a biological theory of race.

The attempted genocide of the Jewish "race" shocked the world into flatly rejecting biological racial theories and condemning the applied racial science of Nazi Germany. The newly formed United Nations created the Educational, Scientific and Cultural Organization ("UNESCO"), which consisted of the leading anthropologists and biologists of the time, and tasked it with issuing an authoritative statement on race. The UNESCO commission determined that racial difference was the result of environmental factors such as genetic drift and isolation, and that race therefore was not "so much a biological phenomenon as a social myth."[30] The UNESCO commission similarly rejected the claims of genetic inferiority of non-white "races" made by Nazi Germany, eugenicists, and others, concluding that "given similar degrees of cultural opportunity to realize their potentialities, the average achievement of the members of each ethnic group is about the same."[31]

In so doing, the UNESCO Statement on Race provided the foundation for modern theories of race. The central principle underlying modern race theory is that race is a social and political construction, devoid of biological meaning. Race is understood as "a concept that signifies and symbolizes sociopolitical conflicts and interests in reference to different types of human bodies,"[32] rather than a biological or genetic category.[33] Professor Angela Harris succinctly describes the prevailing view as one that concludes that "race does not exist in the body but rather is the product of socially-produced understanding."[34] Modern race theory thus explicitly rejects theories that assume that race has a biological or genetic basis:

> Although the concept of race appeals to biologically based human characteristics (phenotypes), selection of these particular human features for purposes of racial signification is always and necessarily a social and historical process. There is no biological basis for distinguishing human groups along the lines of race, and the sociohistorical categories employed to differentiate among these

30. UNESCO, FOUR STATEMENTS ON THE RACE QUESTION 33 (1969).

31. *Id.* at 32.

32. Howard Winant, *Race and Race Theory*, 26 ANN. REV. SOC. 169, 172 (2000); *see generally* Anthony Paul Farley, *All Flesh Shall See it Together*, 19 CHICANO-LATINO L. REV. 163, 166 (1998) ("There is no such thing as 'race' save as a 'social construction.'").

33. The United States Supreme Court has largely adopted the findings of modern race theory. *See*, *e.g.*, St. Francis College v. Al-Khazraji, 481 U.S. 604, 610 n.4 (1987) (finding that race is "for the most part sociopolitical, rather than biological, in nature").

34. Angela Harris, *From Color Line to Color Chart: Racism and Colorism in the New Century*, 10 BERKELEY J. AFR.-AM. L. & POL'Y 52, 68 (2008); *see also* JOE R. FEAGIN & CLAIRECE BOOHER FEAGIN, RACIAL AND ETHNIC RELATIONS 7 (6th ed. 1999) ("Human populations singled out as 'races' are simply groups with visible differences that Europeans and European-Americans have decided to emphasize as important in their social, economic, and political relations. . . . Such racial categorizing is neither objective nor scientific.").

groups reveal themselves, upon serious examination, to be imprecise if not completely arbitrary.[35]

II. POPULATION GENETICS AND DNA RACIAL PROFILING

The modern view of race as socially constructed, however, is increasingly being challenged by the assumption that race can be discerned from genetic testing. Science is once again being invoked to interpret human racial difference. Private genetic testing companies promise to analyze DNA samples to "decipher[ ] . . . an individual's race,"[36] to determine the percentage of genetic racial admixture in a person,[37] and to assign a person to a racial category such as white, Black, or Asian.[38] State and federal law enforcement have also begun to rely on forensic analysis of crime-scene DNA samples to identify the likely "race" of a criminal perpetrator, while prosecutors present expert testimony during criminal trials to present the probability that another person of the same "race" as the defendant could have contributed the crime-scene DNA sample.

a. The Science of Genetics and Human Difference

Deoxyribonucleic acid, otherwise known as "DNA," is a chemical substance that is found in the nucleus of every cell of a person's body. DNA contains the biological information necessary for replicating the human cell, as well as for constructing the enzymes required to maintain functioning cells. The biological information stored by DNA in turn is responsible for dictating individual genetic attributes—such as eye color, hair texture, and skin color.

DNA provides a genetic map of the human body by storing biological information in four subunits of nucleic acid—adenine (A), guanine (G), cytosine (C), and thymine (T). The DNA molecule contains long sequences of these subunits, each in a shape resembling that of a double helix or "ladder." Each DNA molecule consists of two of these strands made up by the four nucleic acids. The two strands always bind together in the same fashion: adenine (A) always binds together with thymine (T), and guanine (G) always pairs with cytosine (C).[39] This general rule of complementary base pairing is heavily relied upon in the forensic analysis of DNA samples.

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35. Winant, *supra* note 32, at 172; *see also* David Brion Davis, *Constructing Race: A Reflection,* Vol. 54, No. 1, WM. & MARY QUARTERLY 7, 7 (1997) (noting that "responsible scientists have long discredited any biological or genetic definition of racial groups" and that "historians have increasingly recognized that the so-called races of mankind are the fortuitous and arbitrary inventions of European and American history, the by-products, primarily, of Europe's religious, economic, and imperial expansion across the seas of the earth").
36. Zach Gaskin, DNA Print Genomics, Determine Race Proportions from Crime Scene DNA, http://bioforensics.com/conference04/Racial_Identification/ (last visited Sept. 4, 2008).
37. C. Abraham, *Molecular Eyewitnesses: DNA Gets a Human Face*, TORONTO GLOBE & MAIL, June 25, 2005 at A6.
38. *Id.*
39. Kahn, *An Introduction to DNA Structure and Genome Organization, in* FORENSIC DNA TECHNOLOGY 25, 26-28 (M.A. Farley & J.J. Harrington eds., 1991).

The DNA bundle itself is tightly compressed into chromosomes, which are located in the nucleus of each human cell. The DNA bundle in the cellular nuclei contains "about three billion chemical nucleotides encoding roughly 30,000 genes, discrete chunks of DNA that are translated into individual proteins."[40] The chromosomes containing DNA genetic material come in pairs, with one chromosome inherited from the father, and the other inherited from the mother. As such, genetic information encoded in nuclear DNA is passed on from one generation to the next.

The vast majority of the human genome consists of genes that are "non-coding," meaning that they do not support protein synthesis. The "coding" portions of the genome do not contain much if any genetic variability, due to the evolutionary pressure to maintain their specific functions without change.[41] In contrast, non-coding portions of the genome are not usually controlled by evolutionary "selection pressure," and thus may transmit the inter-generational mutations and variations that account for human genetic variability.[42] Now that scientific projects, such as the Human Genome Project,[43] have conclusively determined that 99.9% of human genetic DNA material is identical, genetics is now concerned with investigating the .1% of human genetic difference primarily traceable to the non-coding portions of the human genome.[44]

A significant percentage of non-coding genes contain DNA sequences of the nucleic acid subunits that are tandemly repeated—meaning that the sequences are repeated in a head-to-tail manner. The tandemly repeated sequences of DNA often demonstrate significant variation in the number of repeats that occur from individual to individual.[45] For instance, one person may have three repeated nucleic sequences (e.g., A-T-C-G) at one location, while another person may have nine such repeats at the same location. The discovery of DNA sequences that contain variant "repeat regions" opened the door to the ability to perform forensic genome profiling.[46]

The repeated DNA sequences appear in different lengths of repetition. A medium-length repeat sequence is called a "variant number tandem repeat" ("VNTR"), and generally contains between ten and one hundred

40. NATIONAL LIBRARY OF MEDICINE, DNA, www.nlm.nih.gov/exhibition/visibleproofs/education/dna/dna.pdf (last visited Sept. 4, 2008).
41. Angel Carracedo, Beatriz Sobrino, & Maria Victoria Lareu, *Forensic DNA Typing Technologies: A Review*, *in* 6 HANDBOOK OF ANALYTICAL SEPARATIONS: FORENSIC SCIENCE 946 (Ed. M.J. Bogusz, 2d ed. 2008).
42. *Id.*
43. *See* U.S. Dept. of Energy, Human Genome Project Information, http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml (last visited Mar. 9, 2008) (describing the scope and goals of the project, foremost of which is to "identify all the approximately 20,000-25,000 genes in human DNA [and] determin[ing] the sequences of the 3 billion chemical base pairs that make up human DNA . . . .").
44. *See*, *e.g.*, International HapMap Project, About the HapMap, http://www.hapmap.org/thehapmap.html.en (last visited Mar. 9, 2009) (describing the overarching project goal as "to compare the genetic sequences of different individuals to identify the chromosomal regions where genetic variants are shared").
45. *DNA Typing- Criminal and Civil Applications*, 4-37C FORENSIC SCIENCES § 37C.02 (Cyril H. Wecht ed., 1981).
46. *Id.* at § 37C.03-05.

nucleic base pairs.[47] Restriction fragment length polymorphism ("RFLP") was one of the earliest methods of DNA molecular typing that analyzed these individual VNTR differences in a molecular location, or locus.

Polymerase chain reaction ("PCR") analysis is a more efficient method of DNA typing that is currently used by most forensic laboratories. PCR involves amplifying the DNA sample by using a synthesizing enzyme, allowing a specific region of DNA to be replicated into millions of copies. The PCR amplification process allows for the analysis of very minute amounts of DNA. While the RFLP method analyzes variation in VNTR loci, DNA samples amplified via PCR are typically analyzed for variation in short tandem repeat ("STR") DNA markers. STR repeat sequences are much shorter than VNTR repeat sequences, generally containing only two to six base pairs.[48]

b. Forensic DNA Analysis

The analysis of genetic cellular samples, whether through a PCR or RFLP method, is of forensic interest to law enforcement. All people, with the exception of identical twins, have a truly unique molecular signature that can be ascertained through DNA analysis. However, it is currently too time-consuming and expensive to examine the entire genome of a criminal suspect for comparison to a crime-scene DNA sample. Accordingly, forensic scientists utilize RFLP or PCR technology to analyze the tandem repeat sequences of only a few genetic markers in non-coding regions of the genome. The forensic analysis of DNA crime scene samples thus provides law enforcement with an increasingly important tool in the identification of criminal perpetrators.

