DNA Dragnets and Race: Larger Social Context, History and Future

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Background and Context for the Racialized DNA Dragnet

In order to appreciate the current and inexorable future "racialization" of DNA dragnets, it is useful to step back in time and provide some social and historical context of how emerging fields of inquiry most relevant to the new forensics were birthed with the complex issue of the relationship between human taxonomies and DNA markers. For the first decade of the Human Genome Project, from 1989 to 1999, the official position that dominated the whole enterprise was captured in the mantra of human "sameness" (Cook-Degan 1994, Bishop and Waldholz 1990). We heard repeatedly that, since all humans are so alike at the DNA level, it did not matter whose genome was sequenced.

This conventional scientific wisdom obviated the need for any serious or meaningful discussion of how human variation might play a role in determining *which* human (or humans) was (were) to be used as the source of mapping and sequencing. If the DNA sequences of Laplanders, Scots, Sudanese, Aborigines, Canadians, Japanese and Brazilians' are so much alike, then we might as well just sequence some white males from the United States and be done with it.

This position of the complete interchangeability of humans for the purpose of sequencing the genome was officially re-affirmed at the White House press conference of June, 2000 – in which the key players came together to announce

the successful completion of the first draft of the project. President Clinton and British Prime Minister Tony Blair metaphorically joined hands with Francis Collins and Craig Venter to joyfully and officially pronounce that "at the DNA level, there is only one race, the human race."

Yet at that very moment, a new field fusing genomics and pharmacology was just about to emerge -- its whole reason for being: to find *patterned differences* between humans so that pharmaceutical products could be delivered most appropriately to those whose DNA was most resonant with particular drugs. What had this to do with race? The answer lies in this brief excerpt from one of the first papers to lay down the new racialized DNA gauntlet:

> "All pharmacogenetic polymorphisms studied to date differ in frequency among ethnic and racial groups…" (and)
> "The marked racial and ethnic diversity. . . dictates that race be considered in studies aimed at discovering whether specific genotypes or phenotypes are associated with disease risk or drug toxicity." (Evans and Relling 1999)

This shift from "we are basically the same" to a focus on human differences was made possible by a technological breakthrough, the development of a super-computer that could read hundreds of thousands of nucleotide sequences – from which strong claims could be made about definitive differences in identifying specific samples. On the heels of the *Science* article just quoted, this mechanical breakthrough would change and shape the way various fields, from

pharmacotoxicology and epidemiology to clinical genetics and forensic science would soon turn to focus on human difference:

> NuTec Sciences of Atlanta, GA announces the purchase of the new IBM supercomputer to enable researchers '*to solve the mysteries of the human genome*' (Shankland 2000).

And while the announced goal was to be able to deliver individualized medicine based upon a single person's genetic makeup, in practice, this quickly was transformed into finding "specific populations" at greater advantage or higher risk for a response to some drug (Epstein 2007). This development alone might have been insufficient to fuel the new frame for the molecular reinscription of race, but the die was cast when Congress passed the *Minority Health and Health Disparities Research and Education Act* in 2000. On the surface, this seemed to be a relatively benign development, directing the NIH and other federal funding agencies to keep track of health disparities between populations designated by race and ethnicity. However, those with hammers look for nails. Molecular geneticists, epidemiologists and hematologists reporting out data on rate differences between whites and blacks (cancer, hypertension, diabetes, asthma), or between gentiles and Jews, or between Latinos and Anglos – would give the strong impression that those differences could be understood at the *molecular* level. Here are but a few examples:

> Black asthmatic subjects displayed significantly diminished glucocorticoid responsiveness compared to white asthmatic subjects… Similar results were found between black and white control subjects, as follows: median, 1.26 nmol

> (0.70, 2.14) vs 0.95 nmol (0.55, 1.48) [p = 0.01]…. Our observation that black asthmatic subjects and non-asthmatic control subjects require greater concentrations of glucocorticoid *in vitro* to suppress T-lymphocyte activation suggests that blacks have a racial predisposition to diminished glucocorticoid responsiveness, which may contribute to their heightened asthma morbidity. (Federico, *et al* 2005:571)

