Some Social Implications of the Molecular Biological Revolution

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Some Social Implications of the Molecular Biological Revolution

***Troy Duster*[1]**

The revolution in molecular biology has already had considerable impact on how individuals, members of families and social groups think about each other – and it has also influenced how we avoid, insure, stigmatize, and "explain" each other. As developments move along from theory to possible practical application, they engage us in a new kind of urgent dialogue about moral, ethical and social underpinnings of deeply held beliefs that otherwise lie dormant.

There are a number of important markers to highlight both the speed and drama. These include the more sensational developments and breakthroughs, such as the technique of somatic nuclear cell transfer (with the realization of mammalian cloning and the specter of human cloning), and germ-line gene therapy (with its specter of altering the genetic make-up of future generations). But there is the more current and even more likely prospect of growing organs from animals genetically engineered to produce greater compatibility with the new human host's immunological system – and of course, there is the topical controversy of the use of embryonic or adult stem cells to pursue research to help Parkinson's or Alzheimer's sufferers.

Normally, the public health is a fine example of the communitarian claim of a common public/community interest based clearly upon the common health, the commonweal(th), and the common interest. For example, the right of the individual to remain in a community while s/he has a contagious disease such as smallpox or

tuberculosis is trumped by the state's right to protect the general public health of the citizenry. But molecular biology has played a powerful role in fracturing the public health consensus. While we could all agree that it is in our common interest to mainly rid us of cholera, yellow fever, tuberculosis, infectious meningitis, and small pox, this communitarian consensus has been dramatically undermined as we have learned that some groups are at higher risk for a genetic disorder than others. Cystic fibrosis is a genetic disorder that can affect the upper respiratory system in a life-threatening manner, but only those from north European ancestry are at significant risk. Beta-Thalassemia is a blood disorder primarily associated with persons with ancestors from the southern Mediterranean region. Sickle cell anemia is primarily associated, in the U.S., with Americans of West African descent. And so it goes. In the 1970s, the public health consensus about general health screening was disrupted by this development, as group interests began to emerge to demand more funding for research and genetic testing of the gene disorder most associated with "their group" (Duster, 1990).

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If molecular genetics and the emergence of group-based research agendas fractured the public health consensus, we can expect an even more dramatic parallel development when it comes to discussions of the public safety. It is almost inevitable that a research agenda will surface to try to find patterns of allele frequencies, and then create computer-generated genetic profiles of different types of criminals.[2] As I will demonstrate, "ethnic-affiliation estimations of allele-frequencies" is high on the research agenda in forensic science (Lowe, et al, 2001). But like the phrenology of the 19th century, these markers will be precisely that, "markers" and not explanatory of "the causes" of violent crime. Even if the many "causes" of criminal violence (or any human behaviors) are embedded in the full panoply of forces that begin with protein coding, there is interaction at every level, from the cellular environment all the way up through embryological development – to the ways in which the criminal justice system focuses on one part of the town and not another when making drug busts. We are bemused today about tales of 19th century scientists who sought answers to criminal behavior by measuring the sizes and shapes of the heads of convicted felons. The new IBM computers can make 7.5 trillion calculations per second for biological chip analysis. These are sirens beckoning researchers who wish to do parallel correlational studies of "population-based allele frequencies" with "ethnic estimations" and groupings of felons – a recurring seduction to a false precision. Before turning to the complex set of forces converging forensic science and molecular biology, it will be useful to briefly review some of the biomedical controversies that are surfacing.

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[2] I will explain in some detail what is meant by a SNP profile. One could do a SNP profile of rapists and sex offenders, and find some markers that they putatively share.

Drawing lines in the sand: biological, genetic, and moral

In the last half of 1996, the boundary of legitimate gene therapy intervention was drawn at the genetic engineering affecting somatic cells. The latter is a potential therapy for a person with a genetic disorder – but a therapy that affected *only the body of the person being treated*. But in only eighteen months, molecular biologists began to claim in a widely publicized public forum that work with stem cells is the easiest and best way to intervene in genetic disorders.[3] A few months later, in September, 1998, the National Institutes of Health Recombinant DNA Advisory Committee received a proposal to fund *in utero* gene therapy for the treatment for a specific genetic condition:

> "treatment of adenosine deaminase (ADA) deficiency. We propose a direct injection into the 13-15 week fetus of a retroviral vector carrying a normal copy of the human ADA gene controlled by human genomic ADA regulatory sequences. Because it is a direct in vivo injection, an occasional vector particle may enter an egg or sperm, thereby resulting in germline gene transfer. The magnitude of this risk will be determined by animal studies over the next 2-3 years." (Anderson, 1999)

The implications of this would, if fully understood, catch the attention of the laity, because with "germ-line" interventions (as noted above) there can be deliberate and conscious impact upon future generations with the manipulation of the genetic make-up. The application was put "on hold" and American Association for the Advancement of Science (AAAS) immediately convened two national panels and requested that they produce position papers with recommendations. The panels convened, and produced the jointly sponsored monograph, *Human Inheritable Genetic Modifications: Assessing*

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[3] A conference at the Los Angeles campus of the University of California was held in March, 1998, in which

Scientific, Ethical, Religious, and Policy Issues (also available on the AAAS website, at http://www.aaas.org/spp/dspp/sfrl/germline/main.htm), prepared by Mark S. Frankel and Audrey R. Chapman, September, 2000. The result was a call for a moratorium on "germline" modifications, but as with the current controversy over stem cells, this may have its major effect on the public sector funded research.