Law enforcement agencies in the United States and around the world have relied on DNA forensic technology for well over a decade. Congress passed the DNA Identification Act of 1994 to authorize the Federal Bureau of Investigation ("FBI") to operate a DNA database called the Combined DNA Index System ("CODIS"). The CODIS national database became operational in 1998 and allows state and federal law enforcement agencies to upload DNA profiles to the database, as well as to search the catalog of DNA profiles for a "match" to their crime-scene sample. The number of DNA profiles contained in the CODIS system greatly expanded after Congress passed the DNA Analysis Backlog Elimination Act of 2000, which compelled people convicted of specific federal crimes to submit a genetic DNA sample to law enforcement authorities.[49] By October 2007, the CODIS system contained 5,070,473 DNA profiles in its con-

47. JOHN M. BUTLER, FORENSIC DNA TYPING: BIOLOGY, TECHNOLOGY, AND GENETICS OF STR MARKERS 85 (2005).

48. *Id.*

49. 42 U.S.C. § 14135a (2009); DNA Analysis Backlog Elimination Act of 2000, H.R. 4640, 106th Cong. § 3 (2000) (establishing the qualifying federal offenses mandating submission of a DNA sample to include murder, voluntary manslaughter, aggravated assault, child abuse, sexual abuse, kidnapping, burglary, robbery, arson, and conspiracy to commit such crimes.). The Act also provided for $170 million in federal funds to support state efforts to collect DNA samples from state criminal offenders.

victed offender index, and 194,785 DNA profiles in its forensic crime scene evidence index.[50]

CODIS is a distributed database containing local, state, and national index systems.[51] The National DNA Index System ("NDIS") is the highest hierarchal level of CODIS, and allows for the national comparison of profiles contained in Local DNA Index Systems ("LDIS") and State DNA Index Systems ("SDIS"). According to the FBI, "[a]ll DNA profiles originate at the LDIS, then flow to SDIS and NDIS."[52] State or local forensic laboratories typically upload a DNA profile to their own DNA index system, adhering to federal guidelines regarding the collection, care, and analysis of the DNA sample.[53] That same profile is then uploaded to the NDIS to allow for national searches.

A DNA profile is created by analyzing a genetic sample, collected from a crime scene or from a criminal suspect, for the presence of tandemly repeated sequences of alleles[54] located at thirteen specific markers (loci).[55] The thirteen core non-genic locations of short tandem allele repeats used by CODIS can provide a random match probability of close to 1 in 100 trillion.[56]

The DNA profiles contained in CODIS have a variety of law enforcement uses. Law enforcement often compares a crime scene DNA sample to another crime scene DNA sample in order to connect unsolved crimes. The police may also use CODIS to compare a crime scene DNA sample to the DNA profiles of past criminal offenders already maintained in the CODIS system. CODIS may also be used to compare crime scene DNA samples to a DNA sample obtained from a criminal suspect.

The collected DNA samples are generally analyzed by genetic scientists employed by state or FBI forensics laboratories, but such analysis

50. National DNA Index System, NDIS Profile Comparison (as of Oct. 2007), http://www.fbi.gov/hq/lab/codis/national.htm (last visited Sept. 4, 2008).

51. Federal Bureau of Investigation CODIS Combined DNA Index System, http://www.fbi.gov/hq/lab/html/codisbrochure_text.htm (last visited Sept. 4, 2008).

52. *Id.*

53. *See* BUTLER, *supra* note 47, at 98-99.

54. "Alleles" refers to "genic variants" that are responsible for producing certain traits. *See* U.S. DEP'T OF JUSTICE, NAT'L INST. OF JUSTICE, NAT'L COMM. ON THE FUTURE OF DNA EVIDENCE, THE FUTURE OF FORENSIC DNA TESTING 11-12 (2000), http://www.ncjrs.org/pdffiles1/nij/183697.pdf (last visited Sept. 4, 2008) (hereinafter "FUTURE OF DNA TESTING") (providing the example: "[A] specific allele of a particular gene is responsible for the enzyme that converts the amino acid phenylalanine into tyrosine. When this enzyme is missing or abnormal, the child develops the disease, phenylketonuria, or PKU. The result is severe mental retardation unless the child is treated; happily, with a specific diet the child develops normally. A child will develop PKU only if both representatives of the appropriate chromosome pair carry the abnormal allele. If there is only one PKU allele and the other is normal, the child will be normal; the amount of enzyme produced by a single normal allele is enough." Because nearly ninety-seven percent of DNA is non-genic, and because those "regions show the same genetic variability that genes do, in fact usually more . . . the words commonly used for describing genes (e.g., allele) are carried over to [non-genic] DNA regions. . . .").

55. *Id.* at 19.

56. *See* BUTLER, *supra* note 47, at 439.

may also be farmed out to private genetics companies.[57] A DNA profile is created for each genetic sample after undergoing PCR analysis, and a "match" or "inclusion" will only be identified if all of the DNA segments at the thirteen core CODIS short tandem repeat loci are identical.[58] Since the entire genome of the contributor of the DNA sample is not being mapped out, a DNA match is not conclusive evidence that, for instance, the criminal suspect is the only person who could have contributed the crime scene DNA sample. Contrary to popular opinion, a DNA match merely establishes that the criminal suspect potentially could have contributed the DNA sample found at a crime scene.[59] The second step of the DNA identification process therefore involves producing a probability estimate of the chance that someone other than the criminal suspect would have the same DNA profile.[60]

c. Population Genetics and Random Match Probability Analysis

The random match probability analysis can produce two different statistical estimates by relying on two different reference populations. First, the expert can determine the frequency with which the particular DNA profile appears in the general population. This method of statistical interpretation does not appear to create any tension with modern race theory, as the profile is merely compared to the frequency distribution existing in the general population, without regard to race.

The second method of probability analysis involves measuring the frequency with which a DNA profile appears in a particular "racial" group. While the DNA profiles maintained in CODIS are not classified by race, the FBI created a separate population file that estimates STR allele frequencies in five racial population groups: African American, United States' Caucasian, Hispanic, Far East Asian, and Native American.[61] An expert can then estimate the frequency with which a particular DNA profile occurs in a specific racial database. Accordingly, it is now common for probabilistic estimates to be presented in court that only 1 in 2,600 "American Indians,"[62] or 1 in 41 million "Blacks,"[63] or 1 in 35,000 "Caucasians,"[64] would produce a DNA profile matching that of the criminal defendant.

The National Research Council ("NRC") of the National Academy of Sciences published a comprehensive report on forensic DNA technology and probability analysis in 1992 ("*NRC I*"). The NRC tasked the newly

57. *Id.* at 442-43.
58. TONY N. FRUDAKIS, MOLECULAR PHOTOFITTING: PREDICTING ANCESTRY AND PHENOTYPE USING DNA 3 (2008).
59. NORAH RUDIN & KEITH INMAN, AN INTRODUCTION TO FORENSIC DNA ANALYSIS 139-40 (2d ed. 2002).
60. *Id.* at 143.
61. BUTLER, *supra* note 47, at 439. The FBI created its population file based on the findings of the following study: Bruce Budowle, Brendan Shea, Stephen Niezgoda, & Ranjit Chakraborty, *CODIS STR Loci Data from 41 Sample Populations*, 46 J. FORENSIC SCI. 453, 453 (2001).
62. United States v. Martinez, 3 F.3d 1191, 1193 (8th Cir. 1993).
63. Virgin Islands v. Penn, 838 F. Supp. 1054, 1065 (D.V.I. 1993).
64. United States v. Bonds, 12 F.3d 540, 563 (6th Cir. 1993).

formed Committee on DNA Technology in Forensic Science with resolving the "substantial controversy" that had arisen at the time regarding the proper methodology for statistically interpreting the meaning of a DNA "match."[65] The controversy concerned the appropriate reference population to be used in estimating genomic frequency; that is, whether "racial" groups were sufficiently homogenous to serve as reference populations or whether estimates based on the general population were sufficiently precise.

The NRC observed that there were two possible ways to calculate genomic frequency. The first method simply involves counting the occurrences of a particular DNA profile in a random sample of the population and then using classic statistical principles to place upper and lower confidence limits on that estimate. This "straight counting" method thus does not incorporate theoretical assumptions about the population.

The second proposed method of statistical interpretation involves application of theoretical principles derived from the field of population genetics.[66] Under this approach, every "matching allele is assumed to provide statistically independent evidence, and the frequencies of the individual alleles are multiplied together to calculate a frequency of the complete DNA pattern."[67] A key assumption underlying the use of the product rule in this model is that the reference population does not contain subpopulations with distinct allele frequencies. The absence of "population sub-structuring" was thus considered necessary for the application of the product rule to estimate genome frequency.