Notice that in this formulation, what starts off as a difference between groups designated by race is transformed into "a racial predisposition." That alone suggests that the researchers have conflated the surface of racial classification with the molecular. But they go even further, and conclude "Studies suggest black asthmatic subjects have an inherent predisposition to overexpose proinflammatory cytokines such as IL-4 compared to whites." (p. 576) Thus, while the explicit goal of pharmacogenomics was to deliver individualized treatments, reports from these studies "racialized" the ways in which the delivery of clinical medicine was framed:

> Ethnicity affects the average warfarin dose required to maintain therapeutic anticoagulation. …white patients require higher warfarin doses than Asians to attain a comparable anticoagulant effect. --- Chinese patients required a ~50% lower average maintenance dose of warfarin than white patients to obtain comparable anticoagulation. (*Annual Review of Pharmacology & Toxicology* 2001: 818)

The significance of this summary is that it is from an annual review, which distills the literature of field for a full year, not simply from a single published paper.

A full year after the White House news conference noting “the end of race” at the molecular level, there appeared a report in the news media suggesting that the most likely candidates for explaining sharp and dramatic health disparities between different racial grouping are distinctive genetic pathways:

> “Illnesses that seem identical in terms of symptoms may actually be a group of diseases with distinct genetic pathways. This would help explain blacks’ far higher mortality rates for a host of conditions, including diabetes, cancer and stroke.” (*Financial Times*, 2001)

Both the United States and Western Europe initiated the search for population-specific markers that might help drug companies market to ethnic and racial populations. Molecular geneticists in Asia sensed a challenge and an opportunity. Whether this was more a response to perceived exclusion, or was a kind of jockeying for market share, a consortium of Asian countries convened to consider ways that new drugs being developed might be specifically tailored for Asian populations:

> “The goal of this initiative is to uncover the breadth of genetic diversity and the extent of genetic similarity within Asian populations. This information will form the basis for future studies in genomic medicine focused on Asian populations.” (Daar and Singer 2005:243)

While racial issues were now surfacing in the newly christened field of pharmacogenomics, some forensic scientists had anticipated this several years – even before the Human Genome Project’s completion. In the July 8, 1995 issue of the *New Scientist* entitled, "Genes in Black and White," some extraordinary claims

were made about what it is possible to learn about socially defined categories of race from reviewing information gathered using new molecular genetic technology. In 1993, a British forensic scientist published what is perhaps the first DNA test explicitly acknowledged to provide "intelligence information" along "ethnic" lines for "investigators of unsolved crimes." Ian Evett, of the Home Office's forensic science laboratory in Birmingham, and his colleagues in the Metropolitan Police, claimed that their DNA test can distinguish between "Caucasians" and "Afro-Caribbeans" in nearly 85 per cent of the cases. Evett's original work (1993a) was published in the *Journal of Forensic Science Society* and drew upon apparent genetic differences in three sections of human DNA. Like most stretches of human DNA used for forensic typing, each of these three regions differs widely from person to person, irrespective of race. But by looking at all three, the researchers claimed that under select circumstances it is possible to estimate the probability that someone belongs to a particular racial group.

The implications of this for determining, for practical purposes, who is and who is not “officially” a member of some racial or ethnic category are profound. In more recent years, the technology has moved along, and forensic scientists began using VNTR loci, and investigating 12-15 segments of the DNA, not just the earlier 3-7. The computer chip revolution would permit research on specific populations to achieve a single nucleotide polymorphism (or SNP) profile of such a group (Hamadeh and Afshari 2000). There is a dangerous seduction when deploying the technology in this fashion. The computer will inevitably be able to find some patterns for a group of, say, 3,000 burglars. But this is a mere spurious correlation

of markers that can explain nothing about who commits burglaries – while it will have the seductive imprimatur of molecular genetic precision. But just suppose, hypothetically, this aggregated population of burglars was predominantly African American.