While there will be some general public interest in the content and outcome of these deliberations and recommendations, an even more remarkable saga has surfaced for the nation of Iceland.

ICELAND AS A POTENTIAL GENETIC GOLDMINE -- OR IS IT FOOL'S GOLD?

On December 17, 1998, the Icelandic parliament passed a bill that provides legal access for a private company to obtain a comprehensive genetic database for the entire population of the country.[4] Only one among the 41 members of the coalition government voted against the bill (Berger, 1999). The expressed purpose of the legislation is to encourage research on the molecular basis of twelve genetic disorders, where exclusive access to the database has been provided to a U.S.-based biotechnology firm. This company is based in Delaware, and has major financial backing from both American investors, and by the Swiss pharmaceutical company, Hoffman-La Roche.

Just one month before the vote in the parliament, a Gallup poll reported that only 13 per cent of the nation's adults felt that they were sufficiently knowledgeable about the bill to have an "informed" opinion. Nonetheless, 82 percent of the respondents said they were in favor of the database being generated (Enserink, 1998:891). One of the big

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a group of leading molecular geneticists convened to support with near unanimity this position.

[4] The entire nation of Iceland has a population of only 270,000.

issues is personal privacy. Health data and medical detail will be taken from hospital records, and new data will be added from time to time. While the identity will be encrypted, this is quite a departure from making the data entries completely anonymous.[5] But that is only the surface of some of the intractable ethical and social concerns that reverberate around this development. Scientists not working with the private companies will have no access to these data. Another transparently controversial aspect of the deal is the fact that the biotechnology company, named *deCODE*, need not obtain informed consent from those in the database.

Iceland has kept medical data on its population for more than a century, and the database would also contain the records of the deceased. When combined with both stored and newly collected blood and tissue samples, and further supplanted by detailed genealogical charts and records, the biotechnology company that will mine these databases believes that it has a head start in searching for genes that are implicated in human disease. But there is another element to this story that captures the attention of social analysts of science, and that is the putative "ethnic purity" of the database. The *Science* magazine reporter who covered the story had this to say about why Iceland would be a potential genetic gold mine:

> Thanks to its isolated position and several bottlenecks that wiped out large parts of this population, the island has a remarkably homogenic gene pool, making it relatively easy to track down disease-causing mutations that might form the basis for new tests and therapies (Enserink, 1998:891).

The degree to which this is true, of course, is an empirical question that awaits an answer with potentially volatile economic and political consequences. The major point to

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[5] This permits one to conjure up the Tuskegee Syphilis experiments. For example, what if an Icelandic patient is diagnosed with a disorder for which there is possible treatment? The Icelandic Medical Association opposed the bill.

be made here is that this development has generated a considerable amount of interest from a number of sociologists and anthropologists of science. They have been joined by bio-ethicists and political scientists in a Great Trek northward to monitor and study these developments. While the molecular geneticists are concerned primarily with tracking down what they regard as "disease genes," the social analysts of science are focusing in on the wider set of issues that can have a large impact on a full panoply of social relations – not only in Iceland, but as a harbinger of things to come, globally.

Katz Rothman (1998) has pointed out how communication (or lack of it) of the technical intricacies of the molecular genetics revolution are often silencing and disempowering -- intimidating to those not able to follow closely developments at the vanguard laboratories of the field. Yet these technologies are driven by profoundly social, political and economic questions and concerns. It is therefore both useful and necessary to demystify the complexity, and to be able to cut to the core of basic elements of the scientific work. Then we will be better able to understand what the Iceland adventure is all about, and why it has such a powerful grip and portent on the imagination. We will then see why issues of race and ethnicity, health and medicine, and crime and violence will all be impacted in new ways.

A Short But Necessary Primer on SNPs

Although the work is named The Human Genome Project (the mapping and sequencing of all human genes), no one particular DNA sequence constitutes THE human genome. Rather, each person has her or his own unique human genome, or set of complete genes.[6] DNA is made up of four chemical components, called nucleotides. These are strung together in a chain , much like beads on a necklace. The four different nucleotides are represented as "G" "A" "T" "C, and a DNA sequence could look like

GCGCATTAGCTACGG.

A = adenine

T = thymine

C = cytosine

G = guanine

Each molecule is in the form of a disc, and is called a "base." Rungs of the now famous DNA ladder are constructed when two of these nucleotides are connected in a spiral and form what are called a "base pair."[7] The DNA of humans is made up of approximately 3 billion nucleotides that are packaged into 23 nuclear chromosomes and one mitochondrial chromosome. Approximately ten percent of these base pairs are called genes. Each of these codes for the production of a particular protein.