An additional observation of population genetics is that the product rule—allowing for the multiplication of individual allele frequencies—can only be applied when allele frequencies are similar or constant in the reference population. The Hardy-Weinberg principle, which is considered the foundation of all of population genetics, provides a solution to this quandary by assuming that genotype frequencies within a population remain in such constant equilibrium "unless acted on by one of the four evolutionary forces (mutation, selection, gene flow (or admixture), and drift)."[68] The Hardy-Weinberg theory thus states that there is a predictable relationship between genotype frequency and allele frequency in a given population.[69]

Hardy-Weinberg equilibrium is disturbed, however, when a person within the reference population mates with a person from a different population group (admixture), when mating within the population is not random, or when migration occurs within the population. "However, it can be reasonably argued that mating is not random in most human populations, that some mating populations are not large, and that migra-

65. NATIONAL RESEARCH COUNCIL, DNA TECHNOLOGY IN FORENSIC SCIENCE 74 (1992) [hereinafter "*NRC I*"].
66. "Population genetics" refers to the study of genetic differentiation and diversity present in a specific human population, or subset of a particular species.
67. *NRC I*, *supra* note 65, at 76.
68. Mark D. Shriver, *Introduction*, *in* TONY N. FRUDAKIS, MOLECULAR PHOTOFITTING: PREDICTING ANCESTRY AND PHENOTYPE USING DNA 7 (2008).
69. RUDIN & INMAN, *supra* note 59, at 143.

tion is variable among mating populations throughout the world. In fact, it is well accepted that the United States population is a mixture of people of various origins."[70]

The debate at the time *NRC I* was issued concerned whether the racial population groups used by some geneticists to calculate genomic frequencies demonstrated significant sub-structuring and whether Hardy-Weinberg equilibrium could thus be achieved. On one side of the issue, scientists such as Richard Lewontin and Daniel Hartl argued that studies had demonstrated that racial groups were not genetically homogenous due to significant sub-structuring, and thus were inappropriate to use as distinct reference population groups.[71] Other population geneticists, such as Kenneth Kidd and Ranajit Chakraborty, argued that allele heterogeneity and sub-structuring within racial groups was sufficiently minimal to allow frequency estimates based on population groups defined by race.[72]

The Committee did not conclusively resolve the controversy as much as sidestep the scientific debate and assume that significant sub-structuring existed within racial groups. The Committee observed that current "studies have shown that the genetic diversity between subgroups within races is greater than the genetic variation between races," making the existence of substructuring within a racial group highly likely.[73] However, it also called for additional scientific study of racial differentiation in alleles that could support treating racial groups as genetically homogenous.[74] The Committee thus concluded that it had:

> chosen to assume for the sake of discussion that population substructure may exist and provide a method for estimating population frequencies in a manner that adequately accounts for it. Our decision is based on several considerations:
>
> 1. It is possible to provide conservative estimates of population frequency, without giving up the inherent power of DNA typing.
> 2. It is appropriate to prefer somewhat conservative numbers for forensic DNA typing, especially because the statistical power lost in this way can often be recovered through typing of additional loci, where required.
> 3. It is important to have a general approach that is applicable to any loci used for forensic typing. Recent empirical studies pertain only to the population genetics of the VNTR loci in current use. However, we expect forensic DNA typing to undergo much change over the next decade—including the introduction of different types of DNA polymorphisms, some of which might have different properties from the standpoint of population genetics.
> 4. It is desirable to provide a method for calculating population frequencies that is independent of the ethnic group of the subject.[75]

70. *Id.* at 144.
71. *NRC I*, *supra* note 65, at 79
72. *Id.* at 79-80.
73. *Id.* at 82.
74. *Id.*
75. *Id.* at 80.

NRC I found that there was insufficient scientific knowledge regarding the reliability of calculations based on the Hardy-Weinberg and linkage-equilibrium principles.[76] Accordingly, the report recommended using a conservative method of estimation called the "ceiling principle." The ceiling principle as advocated by *NRC I* theorized that "[t]he multiplication rule will yield conservative estimates, even for a substructured population, provided that the allele frequencies used in the calculation exceed the allele frequencies in any of the population subgroups."[77] The report thus recommended that "databases be tested for agreement with [Hardy-Weinberg] expectations and that loci exhibiting statistically significant differences from the expectation be discarded."[78]

Following publication of *NRC I*, many courts in the United States were hesitant to admit expert testimony regarding DNA frequency estimations based on the product rule.[79] The NRC thus felt compelled to revisit and clarify the role of population genetics in forensic DNA estimates in an additional report published in 1996 ("*NRC II*"). *NRC II* directly addressed the controversial "statistical and population genetics issues in the use of DNA evidence."[80] The report was informed by "[n]ew techniques" and "improvements" in DNA technology, as well as the findings of "extensive" additional studies of population subgroups published during the four years since the 1992 report.[81] These new developments in the field of population genetics led *NRC II* to embrace the use of racial population databases to generate random match probability estimates.

The new report initially acknowledged claims that "the word race is meaningless," that "most [racial] populations are mixed, that the definitions are to some extent arbitrary, and that they are sometimes more linguistic (e.g., Hispanic) than biological," and that "sometimes people select their own [racial] classification."

NRC II nonetheless maintained that the major racial groups in the United States – "white (Caucasian), black (African American), Hispanic, East Asian (Oriental), and American Indian (Native American)"[82] – constituted the principal population groups for genetic study for purposes of "convenience, uniformity, and clarity."[83] The report claimed that the use of racial population reference groups was justified due to the findings of

76. *NRC I*, *supra* note 65, at 80.
77. *Id.* at 76.
78. NATIONAL RESEARCH COUNCIL, THE EVALUATION OF FORENSIC DNA EVIDENCE 97 (1996) [hereinafter "*NRC II*"].
79. *See*, *e.g.*, People v. Barney, 10 Cal. Rptr. 2d 731, 743 (Cal. Ct. App. 1992); *see also* D.H. KAYE, AN INTRODUCTION TO THE SYMPOSIUM ON THE 1996 NRC REPORT ON FORENSIC DNA SCIENCE, *available at* http://www.law.asu.edu/?id=8207 (last visited Sept. 4, 2008) (citing letter from William S. Sessions, Director of the FBI, to Frank Press, President of the National Academy of Sciences, dated April 16, 1993, stating, "Since the release of the report, there have been 30 appellate decisions and in 11 of these, the decision relied on the NRC report [*NRC I*] as a basis for ruling DNA evidence not properly admissible in criminal proceedings."); *NRC II*, *supra* note 78, at 49.
80. *NRC II*, *supra* note 78, at 49.
81. *Id.*
82. *Id.* at 57.
83. *Id.*; *see also id.* at 21-22 (illustrating that geneticists should be "using separate databases for different racial groups").

post-*NRC I* studies of "reproducible differences among the races in the frequencies of DNA profiles in forensic settings,"[84] notwithstanding its admission that other studies had determined that "the variability among individuals *within* a population is greater than that between populations."[85]

NRC II also impliedly rejected the notion of using a general population database on Hardy-Weinberg grounds, stating that "[a]llele frequencies are often sufficiently different between racial groups that it is desirable to have separate databases."[86] At the same time, *NRC II* downplayed concerns of population sub-structuring by stating that "[t]he blending in the melting pot is far from complete."[87] Using the "white population" as an example, the report claimed that white people in the United States "still reflect to a greater or lesser extent their European origins."[88]

The new report thus rejected the ceiling principle advocated by *NRC I* as placing "too much emphasis on formal statistical significance" which could lead to the exclusion of large DNA databases.[89] While admitting that Hardy-Weinberg equilibrium was "hardly ever exactly correct" and could not be strictly satisfied, the report determined that any deviations were sufficiently small as to not substantially effect racial probability estimates.

NRC II concluded that the calculation of racialized DNA profile frequency should be made by applying the product rule, notwithstanding deviations from Hardy-Weinberg equilibrium. The report made two recommendations for the calculation of random match probabilities based on whether the race of the contributor to the DNA sample is known. If the race of the person is known, then *NRC II* recommends using the corresponding racial database to estimate genomic frequency.[90] If the race of the DNA contributor is not known, *NRC II* stubbornly still does not recommend resorting to a general population estimate. Rather, *NRC II* recommends that the analyst provide separate estimates using every racial database.[91] *NRC II* thus provided scientific validation of the existing practice by the FBI and other agencies of utilizing racial DNA databases to calculate random match probabilities.

The assumption underlying the NRC reports is that using the general population as the reference point—as opposed to race—would lead to an overestimation of genetic differences for some DNA profiles, and an underestimation of genetic similarity for other DNA profiles.[92] The calculation of random match probabilities while using a general population

84. *Id.* at 57-58.
85. *See id.* at 22.
86. *NRC II*, *supra* note 78, at 98. However, the report also admitted that "many of the differences [between racial population groups] will be small enough to be practically unimportant."
87. *Id.*
88. *Id.*
89. *Id.* at 97.
90. *Id.* at 97-98.
91. *Id.*
92. *NRC II*, *supra* note 78, at 99.

database would thus be presumably less accurate than estimates that are "narrowed" by race. *NRC II* did not claim that Hardy-Weinberg equilibrium could be achieved in the use of racial databases, but that the use of various other genetic theories and procedures could minimize the impact of deviations from equilibrium.[93] The question, then, is why not utilize those same theories to permit statistically reliable genotype estimates based on a general population database? A potential response based on *NRC II* may be that "[s]ufficient data now exist for various groups and subgroups within the United States that analysts should present the *best* estimates for profile frequencies."[94] But, even if we accept the debatable (and incorrect) proposition that a racialized estimate is "better" than a generalized estimate, it does not mean that legally the racial estimate should be used.

III. THE JUDICIAL RESPONSE TO DNA RACIAL EVIDENCE

The forensic testing of DNA samples, as well as its corresponding statistical interpretation, has been overwhelmingly adjudged to be admissible and trustworthy evidence in the state and federal courts of the United States. Leading legal commentators observe that "[t]he theories behind DNA profiling concerning the structure of DNA are so widely accepted in the scientific world that there are very few attempts to contest their reliability."[95] Many state and federal jurisdictions have gone so far as to allow judges to take judicial notice of the reliability of DNA evidence.[96]

Courts have also largely embraced racialized DNA evidence, accepting without question the folk notion that race is a legitimate biological category. Admittedly, many of the early challenges to the admissibility of DNA evidence concerned the reliability of probability estimates based on racial databases. These cases, however, did not interrogate the validity of using racial databases as opposed to a non-racial general population database. Rather, these cases analyzed whether the racial databases employed by the FBI sufficiently took account of ethnic sub-structuring *within* a particular racial group. The courts thus found themselves immersed in the same controversy that embroiled the population genetics community and that the National Research Council sought to resolve.

a. Early Challenges to DNA Evidence: Accounting for Ethnic Substructuring

A federal district court in Northern Ohio had one of the earliest opportunities to legally assess the use of racial DNA databases to develop random match probability estimates. Prior to the publication of either the

93. *Id.* at 104.
94. *Id.* at 122 (emphasis added).
95. WEINSTEIN'S FEDERAL EVIDENCE § 702.06[5][b] (Joseph M. McLaughlin, ed., 2d ed. 1997) [hereinafter "WEINSTEIN'S FEDERAL EVIDENCE"] (collecting cases).
96. *Id.* (citing United States v. Beasley, 102 F.3d 1440 (8th Cir. 1996); United States v. Jakobetz, 995 F.2d 786, 799 (2d Cir. 1992)).