First, there is abundant evidence for claiming that there is systematic bias, by race, of a full range of behaviors displayed across the criminal justice system. This begins with decisions by police at the point of stop, search, and arrest. For a good example, see Harry Levine's paper for this volume, on the discrepancy between marijuana possession and arrest for marijuana possession, by race. This bias extends through the sentencing guidelines and practices, to incarceration (Mauer 2006). Second, there is now a developing forensic science literature that claims to be able to predict "ethnic-affiliation" from population-specific allele frequencies.

Background to "ethnic-affiliation-markers" at the DNA level

At the level of the DNA, recall that the mappers and sequencers of the Human Genome had assured us that humans are 99.9 per cent alike. But if humans are 99.9 per cent alike and "race" is purportedly a concept with no scientific utility, what are we to make of a series of articles that have appeared in the scientific literature over the last decade and a half, looking for genetic markers of population groups that coincide with common-sense, lay renditions of ethnic and racial phenotypes? It is the forensic applications that have generated much of this interest. Devlin and Risch (1992*a*) published an article on "Ethnic Differentiation at

VNTR Loci, with Specific Reference to Forensic Applications"–a research report that appeared prominently in the *American Journal of Human Genetics.* They wrote:

> The presence of null alleles leads to a large excess of single-band phenotypes for blacks at D17S79 (Devlin and Risch, 1992*b*), as Budowle et al. (1991b) predicted. This phenomenon is less important for the Caucasian and Hispanic populations, which have fewer alleles with a small number of repeats (p. 540).
>
> And: [I]t appears that the FBI's data base is representative of the Caucasian population. Results for the Hispanic ethnic groups, for the D17S79 locus, again suggest that the data bases are derived from nearly identical populations, when both similarities and expected biases are considered …. For the allele frequency distributions derived from the black population, there may be small differences in the populations from which the data bases are derived, as the expected bias is .05 (p. 546).

The work of Devlin and Risch (1992*a*, 1992*b*), Evett et al (1993b, 1996), Lowe et al (2001) and others suggest that only about ten per cent of sites in the DNA are "useful" for making distinctions. This means that at the other ninety per cent of the sites, the allele frequencies do not vary between groups such as "Afro-Caribbean people in England" and "Scottish people in England." But it does not follow that because there is no *single* site where allele frequency matches some phenotype that we are trying to identify (for forensic purposes, we should be

reminded), that there is no purpose in trying to locate *multiple* sites (four, six, seven, now thirteen). It is important to understand that the purpose of this work is to aid the FBI, Scotland yard, or the criminal justice systems around the globe in highly probabilistic statements about suspects, and the "likely" identification of the ethnic, racial, or cultural populations from which they can be associated – statistically. Determining the boundaries of discrete categories of race and ethnicity is irrelevant for these purposes.

Thus, there is a surface contradiction between molecular biologists asserting that "race has no validity as a scientific concept" and forensic experts (and various others) using allele frequencies in specific populations that correspond to common public uses of racial categories. It is possible to sort out and make sense of this, and even to explain and resolve the apparent contradiction, but only if we keep in mind the difference between using a taxonomic system with sharp, discrete, definitively bounded categories, and those which show patterns (with some overlap), but which may prove to be empirically or practically useful. When representative spokespersons from the biological sciences say that "there is no such thing as race"–they mean, correctly, that there are no discrete categories that come to a discrete beginning or end, that there is nothing mutually exclusive about our current (or past) categories of "race," and that there is more genetic variation within categories of "race" than between. While all this is true, it is a discussion more appropriate to abstract theorizing in the logic and philosophy of science, and bears little relevance to the practical matter of helping to "solve" a crime or the practical application of molecular genetics to health delivery via

genetic screening. In both real world sets and settings, there is always the messy overlapping of categories. When Scotland Yard or the Birmingham, England police force, or the New York police force, want to narrow the list of suspects in a crime, they are not concerned with tightly constructed taxonomic systems of classification which have no overlapping categories. Their interest is in probabilities.