1992 or 1996 NRC reports, the court in *United States v. Yee*[97] was faced with resolving competing motions *in limine* regarding the admissibility of DNA evidence and random match probability testimony based on racial DNA databases. The case involved a preview of the "battle of the experts" that characterized the debates before the National Research Council, pitting Richard Lewontin against Kenneth Kidd and Bruce Budowle.

The defendants in *Yee*—Wayne Yee, Mark Verdi, and John Ray Bonds—were alleged to have murdered a man they mistakenly believed to be a member of a rival motorcycle gang.[98] While there were no eyewitnesses to the crime, several witnesses reported seeing a "Hispanic-looking" man flee the scene of the crime in a tan-colored van driven by others.[99] The police later found a tan-colored van that contained the gun used in the murder. Both the gun and the van's carpet were splattered with blood. The blood was not that of the victim, but rather was determined to "match" the DNA profile of one of the defendants, John Ray Bonds.[100] The government thereafter sought a pre-trial determination that the DNA "match" evidence was admissible, as well as expert testimony interpreting the meaning of a match through the use of a probability estimate. The defendants filed a corresponding motion to exclude the evidence.

The government sought to introduce evidence at trial that the probability that Bond's DNA profile would be found in the "caucasian population" was only one in thirty-five thousand.[101] The defendants, relying on the expert assistance of Richard Lewontin and other population geneticists, contended that use of the "Caucasian" racial database to create a probability estimate was "flawed because it failed to take into account the likelihood that there is no such thing as an American Caucasian population."[102] The defense argued that the level of population sub-structuring within the Caucasian population was unknown, and that any probability estimates generated using racial databases were therefore too speculative to be scientifically acceptable.[103] Lewontin testified at the pretrial hearing that there was a chance of a substantial understatement in the probability estimate due to the relatively recent arrival of Europeans to America.[104] The government, relying principally on the expert testimony of Kidd, countered that significant sub-structuring within the Caucasian group was unlikely to occur. Even if sub-structuring existed within the population, the government argued that "what substructuring[sic] exists is not a major problem because the frequencies are not that different."[105]

97. 134 F.R.D. 161 (N.D. Ohio 1991), *aff'd.* United States v. Bonds, 12 F.3d 540 (6th Cir. 1993).
98. Bonds, 12 F.3d at 546.
99. *Id.* at 547.
100. *Id.*
101. *Yee*, 134 F.R.D. at 164.
102. *Id.* at 174.
103. *Id.* at 175.
104. *Id.* at 181.
105. *Id.* at 186.

The Northern District of Ohio adopted the conclusions made by the magistrate judge, which recommended that the evidence of a DNA "match" and corresponding probability estimate be found admissible under the *Frye* standard of general acceptance for scientific evidence.[106] The court simply found government's experts (Kidd and Budowle) to be more persuasive than the defense experts (Lewontin) on the issue of whether the scientific community had generally accepted the method of creating racialized probability estimates.[107] The Sixth Circuit later affirmed the district court's holding, stating that concerns of population sub-structure within a racial group "go[ ] to the weight of the evidence, not its admissibility."[108]

While the *Yee* case was decided under the *Frye* standard for assessing scientific evidence, the Ninth Circuit later clarified that DNA racial evidence was similarly admissible under the then-new *Daubert* framework.[109] The court in *United States v. Chischilly*[110] addressed a challenge to the admissibility of DNA "match" and probability evidence. The defendant—a Native-American member of the Navajo tribe—was found guilty by the district court of rape and murder after evidence was admitted that there was a DNA match between the sample provided by the defendant and that found at the crime scene. A government expert testified at trial that the probability of a similar match between the DNA of another Native-American and the DNA found at the crime scene was 1 in 2,563.[111] The defendant argued on appeal that the DNA match evidence was unreliable under *Frye* since the FBI method for determining statistical probability was not generally accepted in the scientific community. In particular, the defendant argued that sub-structuring within the Native-American population invalidated the FBI's use of the product rule and the Native-American racial database. The defendant also argued that the Native-American database was inadequate to generate an accurate statistical estimate since it did not contain enough DNA profiles of Navajos, a sub-population of the larger Native-American racial group.

The Supreme Court displaced the *Frye* standard in favor of the *Daubert* framework during the pendency of the appeal, and the Sixth Circuit thus analyzed whether admission of the DNA evidence was erroneous under the new legal standard. The court held that both the DNA match evidence and the racial probability estimate satisfied the new *Daubert* test for

106. Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).
107. *Yee*, 134 F.R.D. at 165-66.
108. *Bonds*, 12 F.3d at 564.
109. *Frye*, 293 F. 1013, created the *Frye* test, which required that the party asserting scientific evidence establish that the theory and method used by the expert witness were generally accepted within the relevant scientific community. Seventy years later, the United States Supreme Court, in *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993), determined that FED. R. EVID. 702 had superseded the *Frye* test, and described new factors to be used in determining the admissibility of novel scientific evidence. Many states use *Daubert*, or a similar test (*see, e.g.*, Green v. Cessna Aircraft Co., 673 A.2d 216 (ME 1996)), although some states continue to apply the *Frye* test (*see, e.g.* People v. Wooten, 2001 WL 456790 (N.Y. App. Div. 2001)), and still others have not rejected *Frye*, but apply the *Daubert* factors.
110. 30 F.3d 1144 (9th Cir. 1994).
111. *Id.* at 1149.

scientific evidence.[112] Taking note of the "raging controversy in the scientific community over DNA testing," the court acknowledged that the DNA evidence in the case might be excluded under the old *Frye* test of general acceptance.[113] Nonetheless, the court held that the DNA profiling involved in the case passed *Daubert's* "more liberal admissibility test."[114]

The *Yee* and *Chischilly* decisions established the admissibility of racial probability estimates under the Federal Rules of Evidence. The declaration that concerns over possible intra-racial population sub-structure went to the weight of the evidence rather than its admissibility would soon become a familiar refrain in state and federal case law.[115]

b. The California Cases: From *Pizarro* to *Wilson*

The state courts of California have widely been regarded as being at the vanguard of addressing the complex legal issues arising from the introduction of DNA racial evidence.[116] Following the publication of *NRC I*, the California Court of Appeals initially rejected the introduction of random match probability estimates based on racial DNA databases. In *People v. Barney*, the court deemed inadmissible racial probability estimates interpreting DNA match evidence based on the lack of general acceptance in the scientific community over use of the product rule.[117] Applying its state's version of the *Frye* general acceptance test, the court noted the substantial controversy in the scientific community surrounding the selection of reference population groups and the application of the product rule in interpreting DNA match evidence, as reflected by *NRC I* and the public debates between Richard Lewontin/Daniel Hartl and Kenneth Kidd/Ranajit Chakraborty.[118] The court specifically noted the opinions of Richard Lewontin and Daniel Hartl that it is "inappropriate to use broad data bases to which all Caucasians, Blacks, and Hispanics may be referred for estimating frequencies."[119] The court accordingly held that "the determination of the statistical significance of a match" using racial databases

112. *Id.* at 1153.
113. *Id.* at 1155.
114. *Id.* at 1156.
115. *See, e.g.*, United States v. Santiago, 156 F.Supp.2d 145 (D.P.R. 2001) (finding racialized DNA probability estimate admissible under *Daubert* and rejecting ethnic substructuring argument that the FBI's Hispanic racial database was unreliable for failing to adequately account for "Puerto-Rican DNA"); Virgin Islands v. Byers, 941 F.Supp. 513 (D.V.I. 1996) (holding that the racialized DNA probability estimate provided by Dr. Bruce Budowle—chief of the FBI Forensic Research Institute—was admissible under *Daubert* and rejecting the defendant's argument that the FBI's "black" racial database failed to account for Afro-Caribbean sub-structuring); United States v. Coronado-Cervantes, 912 F.Supp. 497 (D.N.M. 1996) (finding racialized DNA probability estimate admissible under *Daubert* and rejecting defense argument that FBI's Native-American racial database was unreliable for failing to account for tribal sub-structuring); Virgin Islands v. Penn, 838 F. Supp. 1054 (D.V.I. 1993) (holding that racialized DNA probability estimate was reliable under *Daubert*, notwithstanding the defendant's argument that the FBI's "black" racial database failed to account for a Caribbean black sub-population).
116. *See, e.g.*, KAYE, *supra* note 79.
117. 10 Cal. Rptr. 2d 731 (Cal. Ct. App. 1992).
118. *Id.* at 733.
119. *Id.* at 740.

had not been generally accepted in the scientific community, and thus was inadmissible at trial.[120]

As previously noted,[121] the publication of *NRC II* was in large part inspired by the growing post-*NRC I* rejection of racial DNA evidence by state courts such as *Barney*. The *NRC II* report thus sought to clarify the debate surrounding population genetics, and to facilitate the judicial admission of racial probability estimates in future criminal trials. *NRC II* was incredibly successful in achieving its goals, and by 1999 the Supreme Court of California effectively overruled *Barney* by ruling that racial DNA probability estimates were admissible evidence. The court held in *People v. Soto* that the use of an unmodified product rule in calculating racial probability estimates had since gained general acceptance in the scientific community, as reflected by *NRC II*.[122]

As in the vast majority of state and federal jurisdictions around the United States, racial DNA probability estimates were largely accepted as admissible and reliable evidence.[123] Defense arguments based on intra-racial ethnic sub-structuring were largely shot down,[124] allegations of laboratory contamination were mostly unsuccessful, and calls for the use of a non-racial general population database were either unmade or ignored. The nearly automatic judicial admission enjoyed by racial DNA probability estimates, however, would be interrupted in 2003 by a key California state case.