In 1997, Mark Shriver published a paper in which he trumpeted the possibility of using DNA markers to predict race (Shriver 1997). A few years later, the following paper appeared in the *International Journal of Forensic Science*:

> "The purpose of this paper is to report a method for inferring the ethnic origin of a DNA sample profiled using 6 STR loci. …Information regarding the probable ethnicity of an unknown offender may assist in targeting investigations and setting priorities for mass screens." (Lowe et al 2001)

> "We report the use of DNA profiles from six STR loci for inferring the ethnic origin of a crime stain…and discuss how such inference may be used as intelligence information to reduce the expected number of interviews to resolve a case." (Lowe et al 2001)

So from the very beginning, the forensic science interest in "ethnic estimation" was to permit the police to focus in more narrowly on a specific population of possible suspects. If the tissue sample left at the crime scene could be determined, even with a modest probability of only 75 per cent (to be from group X or Y), that would "aid in the limits of mass screens." And that is precisely

what occurred when the technology was deployed in helping to solve a number of cases of serial rapists and murderers.

The "Tamiami Strangler" -- Race and DNA Forensics

Miami, Florida was the scene of the most notorious and widespread racial DNA dragnet. Between September 1994 and January 1995, six women were killed and their bodies were left just outside the Miami city limits on a street known as the Tamiami Trail. More than 2,300 men were stopped by the police as they drove down streets in the area, each asked to provide saliva samples to determine a possible DNA match (Pan 1998). While the so-called "Tamiami Strangler" was identified through other means, this dragnet is of particular relevance to the issues raised here because (1) almost all of the men who were asked for DNA samples were African Americans, and (2) their DNA samples were stored.

As noted above, some forensic scientists claim they can make an "ethnic estimation" of the suspect's probable identification with some specific population group from DNA evidence at a crime scene. As we shall see, this often means "race" or an effective proxy for race. Others are pursuing work in forensic science with the hope of finding particular allelic frequencies more common in one group than another (Lowe et al, 2001). Readers interested in pursuing these arguments for the merits of the case should consult the following literature (Braun 2002; Risch et al, 2002; Rosenberg et al, 2002; Frank 2001; Lee et al, 2001; Evans and Relling 1999). The use of this technology in high profile cases has led to a full set of arguments for widening the net of the DNA database, so that more and more

samples can be included, ranging from convicted felons to suspects to arrestees to the whole population (Smith and Kaye, 2006). What more objective way could there be of exculpating the innocent and convicting the guilty? However, this conflates three quite distinct strategies and practices of the criminal justice system that need to be separated and analyzed for their disparate impact on different populations. The first is the use of DNA in post-conviction cases to determine whether or not there was a wrongful conviction, the kind of situation that would help to free the innocent. The second is the collection of DNA of "suspects" or arrestees in pre-trial circumstances to increase the DNA database – which in turn is designed to help law enforcement to determine if there is "match" with tissue samples left at some unsolved crime – the net to catch the guilty.

Third is the advocacy of increasing the collection of DNA from a wider and wider band of felons and misdemeanants in the post-conviction period, so that there is a record on file in the event of recidivism. Much like the current situation in which the police can stop a driver and determine whether there are outstanding warrants or traffic ticket violations that have piled up, the new technology would permit authorities to see if the DNA of the person stopped and arrested "matched the DNA" on file for someone at an unsolved crime scene. This is not hypothetical. In early 2000, the New York Police Department began a pilot project experimenting with portable DNA laboratories (Flynn 2000). The police take a buccal swab – some saliva from inside the cheek of the person stopped – and place it on a chip the size of a credit card. They then put this card through a machine no larger than a hand-held compact disc player, where the DNA is read via a laser in two

minutes, isolating about 13 DNA markers to create a profile of the suspect. When this task is completed, the police can then transmit these data to a central database, where it currently requires about twelve minutes to determine if there is a "match" with a sample. Who could possibly be opposed to the use of these technologies for such crime-fighting purposes? The answer is a bit complex, but it has to do with (a) some hidden social forces that create a patterned bias determining that certain populations will be more likely subjected to DNA profiling, and (b) the resuscitation of some old and dangerously regressive ideas about how to explain criminal behavior.