The California Court of Appeals determined in *People v. Pizarro* that racial DNA probability estimates were inadmissible when the race of the perpetrator is unknown.[125] In *Pizarro*, the defendant was convicted of murder and rape following the introduction of DNA evidence indicating that there was only a 1 in 250,000 probability that another "Hispanic" person contributed the DNA sample found on the victim's body.[126] The defendant initially appealed on the grounds that the use of an unmodified product rule was not yet generally accepted, but the appeal was rejected based on the holding in the recent *Soto* decision.[127] The defendant next appealed on the grounds that, *inter alia*, evidence of the Hispanic profile estimate was improperly admitted without first establishing that the perpetrator was Hispanic.[128]

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120. *Id.*
121. *See NRC II, supra* note 78.
122. 981 P.2d 958, 960 (Cal. Ct. App. 1999) (explaining that expert testimony admitted that there was only a 1 in 189 million chance of a random "Hispanic" person sharing the same DNA profile as that of the defendant).
123. *See, e.g.*, United States v. Shea, 159 F.3d 37, 41 (1st Cir. 1998); United States v. Lowe, 145 F.3d 45, 51 (1st Cir. 1998); United States v. Johnson, 56 F.3d 947 (8th Cir. 1995); Virgin Islands v. Penn, 838 F. Supp. 1054, 1073-74 (D.V.I. 1993).
124. *See, e.g.*, United States v. Santiago, 156 F. Supp.2d. 145, 150 (D.P.R. 2001); United States v. Coronado-Cervantes, 912 F. Supp. 497, 501 (D.N.M. 1996) (finding that intertribal differences were "at best equal to that of ethnic populations within a broad racial group" and such differences did "not result [in] a wrong forensic inference").
125. 3 Cal. Rptr. 3d 21 (Cal. Ct. App. 2003).
126. *Id.* at 38.
127. *Id.* at 101.
128. *Id.* at 40.

The court agreed with the defendant that the prosecution had presented an "insufficient *evidentiary foundation*" to warrant the admission of the racialized DNA probability estimate.[129] The court chastised the lower court for improperly assuming "that *defendant was in fact the perpetrator* and that defendant's traits therefore could be relied upon to provide or clarify those traits of the perpetrator forming the basis of the DNA evidence."[130] This assumption, according to the court, violated the defendant's presumption of innocence.[131]

Furthermore, the relevant reference population from which to derive a probability estimate was the perpetrator's population and not the defendant's population.[132] The relevance of the DNA evidence at issue depended on first establishing as a preliminary fact that the perpetrator shared the same racial group as that of the defendant. The probability estimate presented in court that only one in 250,000 Hispanics would share the same DNA profile as that of the defendant was *conditionally relevant* only upon first demonstrating that the perpetrator was also Hispanic. Since there was no evidence presented regarding the race of the perpetrator, the racial probability estimate was erroneously admitted at trial.[133] The court keenly observed that what may be scientifically relevant may not be legally admissible.[134]

The *Pizarro* court further faulted racial probability estimates for "unfairly and unjustifiably encourag[ing] the jurors to focus on ethnicity and race—specifically the ethnicity and race of the defendant, the only suspect before them."[135] The court articulated three methods of presenting relevant probability estimates: "(1) establish that the perpetrator more likely than not belongs to a particular ethnic population, then present only the frequency in that particular ethnic population; (2) present only the most conservative frequency, without mention of ethnicity; or (3) present the frequency in the general, nonethnic population."[136]

The reasoning of the California Court of Appeals in *Pizzaro* was soon rejected by the Supreme Court of California in *People v. Wilson*.[137] In *Wilson*, the defendant was convicted of murder after DNA match and probability evidence were admitted at trial.[138] An expert testified that the

129. *Id.* at 29.
130. *Id.* at 30.
131. *Id.* at 32 (noting that the lower court and prosecution presumed "that because the defendant possesses certain traits, the perpetrator also possesses those traits.").
132. *Id.* at 30 (the "purpose of the statistical evidence is to establish *how few people* in the relevant population genetically match the perpetrator. The relevant population is the population of possible perpetrators – the *perpetrator's* population.").
133. Notably, the defendant in the *Pizzaro* case was described as being "half Hispanic and half Caucasian." *Id.* at 98. In situations involving mixed-race persons, the forensic expert typically calculates a probability estimate using the racial database that is less detrimental to the defendant.
134. *Id.* at 29 ("This case demonstrates how DNA evidence brings to the fore the distinction between science and law. In the criminal legal setting, theoretical conclusions inherent to scientific discourse have different consequences.").
135. *Id.* at 105.
136. *Id.* at 105 n.85.
137. 136 P.3d 864 (Cal. 2006).
138. *Id.* at 866.

defendant's DNA profile (which matched the crime-scene samples) could be expected to occur in "one of 96 billion Caucasians, one of 180 billion Hispanics, and one of 340 billion African-Americans."[139] Notably, while the defendant was described as a "light skinned Black man," the defendant's DNA profile was actually more prevalent in both the "Caucasian" and "Hispanic" racial populations according to the estimates admitted at trial.[140] The defendant appealed his conviction on the *Pizarro* grounds that the prosecution had failed to lay a sufficient foundation by demonstrating the likely race of the perpetrator.

The California Supreme Court held that the racial probability evidence was properly admitted. The court assumed without question that racial databases are necessary to base probability estimates due to the significant genetic variability among the major racial groups.[141] The court agreed with *Pizarro* that the relevant reference population group is the "entire class of plausible perpetrators" and not simply that of the defendant.[142] The court, however, rejected *Pizarro's* finding that any evidence of DNA ethnic frequency is irrelevant in the absence of sufficient evidence of the perpetrator's race.[143] Relying on *NRC II*, the court held that even when the race of the perpetrator is unknown, providing the genome frequencies for each racial group is still relevant for interpreting the rarity of that DNA profile.[144]

The *Wilson* court similarly rejected the *Pizarro* court's concerns that racialized probability estimates could prejudice the defendant. The court believed that the presentation of probability estimates for each of the three major racial groups adequately diminished any such prejudice, as the "focus is removed from the race of the defendant."[145] In evaluating the prejudice inherent in bringing race into the courtroom, the court notably cited the need to present racial probability estimates given the "objectively established physical differences among racial populations."[146]

The California decisions reflect the judicial embrace of racial DNA probability estimates and its concomitant belief in the biology of race. While the *Pizarro* court removed the veil long enough to reflect on the inherent irrelevancy and prejudice of racial DNA probability estimates, the *Wilson* court chose to sheepishly follow the lead of the majority of federal and state courts and ascribe to a biological conception of racial difference.

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139. *Id.* at 867.
140. *Id.* at 868.
141. *Id.*. at 867.
142. *Id.* at 868 (quoting D.H. KAYE, *Logical Relevance: Problems with the Reference Population and DNA Mixtures in* People v. Pizarro, 3 LAW PROBABILITY & RISK 211 (2004)).
143. *Wilson*, 136 P.3d at 869.
144. *Id.* (quoting *NRC II* as recommending that "[i]f the race is not known or if the population is of racially mixed ancestry, the calculations can be made with each of the appropriate databases and these presented to the court").
145. *Id.* at 870-71.
146. *Id.* at 871 (quoting the concurring opinion of Justice Pollak in the underlying Court of Appeals case, 21 Cal. Rptr. 3d 102, 113 (Cal. Ct. App. 2004)).

IV. THE INADMISSIBILITY OF DNA RACIAL EVIDENCE

There has long been an intoxicating allure to conceiving of race as a stable and natural biological truth. From Linnaeus to Blumenbach, from pre-modern anthropologists to nineteenth century physiognomists, and from the pre-World War II eugenicists to some modern geneticists, science has provided pseudo-empirical backing to folk notions about the fixed and immutable nature of race. That race is a *social construction*, developed over time to justify the unequal treatment of non-white human groups based on supposed human difference, has been conclusively established by both social scientists (see *supra* Part I) *and* natural scientists (see *supra* Part III). The belief, supposedly confirmed by genetic science, that "race" has a discernable biological essence clearly conflicts with modern race theory.

So why then are geneticists, prosecutors, and law enforcement still insisting upon a biological conception of race? Why have our courts largely failed to interrogate the shaky legal ground upon which racial DNA probability estimates rest? Why have population geneticists and the FBI chosen to rely on racial DNA databases to form random probability estimates rather than a general, non-racial DNA database?

One answer to these questions lies in the enduring folk appeal and historical pedigree of understanding race to represent a natural and biologically-based method of human categorization. Our society's judges, lawyers, prosecutors, and geneticists are all deeply susceptible to culturally learned assumptions about race and racial taxonomy. Similar to the nineteenth-century race scientists, cultural attitudes continue to unconsciously shape the manner in which many people interpret race. The racial classification scheme adhered to by the United States—generally recognizing the three "major racial groups" of Caucasian, Black, and Hispanic that form the basis of the FBI's racial DNA databases—is neither universal nor scientifically mandated. The world maintains varying conceptions of both the meaning of race and the number of races. While in the United States people are generally categorized as White, Black, Hispanic, or Asian, there exist hundreds of racial categories in other countries such as Brazil. Whereas a light-skinned person may be categorized as Black in the United States based on a historical adherence to hypodescent rules,[147] that same person may be racially categorized as White in India or Africa. The very malleability of race in the global context undermines any claim that there is some legal or scientific basis for racially categorizing DNA samples.

The desire to maintain systems of racial differentiation is deeply rooted to an often unspoken and unconscious need to preserve racial hi-

147. The term "hypodescent" refers to the social practice of classifying the race of a "mixed person" by reference to the race of their socially subordinate parent. As F. James Davis explains, "[i]n the South it became known as the 'one-drop rule,' meaning that a single drop of 'black blood' makes a person a black. It is also known as the 'one black ancestor rule,' some courts have called it the 'traceable amount rule,' and anthropologists call it the 'hypo-descent rule,' meaning that racially mixed persons are assigned the status of the subordinate group." F. JAMES DAVIS, WHO IS BLACK? ONE NATION'S DEFINITION 5 (1991) (citations omitted).

erarchy and privilege.[148] After all, what becomes of racial hierarchy if there are no racial categories? Using science to interpret racial difference and validate folk notions of the supposed fixed nature of race inevitably protects "whiteness" and the racial status quo. The historical development of the race concept[149] demonstrates how the science of racial difference has long been used to establish the genetic, cultural, and moral bases of white superiority and non-white inferiority.