The Dangerous Intersection of "Allele Frequencies in Special Populations" and "Police Profiling via Phenotype"

The conventional wisdom is that DNA fingerprinting is just a better way of getting a fingerprint. That is wrong. The traditional physical imprint of your finger or thumb provides only that specific identifying mark, and was widely believed to be attached to you and you alone. However, recent research indicates that the actual physical fingerprint was never as definitive as forensic scientists claimed (Cole 2001). Quite unlike the actual fingerprint, the DNA contains information about many other aspects than simply a marker for identification. It contains information about potential or existing genetic diseases or genetic susceptibilities one may have, and also contains information about your family. These can involve data of interest to one's employer and of course, to insurance companies. For these reasons, law enforcement officials claim that they are only interested in that part of the DNA that will permit them to provide identifying markers that are not in

coding regions. Coding regions are only ten per cent of the DNA, and it is in these regions that the nucleotides code for proteins that might relate to a full range of matters of concern to researchers, from cancer or heart disease–to neuro-transmission and thus, for some, to *possible "coding" for "impulsivity" or biochemical outcomes that might relate to violence.* While the FBI and local and state law enforcement officials tell us that they are only looking at genetic markers in the non-coding region of the DNA, twenty-nine states now require that tissue samples be retained in their DNA data banks after profiling is complete (Kimmelman 2000:211).

Only one state, Wisconsin, requires the destruction of tissue samples once profiling is complete. The states are the primary venues for the prosecution of violations of the criminal law, and their autonomy has generated considerable variation in the use of DNA databanks and storage. Even as late as the mid 1980s, most states were only collecting DNA samples on sexual offenders. The times have changed quite rapidly. All fifty states now contribute to the FBI's Combined DNA Index System (CODIS). Moreover, there has been rapid change in the inter-linking of state databases. In just two years, the database went from a total of nine states cross-linking "a little over 100,00 offender profiles and 5,000 forensic profiles" to 32 states, the FBI, and the US Army now linking "nearly 400,000 offender profiles, and close to 20,000 forensic profiles" (Gavel 2000). States are now uploading an average of 3,000 offender profiles every month. If this sounds daunting, computer technology is increasingly efficient and extraordinarily fast. It takes only 500 microseconds to search a database of

100,000 profiles. As we increase the numbers of profiles in the databases, there will be researchers proposing to provide SNP profiles of specific offender populations. Twenty states authorize the use of databanks for research on forensic techniques. These stored samples can be used in subsequent criminal investigations, of course, but they can also be used in behavioral genetics research – with its new turn to the molecular level of DNA markers associated with different behavior. It is important to address the serious implications *for behavioral genetics* of having race re-enter the scientific and medical literature through the DNA, particularly in research linking proclivities to violence, impulsivity, and crime with between-group differences.

DNA Dragnets

DNA dragnets originated in England, and are most advanced in Europe and the United Kingdom. The first DNA dragnet was conducted in Leicester, England in 1987. Two teenage girls were raped and murdered in the same area, and police requested voluntary blood samples from more than 4,500 males within a certain radius of the crime scene. When a man asked a friend to submit a DNA sample in his place, he immediately became a prime suspect, and turned out to be the killer (Wambaugh 1989). Germany is the site of the largest DNA dragnet ever conducted. In 1998, the police collected samples from more than 16,000 people, and finally matched the DNA of a local mechanic to the sample collected a the crime scene of the rape-murder of an eleven year old (Hansen 2004).

While the United States has only conducted about a dozen DNA dragnets, most notable about them is their focus on specific racial groups. San Diego was among the first jurisdictions to conduct the practice, when, in the early 1990s, a serial killer stabbed six persons to death in their homes. The suspect was African American, and more than 750 African Americans were tested. In 1994, Ann Arbor, Michigan police obtained nearly 200 samples from African Americans in the hunt for yet another serial rapist and murderer. In both the San Diego and Ann Arbor cases, the suspect was apprehended and convicted for committing another crime, not as a result of the success of the dragnet. Then in 2004, Charlottesville, Virginia had a racially-driven dragnet that generated a controversial response from civil liberties groups that ultimately convinced the police to temporarily abandon the dragnet strategy (Glod 2004).

A serial rapist had been active in the Charlottesville area for six years, from 1997 through 2003, frustrating police investigations at every turn. The DNA evidence linked the rapist to at least six assaults. From a number of leads, the police believed the rapist to be African American, and so in the winter of 2003, the chief of police initiated a project to obtain saliva samples from 187 men – 185 of whom were black (the two others were Latinos).

However, when two men, both students at the University of Virginia, refused, they raised the whole issue of what constitutes voluntary submission of a DNA sample. In so doing, they brought pressure on both the university and the local black community to take a position. The Dean of the University of Virginia's Office of African American Affairs organized a forum to discuss the situation –

drawing national media attention. At one point, the Dean said: “Because the suspect is black, every black man is suspect. What are we going to do about this in the community?” In mid-April of 2004, the police chief suspended the dragnet, and restricted its use to a much narrower use of police discretion based more on whether a suspect resembled a composite profile than on race (Glod 2004).

Racial taxonomies and DNA Databanks

If the United Kingdom was first off the block with DNA Dragnets, and also led the world’s nations in the largest DNA databank and the highest proportion of its citizens who are enrolled in its national DNA database, it also enjoys another distinction. An extraordinary 4 in 10 of the black male population have their DNA in the police database. This is in sharp contrast to the less than one in ten whites in the database (Randerson 2006). Of course one of the responses to these kinds of figures is the speculation that they merely reflect who is committing the crimes. Perhaps blacks are committing about forty per cent of all the crimes in the UK. I shall return to this matter, and point to some data that suggest an answer to this kind of speculation as relates to data collection on race and crime in the United States. However, before turning to this matter, it is instructive to report the evolving and shifting response of the president of the National Black Police Association in the UK, Keith Jarrett – to the data about racial disparities in arrest rates and DNA collection. This shift occurred over a very short time period of two years:

> Since April (2005), police have had the power to take DNA from anyone arrested on suspicion of a recordable offence – one that would involve a custodial sentence – meaning the database is not simply a reflection of those convicted of crimes. (Renderson 2006)

At the time, in 2005, Jarrett said that this development was "very worrying" and recommended "an investigation into how the database is compiled." However, in October of 2007, Jarrett delivered a speech in which he urged increased stop-and-search police work when dealing with racial and ethnic minorities:

> Speaking at the group's annual conference, Keith Jarrett (asked) Police Minister Tony McNulty and Sir Ian Blair, Commissioner of the Metropolitan Police, to consider escalating stop-and-searches among black people to reduce the number of shootings that have claimed the lives of another two teenagers in the past week (Townsend 2007).

But Jarrett went even further, claiming that in the new climate of fear about rampant violence, the Black community would welcome random stop-and-search practices by the police:

> …Jarrett said he would not oppose a random use of stop-and-search when officers had 'reasonable suspicion' an offence had been committed. He argued that as long as police officers used the powers courteously and responsibly, many within the Black community would accept it as a necessary evil (Townsend 2007).

This remarkable turn-around in the short space of two years reflects the shifting mood in weighing the trade-offs made in the balancing act between security and freedom. And while the British have been in the lead of collecting DNA from its population, whether or not there has been a felony conviction, several states in the US have embarked upon data collection of arrestees as well. The most aggressive programs are in Louisiana and California, but the trendline is clear, so some states are debating whether to include ALL arrestees:

> "Lawmakers in South Carolina are considering a bill that would create the nation's most aggressive DNA collection program, instructing police to take genetic samples from people arrested in any crime — including misdemeanors such as shoplifting — and enter them into state and national DNA databases ." (Fausset 2007)

There are dramatic implications of this prospective development for how such a database would be heavily racialized. First, consider that incarceration rates for blacks and Latinos are now more than six times higher than for whites; 60% of America's prison population is either African-American or Latino. Just over 20% of black males between the ages of 25 and 44 have served a sentence at some point in their lives, and 8% of black men of working age are now behind bars (Austin, et al 2007). At current rates, a third of all black males, and one-sixth of Latino males will go prison at some point during their lives, while the figure for whites is one in 17. These are national figures, but depending upon the urban area, things can look even more heavily racialized. For example, in Baltimore, one in five of black men between ages 20 and 30 is incarcerated, and 52% are under

some form of correctional supervision (Ziedenberg and Lotke 2005). In this kind of setting, familial searching and DNA Dragnets take on a particularly ominous racial character:

> "Six of those 44 states, including California, have approved taking samples from people arrested on suspicion of certain crimes. States maintain their own DNA databases, which are linked to form the national network ." (Faussett 2007)

The Bearing of Cold Hits vs. Cold Facts in Racialized Dragnets

John Davis is a California state prisoner who had been linked, by a "cold-hit" to a 1985 rape-murder in San Francisco. Davis had been arrested for robbery, and thus his DNA had been collected and was entered into the state's database.

> "The only evidence against him was the DNA (match), plus the fact that he'd lived in the area at the time." – the… match occurred after DNA was eventually extracted from semen found on the body of the murder victim. The cold-hit match held good across 13 different sections, or loci… (and) a 13-locus match seemed unassailable…" (Jefferson 2008).

However, Davis' defense attorney, Bicka Barlow, is not only a lawyer, she also holds an advanced degree in genetics. Barlow had read about an interesting case in Arizona, where two people matched at nine loci. Conventional and prevailing statistical wisdom says that the odds of a random match at nine loci would be one in a billion. She filed a subpoena seeking more data on this case,

and learned in November, 2005 that Arizona's offender database contained genetic profiles of 65,493 offenders, and "within that pool, 122 pairs of people had DNA that matched at nine loci – and 20 pairs had profiles that matched at 10 loci (Jefferson 2008:32).

Now the story turns into an interesting melodrama about the search for truth versus the organizational imperatives of the FBI and prosecuting attorneys' interest in protecting the image of DNA cold-hit technology as definitive. Barlow posted her results on a website in order to alert other public defenders of her findings. Then she subpoenaed California's Department of Justice to compel the state's crime lab to analyze how common such unexpected pair matches were in the California offender database. "The FBI sent out a nationwide alert [to state crime labs] saying, 'notify us if you get any requests like this,'" she says, and "…the Arizona Attorney General faxed me a letter from CODIS that said basically, 'if you don't take this [Barlow's web posting] down, we'll bar your state from participation in the national database" (Jefferson 2008:33). A San Francisco judge refused to permit her to probe California's database.

This is hardly an isolated case. In July, 2006, defense attorneys for a murder suspect in Chicago requested a search of the Illinois database.

> …the FBI's Callaghan held a telephone conference with Illinois crime lab officials. The topic was "how to fight this," according to lab officials' summary of the conversation, which later became part of the court record. Callaghan suggested they tell the judge that Illinois could be disconnected from the national database system, the summary shows. Callaghan then

> told the lab officials that "it would in fact be unlikely that Illinois would be disconnected," according to the summary (Felch and Dolan 2008).

In any event, a judge ordered that the search be permitted, and the result was a finding of “903 pairs of profiles matching at nine or more loci in a database of about 220,000.” Even though state officials were able to get a court order to prevent distribution of these results, “*the Los Angeles Times* obtained them from a scientist who works closely with the FBI” (Felch and Dolan 2008).

Forensic Science vs. Science

Barlow is hardly alone in her skepticism about DNA cold-hit technology. In a recent law review article, Erin Murphy (2007) has raised similar issues of the limits of asserting just how definitive DNA matches can be in “cold hit” cases. Yet, this is a world in which the “CSI effect” has captured the public imagination, and where DNA evidence has come to be seen as nearly infallible (Willig 2004).