It is unsurprising, though disappointing, that the specter of nineteenth century "race science" has reappeared in the criminal context with the modern use of racial DNA probability estimates. Non-whiteness, and more specifically blackness, has been closely linked to criminality as part of a broader project of non-white racial oppression: "the prevailing image of Blackness as something loathsome, marginal, and deviant—the criminalblackman—persists."[150] Professor Frank Rudy Cooper summarizes the historical racist linkage of blackness with criminality as follows:

> Early European observers linked blackness to criminality. During United States chattel bondage, states criminalized the very property of being black. That resulted in an association of blackness with a criminal propensity. The success of the notion that blacks are inherently criminal was seen in white people's panic over the possibility of crime waves by recently freed blacks. With respect to black men, the image of black criminality merges with the myth of black men has having unrestrained sexuality to form the image of black men as incipient rapists.[151]

The continued judicial acceptance of racialized DNA random match probability estimates reinforces this connection between non-whiteness and criminality. As racial difference is interpreted as genetically meaningful and discernable through DNA testing, racial probability estimates admitted against non-white criminal defendants provide a "scientific" testament to deep-seated associations of blackness with criminality and biological inferiority.

Random match probability estimates based on race are simply irrelevant, unreliable and unfairly prejudicial in the state and federal courts of the United States. The heretofore judicial embrace of racialized probability estimates reflects an unyielding protection of whiteness as a meaningful genetic category rather than an arbitrary social construction. While this racial project should not be given legal acceptance on normative grounds, it is similarly objectionable under many of the doctrinal rules of federal evidence.

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148. Charles R. Lawrence, *The Id, the Ego and Equal Protection: Reckoning with Unconscious Racism*, 39 STAN. L. REV. 317, 322 (1987).

149. *See* Part I, *supra*.

150. Katheryn Russell-Brown, *Black Protectionism as a Civil Rights Strategy*, 53 BUFF. L. REV. 1, 3 (2005).

151. Frank Rudy Cooper, *Against Bipolar Black Masculinity: Intersectionality, Assimilation, Identity Performance, and Hierarchy*, 39 U.C. DAVIS L. REV. 853, 877-78 (2005); *see* N. Jeremi Duru, *The Central Park Five, the Scottsboro Boys, and the Myth of the Bestial Black Man*, 25 CARDOZO L. REV. 1315 (2004).

The determination of whether scientific evidence is admissible is entrusted to the trial judge as part of its "gatekeeping" role, as elucidated by the United States Supreme Court in the seminal *Daubert v. Merrell Dow Pharmaceuticals, Inc.* case.[152] The *Daubert* court stressed that the trial judge must screen scientific evidence prior to its presentation to the jury, to ensure that such evidence is relevant, reliable, and not unfairly prejudicial.

a. The Irrelevance of DNA Race Science

Scientific evidence is admissible in the courts of the United States so long as it is relevant.[153] Relevancy is defined as "evidence having any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence."[154] Relevant evidence has also been interpreted as involving an alteration of "the probabilities of a proposition to be proved."[155] As such, one "test for determining relevance is whether the proffered evidence could reasonably affect an assessment of the probability of the fact to be inferred."[156] Applying the language of Federal Rules of Evidence 401 and 402 to the current issue, it is clear that racial random match probability estimates should be deemed irrelevant evidence. The provision of a racial probability estimate in court does not make the identification of the defendant as the criminal perpetrator any more likely than if the only statistical evidence presented was a probability estimate relying on the general population as a reference point. Put another way, a racial probability estimate does not *reasonably* affect the trier of fact's assessment of the defendant's guilt. The courts have sidestepped the crucial threshold issue of whether racial differentiation within the general population provides any reasonably relevant information. Race is simply not a relevant criterion for assessing genomic frequencies, as it does not alter the probability of a defendant's guilt in any reasonable way.

The use of distinct racial DNA databases was initially understood to be a seemingly natural way to account for genetic differentiation within the general population. Population geneticists, relying on their own cultural understanding of race, assumed that there were scientifically observable genetic differences between the three "major racial groups" in the United States and then sought out to validate those assumptions. Accordingly, the major racial groups were soon regarded as the proper reference populations for basing probability estimates using the product rule. The fear was that the use of the general population as a reference point would lead to an underestimation of the frequency of a DNA profile. As explained by *NRC I*:

152. 509 U.S. 579 (1993).
153. FED. R. EVID. 402; *see also* FED. R. EVID. 702 (scientific evidence must "assist the trier of fact to understand the evidence or to determine a fact in issue").
154. FED. R. EVID. 401 (defining "relevant evidence").
155. WEINSTEIN'S FEDERAL EVIDENCE, *supra* note 95, at § 401.04(2)(b), at 401-21.
156. *Id.* ("The question to be asked in determining the relevance of evidence is whether a reasonable person might believe the probability of the truth of the consequential fact to be different if that person knew of the proffered evidence.")

> If a population survey of Europe showed that 1 of 10 people had blond hair, 1 of 10 had blue eyes, and 1 of 10 had fair skin, one would be wrong to multiply these frequencies to conclude that the frequency of people with all three traits was 1 in 1,000. Those traits tend to co-occur in Nordics, so the actual frequency of the combined description is probably higher than 1 in 1,000. In other words, the multiplication rule can produce an underestimate in this case, because the traits are correlated owing to population substructure—the traits have different frequencies in different population groups.[157]

A racial probability estimate is therefore often assumed to be more statistically accurate than a general probability estimate. Putting aside for the moment questions regarding the scientific validity of this assumption (see *supra* Parts II and III), it is nonetheless clear that racial probability estimates do not alter the "probabilities" in any *legally* significant or relevant manner. The small difference between a racial probability estimate (e.g., 1 in 50 billion) and a general probability estimate (e.g., 1 in 200 billion) is legally insignificant. The *Pizarro* court was aware of the distinction between scientific significance and legal relevance:

> This case demonstrates how DNA evidence brings to the fore the distinction between science and law. In the criminal legal setting, theoretical conclusions inherent to scientific discourse have different consequences. What may be an intellectual discussion in the scientific setting becomes the basis for the deprivation of a person's liberty in the legal setting.[158]

Modern forensic DNA typing is capable of generating general probability estimates in the billions,[159] eliminating any need to provide a purportedly narrower racial estimate to juries. The National Commission on the Future of DNA Evidence has already endorsed the replacement of separate racial databases with a single general population database to develop probability estimates:

> It is already apparent that most of the STR variability is within groups. Although groups differ, the mean differences between groups are less than the individual differences within groups; profiles that are rare in one group tend to be rare in others. With enough loci it may be possible to have a single database for all the major groups in the United States.[160]

As modern forensic DNA analysis now uses 13 STR loci in the CODIS system, astronomical probability estimates are now possible using just the general population as the reference point. The FBI's Bruce Budowle

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157. *NRC I*, *supra* note 65, at 76.
158. People v. Pizarro, 3 Cal. Rptr. 3d 21, 29 (Cal. Ct. App. 2003).
159. Bruce Budowle et al., *Source Attribution of a Forensic DNA Profile*, 2 FORENSIC SCI. COMMC'NS. 3 (2000), *available at* http://www.fbi.gov/hq/lab/fsc/backissu/july2000/source.htm.
160. NATIONAL COMMISSION ON THE FUTURE OF DNA EVIDENCE, NATIONAL INSTITUTE OF JUSTICE, THE FUTURE OF FORENSIC DNA TESTING: PREDICTIONS OF THE RESEARCH AND DEVELOPMENT WORKING GROUP 27 (2002), *available at* http://www.ncjrs.gov/pdffiles1/nij/183697.pdf.

noted in 2000 that the "average random match probability for unrelated individuals for the 13 STR loci is less than one in a trillion, even in populations with reduced genetic variability."[161] Dr. Budowle further explained that a DNA "profile would be considered rare whether it had an estimated frequency of 1/5,000,000, 1/50,000,000, or 1/500,000,000. Obviously, the difference in the rarity of such estimates would have little consequence in a forensic context."[162]

Moreover, expert witnesses testifying in court have often acknowledged the insignificance of differences in probability estimates. The population geneticist Kenneth Kidd, while generally in favor of using racialized estimates, admitted in the *Soto* case that "any difference in estimates over one in a million was pragmatically meaningless."[163] An expert in the *Wilson* case similarly observed that a DNA random match probability estimate "would be a 'pretty discriminating number' no matter what population data base was used."[164]

The racial probability estimates admitted in *Wilson* illustrate the problem of legal irrelevancy. In *Wilson*, expert testimony was admitted that stated that the defendant's DNA profile would occur in "one of 96 billion Caucasians, one of 180 billion Hispanics, and one of 340 billion African Americans."[165] Therefore the defendant's genetic profile would be slightly more common in Caucasians than in African Americans. However, the defendant was described by the court and witnesses as being a "light-skinned Black man."[166] This mismatch between the identified race of the defendant and the racial probability estimates presented at trial demonstrates the inherent irrelevancy of using race in forensic DNA analysis. The racial probability estimates admitted in *Wilson* simply did not add anything relevant to the analysis.

The *Wilson* court, while not acknowledging the mismatch, nonetheless observed that "as the science underlying DNA comparisons continues to improve, the practical significance of the different racial frequencies diminishes."[167] The court stated that whether the jury focused on the probability estimate most favorable to the defendant (e.g., the Caucasian estimate of one in 96 billion) or the estimate most damaging to the defendant (e.g., the African-American estimate of one in 340 billion) "is of little moment."[168] The court reasoned that "[s]ince there are no more than 7 billion people on the planet, it is rather unlikely, to say the very least, that a jury's evaluation of the significance of the match between defendant's DNA and the crime scene DNA would differ whether the jury focuses on

161. Budowle, *supra* note 159, at 3.
162. Bruce Budowle & Kenneth L. Monson, Accepted Practices by the Forensic DNA Community Supported by NRC II Report, http://www.promega.com/geneticidproc/ussymp7proc/0703.html (last visited Apr. 1, 2009).
163. People v. Soto, 981 P.2d 958, 973 (Cal. 1999).
164. *Wilson*, 136 P.3d at 867.
165. *Id.*
166. *Id.* at 868.
167. *Id.* at 871 (quoting Justice Pollak's concurring opinion in the lower court decision *People v. Wilson*, 124 Cal. App. 4th 38, 54 (Cal. App. 1st Dist. 2004)).
168. *Id.* at 872.