We know African Americans are being arrested at a rate of at least five times greater than whites for minor violations such as marijuana possession, even though the best available evidence suggests that whites are more likely than blacks to use (and thus possess) marijuana at every age level. The DNA of arrestees is being collected more and more routinely (12 states now collect DNA from those merely arrested), and thus we are witnessing a new kind of convergence with portents for even greater racial disparities in convictions and rates of incarceration. The vast majority of persons convicted of crimes plead guilty, without their case ever going to trial. The reason is simple. The prosecuting attorney engages in a “plea bargain” in which the accused agrees to a lesser

sentence in return for pleading guilty to a lesser crime. It has been known for more than three decades that approximately ninety per cent (or more in some jurisdictions) of defendants plead guilty to a crime rather than take their case to a jury (Heumann 1978; Altschuler 1979). This saves the state the problem of convening a jury and going through a lengthy trial. Indeed, if even a third of those in prison requested jury trials, the system would be clogged up for decades. So, the plea bargain is a Faustian bargain of sorts – and everyone in the criminal justice system knows it. The segment of the society that is surprised by the ubiquitous nature of the plea bargain is – everybody else, i.e., the general public. Mesmerized by decades of radio and then television portrayals of criminal court jury proceedings, from *Perry Mason* to *Law and Order*, from *Closer* to *Crime Scene Investigation*, the public is more likely to think that juries play a decisive role in who the determination of guilt or innocence. Indeed, the so-called "CSI effect" – the idea that the prosecution needs to come up with DNA evidence has penetrated into jury selection and jury members (Willig 2004).

This has two direct kinds of relevance to racialized dragnets and racialized databases? First, we have data that show that defendants confronted with the "information" that there is DNA evidence against them are far more likely to see this as "definitive evidence" – and thus more likely to accept a less advantageous plea bargain (Prainsack and Kitzberger 2008). Murphy (2007) and others have noted the successful "creep" of the CSI Effect on the general public. But Prainsack and Kitzberger(2008) have discovered that defendants are perhaps even more susceptible to the CSI effect, i.e., the tendency to believe that DNA evidence is

sufficient to secure a conviction. Their work with prosecutors and interviews with defendants in the United Kingdom document just how much the technology of the *DNA Mystique* (Nelkin and Lindee 2004) has become a part of the taken-for-granted features of the *zeitgeist*. Since prosecutors have become increasingly aware of this, they can and do tell those arrested and accused of a crime that "they have the DNA fit" – whether or not they do!! This is legally permitted, and there are also documented cases in the United States where this has been a practice (LaDuca 2007).

Second, more and more cases will be brought before prosecutors using "cold hits" (that match "known offenders" – which will increasingly include those merely arrested). We know that those "merely arrested" will by heavily distorted by race. From the Arizona database noted above, there were 120 matches, not one in a billion, at 9 loci.

Which brings us to a crucial distinction between science and forensic science. One of the most essential elements of science is replication of findings by an independent investigator. If a researcher claims to have discovered some empirically derived finding (think of cold fusion), s/he must make available the method of investigation, and open up for scrutiny the procedures so that other scientists can determine whether the finding was spurious, unique, doctored, a fluke, etc. Not so with empirical evidence on DNA matches in a court of law. The crime labs are routinely held proprietarily, where the government agency *refuses* to permit independent laboratory work by "outsiders" who could use the same "scientific methods" to either corroborate or refute a finding of a DNA match

(Murphy 2007). This barrier to comparative laboratory analysis is not science – but it is the current state of forensic science. The stakes are not just scientific reputation of some principal investigator – the stakes can involve the death sentence to an innocent person – the life imprisonment of a citizen falsely accused of rape, a long-term prison sentence.

Thus we can begin to get a glimpse into the future to see how these various forces (racialized dragnets, expanding offender databases to include arrestees, and the CSI effect – on both prosecutors and defendants) can and will further distort the racial bias in the criminal justice system. The vast majority of young persons of African American and Latino descent who are brought into the criminal justice apparatus can not afford representation by private attorneys –and are thus doubly victimized by a system that dramatically over-selects them at point-of-arrest by ratios from 5 to sometimes even 8 to 1 (Austin, et al 2007). The seemingly inexorable move now gaining momentum to include those merely arrested in the national DNA database will only increase the current disparities – for the full range of reasons chronicled above. What is to be done? The first twinned task is to a) start to rollback the "function creep" of adding those merely arrested into a database that now totals nearly six million, and b) use this as an opportunity to explain to an unsuspecting public that "cold hits" are not nearly what they seem to be on their favorite crime television programs.

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