1 in 96 billion, 1 in 340 billion, or any number in between, as the likelihood of a random match with another person."[169]

Race is an irrelevant legal concept when assessing criminal guilt based on genetic analysis. Probability estimates relying on a general population database are sufficiently accurate to eliminate any need for a supposedly more accurate estimate using race. Simply put, a random match probability estimate relying on race does not reasonably make the identification of the perpetrator any more probable or assist the trier of fact.

b. The Unreliability of DNA Race Science

Scientific evidence, such as DNA probability estimates, must also be deemed to be "reliable" under *Daubert* and the federal rules of evidence in order to be admissible. The *Daubert* court suggested a number of nonexclusive factors to consider when assessing reliability: (1) whether the expert's technique or theory can be or has been tested; (2) whether the technique or theory has been subject to peer review and publication; (3) whether the technique or theory has been generally accepted in the relevant scientific community; (4) the potential rate of error for the technique or theory; and (5) whether adequate standards or controls exist and were followed.[170]

The vast majority of federal and state courts routinely hold racial DNA probability estimates to be reliable in the scientific community. The science underlying DNA profiling, even when utilizing racial databases, has been held reliable by the courts for nearly twenty years. As such, most courts readily accept racial DNA evidence as reliable on the basis of past precedent. The *Pizarro* court observed that "[t]he question of general scientific acceptance may be answered by prior case law: 'Once a trial court has admitted evidence based upon a new scientific technique, and that decision is affirmed on appeal by a published appellate decision, the precedent so established may control subsequent trials, at least until new evidence is presented reflecting a change in the attitude of the scientific community.'"[171]

Despite the continued judicial reliance on precedent, it is clear that the majority of geneticists have determined that race has no biological meaning. Geneticists have conclusively established that great genetic variation occurs *within* so-called "racial" population groups.[172] Various population geneticists have demonstrated that "allele frequency comparisons among human populations rarely show discontinuities that map onto racial boundaries,"[173] and that there is no scientific basis for a division of humans into genetically defined groups. Even Kenneth Kidd, an ardent supporter of using racial databases to calculate genomic frequency, has

169. *Id.* (quoting Justice Pollack's concurring opinion in the lower court decision, *People v. Wilson*, 124 Cal. App. 4th at 54).
170. *Daubert*, 509 U.S. at 593-94; *see also* FED. R. EVID. 702 advisory committee's notes.
171. *See, e.g.*, *Pizarro*, 3 Cal. Rptr. 3d. at 42 (quoting People v. Kelley, 17 Cal. 3d. at 32).
172. *See* Ossorio & Duster, *supra* note 4, at 116 (2005); Feagin & Feagin, *supra* note 34 at 32; UNESCO, FOUR STATEMENTS ON THE RACE QUESTION 36-49 (1969); Madrigal & Barbujani, *supra* note 5, at 21 (citing studies); see also *NRC I*, *supra* note 65, at 12.
173. Ossorio & Duster, *supra* note 4, at 116 (citing genetic studies).

admitted that there is "a virtual continuum of genetic variation" throughout the world, and that "there's no such thing as race in . . . *Homo sapiens*."[174]

The National Research Council in its 1996 report *endorsing* the use of racial databases, nonetheless admitted that "some assert that the word *race* is meaningless," that "most [racial] populations are mixed, that the definitions are to some extent arbitrary, and that they are sometimes more linguistic (e.g., Hispanic) than biological," and that "people often select their own [racial] classification."[175] *NRC II* also acknowledged that the "variability among individuals *within* a [racial] population is greater than that between populations."[176] Furthermore, most courts fail to understand the distinction between "race" (a social construction devoid of genetic meaning) and differences in phenotype or ancestry (which are not per-se encoded with racial meaning). As the anthropological geneticists Lorena Madrigal & Guido Barbujani state, it is "[a] widespread misconception is that the analysis of morphological traits, such as skeletal measures or skin colour, demonstrates a clear racial subdivision of humankind."[177] The FBI, some geneticists, and the courts have readily assumed that there has been some consensus on the meaning and number of each racial category. "As our troubled history of race science demonstrates, scientists at various times have estimated the number of human races to be as little as three and as many two hundred."[178] Modern genetic studies continue to rely on different assumptions regarding the number of races.[179] The presentation of probabilistic estimates derived from racial databases must be viewed as unreliable if the definition of race itself remains unsettled. "If races are biological realities, they must be the same everywhere, whereas forensic race catalogues differ across countries."[180]

Recent scientific studies have also indicated that the racial population groups within the United States are genetically admixed, and should not be represented as genetically homogeneous and distinct groups.[181] *NRC I* thus noted that there were scientific concerns that:

> [The] census categories—such as North American Caucasians, blacks, Hispanics, Asians, and Native Americans—are not homogeneous groups, but rather that each group is an admixture of subgroups with somewhat different allele frequencies. Allele frequencies have not yet been homogenized, because people tend to mate within their subgroups.[182]

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174. Eliot Marshall, *DNA Studies Challenge the Meaning of Race*, 282 SCIENCE 654, 654 (Oct. 23, 1998).
175. *NRC II* at 57; *see also supra* Part I.
176. *Id.* at 21 (emphasis added).
177. *Id.* at 20.
178. *See* Sundquist, *supra* note 7.
179. *Id.*
180. Madrigal & Barbujani, *supra* note 5, at 27.
181. *Id.* at 31 (collecting studies).
182. *NRC I*, *supra* note 65, at 12.

The anthropological geneticists Lorena Madrigal and Guido Barbujani conclude that "it is impossible to claim that a discontinuous population structure with well-identified clusters has emerged so far. . . ."[183] These scientists also point out that most of the population genetics studies rely on DNA sampling based on "diverse" population groups which merely reflected folk conceptions of race.[184]

One could also argue, with a straight face, that such racial estimates are not generally accepted if we re-define the relevant scientific community. The scientific community identified as relevant by most courts is that of population geneticists.[185] While the conclusions of population geneticists surely are an important consideration, so are the findings of sociologists and anthropologists regarding the nature of "race." As examined in Part I of this Article, the overwhelming consensus of sociologists and anthropologists maintains that "race" is a socio-political construction devoid of any biological meaning. If the courts were to expand their consideration of the relevant scientific community to include social scientists such as sociologists and anthropologists, the error in ascribing genetic content to a malleable concept such as race would soon become clear.

The methodology underlying the creation of racial probability estimates of genome frequency is similarly troublesome. Initially, it must be noted that the racial genome estimates violate both the Hardy-Weinberg and linkage-equilibrium principles of population genetics. The Hardy-Weinberg principle requires that allele frequencies be stable within a population before allowing for application of the product rule. The absence of population sub-structuring is therefore a necessary prerequisite to allowing for probability estimates using the product rule.[186] Given that most human genetic variation occurs intra-racially, Hardy-Weinberg equilibrium is simply not possible in the context of racial probability estimates.[187] The treatise *Weinstein's Federal Evidence* summarizes the dangers of not adhering to the Hardy-Weinberg principle:

> Another consideration is that the method of computing the probability may not be very reliable under certain circumstances. The trial court, in making its reliability determination, needs to recognize that the random probability evidence is dependent on the assumption that it is scientifically legitimate to multiply together the probabilities of each of the eight or 10 DNA strands from each of the four or five locations on the DNA helix. The legitimacy of the performance of that multiplication, by which the astronomically small numbers are obtained, depends on the assumption that each of the characteristics represented by each of the DNA strands is genetically and statistically independent of the other. That assumption may not be appropriate for certain cul-

183. Madrigal & Barbujani, *supra* note 5, at 25.
184. *Id.* at 26.
185. *See generally Bonds*, 12 F.3d at 565; *Yee*, 134 F.R.D. at 181.
186. *See supra* Part III.
187. *See NRC II*, *supra* note 78, at 97 (admitting that Hardy-Weinberg equilibrium was "hardly ever exactly correct" and could not be strictly satisfied).

tural groups or sub-populations included within the population data base.[188]

A second *Daubert* reliability concern lies in the lack of an empirical method to classify DNA samples by race. Racial categorization is a social practice, and the construction of race is dependent on many variables such as skin color, phenotype, language, dress, and racial performance. It is simply unclear how the DNA samples used in racial databases are racially categorized. There are two basic methods to determine race: self-reported or other-ascribed racial identification.[189] Are the DNA samples classified by race according to the self-identification of the person providing the sample? Or is the race of that same person subjectively determined by an outsider? If so, what racial criteria does that outsider rely on?

The DNA samples contained in racial databases originate from a variety of sources. Many of the DNA samples are obtained from "anonymous donors at blood banks and paternity testing labs,"[190] others are obtained from persons convicted of certain felonies,[191] and still other DNA samples were collected from FBI agents.[192] The methodology employed to classify the race of these DNA samples, however, remains unclear.[193]

Assuming that the DNA samples are racially classified on the basis of self-identification does not support a determination of reliability. A loosely-based "methodology" centered around subjective self-identification simply does not pass muster under the stringent demands of *Daubert* and Federal Rule of Evidence 702. Racial self-identification, after all, is a deeply personal question of identity formation that depends on a number of social and cultural variables. For instance, in the United States cultural attitudes towards hypodescent and the "one-drop rule" may lead many light-skinned African-Americans to identify as "black" even if they are "light, bright, and damn near white."[194] Similarly, evolving conceptions of race mean that there is no guarantee that a "mixed" person will automatically identify as non-white as opposed to white. One person may self-identify as black in America, yet the same person may identify as white in Brazil. Even if we disregard these not so extreme examples of racial identification, many persons who fit within a stereotypical racial

188. WEINSTEIN'S FEDERAL EVIDENCE, *supra* note 95, at §702.06[5][b] at 702-148-49 (citing to United States v. Chischilly, 30 F.3d 1144 (9th Cir. 1994)).

189. *See, e.g.*, Christopher A. Ford, *Administering Identity: The Determination of "Race" in Race-Conscious Law*, 82 CAL. L. REV. 1231, 1239 (1994).

190. *Byers*, 941 F. Supp. at 520.

191. DNA Act of 2000, 42 U.S.C.A. §§ 14135-36 and 10 U.S.C.A. § 1565.

192. *See Bonds*, 12 F.3d at 550 ("[b]y conducting DNA studies on FBI agents, the FBI has developed a table of DNA allele frequencies for each of three racial groups – caucasian, black and hispanic . . . "); Jakobetz, 955 F.2d at 793.

193. Some population genetics studies rely on either other-ascribed or self-reported racial identification. *See* Madrigal & Barbujani, *supra* note 5, at 26 (citing studies). Other studies that rely on blood bank DNA samples tend to rely on self-reported race. *See, e.g.*, Peter M. Vallone, Amy E. Decker & John M. Butler, *Allele Frequencies for 70 Autosomal SNP Loci with U.S. Caucasian, African-American, and Hispanic Samples*, 149 FORENSIC SCI. INT'L 279 (2005) ("Anonymous liquid blood samples with self-identified ethnicities were purchased. . . .").

194. *See* IAN HANEY LOPEZ, WHITE BY LAW: THE LEGAL CONSTRUCTION OF RACE 155 (2006).

phenotype likely have a mixed "racial" background. *NRC II* suggested that in cases involving a "mixed race" defendant, the court should rely on the racial probability estimate least damaging to the defendant. Surely this is not a sound scientific method of ensuring that a reliable racial estimate is presented in court. Accordingly, an implied system of racial self-identification simply does not satisfy the rigorous *scientific* methodology demanded by *Daubert.*

Assuming instead that the DNA samples are racially classified by outsider-reference also does not free us from the reliability quagmire. What protocols are followed when assigning a race to a DNA sample? Who makes the racial determination, and on the basis of what evidence? The process of assigning a racial label to DNA samples is too speculative, resting on an uneasy and often unspoken factual ground, to be deemed reliable.[195] It is just not reasonable, under *Daubert* or Federal Rule of Evidence 702 or 703, for an expert to rely on "speculative facts" or "[u]nsubstantiated facts, data, or assumptions."[196]

c. The Unfair Prejudice of DNA Race Science

Probability estimates of genomic frequency that use racial reference populations, even if deemed relevant and reliable, should nonetheless be excluded on grounds of unfair prejudice. Scientific evidence may be excluded if "its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by consideration of undue delay, waste of time, or needless presentation of cumulative evidence."[197] "Unfair prejudice" is defined by the Advisory Committee Notes to Rule 403 as involving an "undue tendency to suggest decision on an improper basis, commonly, though not necessarily, an emotional one."[198] Prejudice is thus "unfair" if the evidence has "some other effect other than tending to prove fact or issue that justifies its admission."[199] Courts are also encouraged to pay special attention to statistical evidence of probabilities, which can give off an unfair "aura of scientific infallibility."[200] Probability estimates of genomic frequency are particularly "suggestive to the jury that not only was the defendant undeniably the source of the DNA found at the crime scene, but that the defendant is guilty of the crime."[201]

The United States Supreme Court has provided detailed guidance for balancing the probative worth of an item of evidence against its unfair prejudice. In *Old Chief v. United States*, Justice Souter laid out the framework for assessing Rule 403 issues: (1) decide whether the evidence involves a danger of unfair prejudice; (2) if so, evaluate the degrees of

195. *See, e.g.,* WEINSTEIN'S FEDERAL EVIDENCE, *supra* note 95, at § 702.05[2][b] at 702-83 (Under FED. R. EVID. 702 "an expert's testimony is inadmissible if it is based on suppositions rather than facts.").
196. *Id.* at 703.04[4] at 703-21.
197. FED. R. EVID. 403.
198. FED. R. EVID. 403, advisory committee's notes.
199. WEINSTEIN'S FEDERAL EVIDENCE, *supra* note 95, at § 403.04[1][b] at 403-37.
200. *Id.* at § 403.05[3][c] at 403-66.5.
201. *Id.* at § 702-148.

probative value and unfair prejudice attached to the evidence; (3) discount the probative worth of the evidence if an actually available substitute for the evidence is available; and (4) exclude the evidence if its probative worth is substantially outweighed by the risk of unfair prejudice.[202]

Racial probability estimates of genome frequency are clearly unfairly prejudicial. Racial probability estimates are generally admitted in criminal trials, where the defendant is often accused of committing a violent and reprehensible crime. Such evidence unnecessarily injects issues of race and ethnicity into the trial, thereby leading the trier of fact to improperly focus on the race of the defendant and, at times, victim.[203] A racial probability estimate clothed in science also reifies the folk association of race with biology. This pseudo-scientific evidence facilitates a "molecular reinscription of race in the biological sciences,"[204] further feeding the folk myth that the races are real, natural, and fixed genetic categories. The damage borne by the defendant and society cannot be understated.

The clear risk of racial bias stemming from the introduction of racial DNA estimates is highlighted by the unfortunate historical association of crime and race.[205] Racist ideology has long sought to establish the biological inferiority of non-white persons by claiming that non-white people are naturally predisposed to committing crimes against society. The introduction of "*scientific*" evidence against a criminal defendant that purports to assess genetic probabilities based on race, therefore, threatens to resurrect an enduring racial prejudice. This is the very type of "unfair" prejudice that Federal Rule of Evidence 403 seeks to disallow, as there is a historically documented risk that the jury will reach their decision on a wholly improper basis.[206]

While the unfair prejudice attached to racial DNA probability estimates is undoubtedly high, the probative value of such evidence is *de minimis*. Applying the *Old Chief* framework to our analysis, there is clearly an "actually available" substitute for the prejudicial evidence of equal or greater probative value. A DNA probability estimate using the *general population* as the reference database is just as probative as a racial estimate as to the defendant's criminal guilt.[207] A non-racial DNA

202. 519 U.S. 172, 191-92 (1997).

203. *See Pizarro*, 110 Cal. App. 4th at 632 ("[T]he improper mention of ethnicity unfairly and unjustifiably encourages the jurors to focus on ethnicity and race – specifically the ethnicity and race of the defendant, the only suspect before them.").

204. Troy Duster, *The Molecular Reinscription of Race: Unanticipated Issues in Biotechnology and Forensic Science*, 40 PATTERNS OF PREJUDICE 427, 427 (2006).

205. Frank Rudy Cooper, *Against Bipolar Black Masculinity: Intersectionality, Assimilation, Identity Performance, and Hierarchy*, 39 U.C. DAVIS L. REV. 853, 877-78 (2006); *see also* N. Jeremi Duru, *The Central Park Five, the Scottsboro Boys, and the Myth of the Bestial Black Man*, 25 CARDOZO L. REV. 1315, 1320 (2004); *see also supra* Part I.

206. *See generally* McClesky v. Kemp, 481 U.S. 279, 309 (1987) ("Because of the risk that the factor of race may enter the criminal justice process, we have engaged in 'unceasing efforts' to eradicate racial prejudice from our criminal justice system.").

207. *See supra* Part IV.

probability estimate also does not suffer from the unfair prejudice and improper emotional appeal that characterizes racial DNA estimates.

The significantly discounted probative value of racial DNA probability estimates is substantially outweighed by clear danger of unfair prejudice. The likelihood of introducing enduring racial stereotypes, prejudice and imagery in the trial, which may cause the jury to improperly reach their decision on a racially-tinged emotional basis, strongly cautions against the admission of racialized probability estimates.

V. CONCLUSION

Science has a long and regrettable history of inappropriately taking it upon itself to interpret racial difference. Science—whether it be phrenology, anthropometrics, anthropology, biology, eugenics or now genetics—has steadfastly heeded the call to provide empirical validation to folk beliefs of white superiority and non-white inferiority. Following World War II, prominent scientists from around the world uniformly rejected the biological theories of race that had led to the death and oppression of countless millions. Race was established, not simply theorized, to be a social construction that has no biological or genetic meaning.

The rise of DNA profiling and population genetics, however, has ushered in a modern era of "race science." Genetics has once again been relied on to scientifically interpret racial difference, notwithstanding the unfortunate lessons of history. Modern science and the courts apparently are easily lured by the folk notion that racial classifications in society are not simply arbitrary artifacts reflecting historical social and political processes, but rather account for enduring and naturally-occurring biological differences. It is thus now common and widely accepted for courts in the United States to admit statistical evidence claiming the *scientific* ability to interpret genetic racial difference.

Such evidence, however, is objectionable on both normative and doctrinal grounds. The allure of believing there is a biological dimension to race is deeply tied to an often unspoken and unconscious desire to preserve existing structures of racial classification and privilege. The use of science to validate folk notions of race inevitably protects both the racial status quo and the social benefits that accrue from whiteness. The reemergence of "race science" in the forensic genetics context is, however, somewhat unsurprising, given the long-standing racist history of linking criminality with non-whiteness (more specifically, blackness).

Probability estimates of genomic frequency interpreted through the lens of race simply provide no relevant information to the finder of fact. The lack of a reliable methodology to racially classify DNA sample, combined with irrefutable scientific evidence that race has no genetic component, are further grounds for inadmissibility. Racial probability estimates also introduce an unnecessary risk of unfair prejudice at trial by cultivating racial bias and reifying biological folk theories of race. The continued judicial acceptance of racial DNA probability estimates not only serves to reinforce racial hierarchy, but also runs counter to basic evidentiary principles concerning the admission of scientific evidence.