If someone is missing a "correct" sequence of DNA in one of those segments, that particular protein will not be made. That could prove vital, fatal, or painful. For example, hemophilia is a condition where blood does not clot properly. Those with hemophilia have stretches of the DNA with "errors"[8] that inhibit the protein that would instruct blood to clot properly.

Maps of the genome allow researchers to locate a piece of DNA someplace in the genome, but that map will not indicate the precise arrangement of the nucleotides in that piece of DNA. The precise arrangement, or linear order, of nucleotides is called the **DNA sequence**. The DNA sequence is important because different sequences encode

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[6] The exception, of course, is monozygotic (identical) twins

[7] adenine pairs with thymine; cytosine pairs with guanine

[8] Quotation marks have been placed around "correct" and "errors" for an important reason. While there may be a relatively high consensus about what constitutes a debilitating or fatal disease condition (e.g., Tay-Sachs is a neurological disease that is fatal by age four), that consensus falls away for many other conditions. Setting a single standard of "normality" is always about power and position to do so. In the United States and Europe, many communities of deaf persons resist the idea of being "corrected". This raises the question of who shall set the standard of "the normal" human genome.

different information. One of the main reasons to study DNA is because it encodes information that specifies how cells should make biologically useful molecules, such as proteins.

If we compare the complete DNA sequence of any two people we will find a difference approximately one time in every 1000 nucleotides. The simplest kind of difference is when one nucleotide differs between the two people, for instance, when one person has a G at a certain position in the sequence and another person has a T there. In some cases, such differences will cause a slightly different protein to be made. In other cases, these differences have no known impact on which protein is made or on any other biological functions.

Places where people's genomes differ by one nucleotide are called "single nucleotide polymorphisms" or commonly shortened to SNPs. The search for SNPs is now in full bloom because these SNPs can be used as "markers" on chromosomes. These markers can be used to make genetic maps which may allow us to locate genes of interest, such as genes involved in diseases. But they can also be used to identify and mark both individuals and groups of individuals, a technological capacity that will prove to be of extraordinary significance and consequence to social studies of science.

SnPs ON CHIPS

Many things that molecular geneticists want to study, including many (if not most) human diseases, are caused by a complex interaction between things in the person's environment and the person's biology, including many different genes. In the last decade, media accounts of "the gene for" this or that disease, condition, attribute, or behavior have become common, sometimes weekly reports. This has led many lay

persons to believe that a single gene is the cause of a host of diseases, attributes, and conditions.[9] Yet it is only in rare cases that a single gene has a very strong, identifiable effect on whether or not a person contracts or develops a disease. Such cases are generally called "single gene disorders."

In most cases, when genes play a role in the development of a disease, such as a particular kind of heart disease, the role of any single gene will be very small. To study the genetics of complex conditions such as heart disease, methods must be devised for finding a constellation of genetic differences between people that correlate with that disease. One method for examining many different pieces of DNA all at once, and for detecting more that one genetic difference in a single experiment, is to put many different genes or parts of genes on a computer chip.

DNA chips are useful for doing the equivalent of 100 or even 1000 experiments all at one time, in one simple procedure. The chip with dimensions less than one square centimeter may have 1000 or 10,000 different sectors. The technology is now available to attach DNA of a slightly different sequence to each sector. For instance, suppose that a group of researchers had found 2000 different SNPs; that is, 2000 identifiable places in the genome where people's DNA sequences could differ by one nucleotide. Then, somebody could make a DNA chip that would have all of the possible SNPs (at least 4000, but it could be more because each SNP will have between two and four possibilities), each in its own separate and identifiable place on the chip. Then, if my DNA were exposed to the chip (actually, DNA or RNA are hybridized to the chips), one

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[9] In September, 1992, the March of Dimes published results of their study, a Lou Harris poll, entitled "Genetic Testing and Gene Therapy". The study summarized findings of a national survey of attitudes of the U.S. population about the new genetic technologies, and found the overwhelming majority of Americans (more than seven in ten) strongly favored genetic therapy. This of course presumed that one could locate "the gene for" and then provide therapeutic intervention.

experiment could determine which SNP I had at all 2000 different places in the genome. We could make a "SNP profile" for me. If we did this for 5000 people, 2500 of whom had a certain kind of heart disease and 2500 of whom did not, then we might be able to find 5-10 SNPs that were correlated with a high likelihood of developing heart disease. That is the core of the methodological strategy of SNPs on Chips.

SNPs, Human Diversity, and Social Groupings

Approximately eighty-five percent of human genetic diversity can be found in any population, even a very small, village sized population (Cavalli-Sforza, in Smith and Sapp: 1997:55). For instance, if we were looking at SNPs, we would find that most are in all populations throughout the world. However, there will be some SNPs that are found in some people from Finland but probably not in people of Native American descent. This does not mean that a certain sequence is found in all people from Finland, or that it is never found in people who are not from Finland.

There are social implications of creating SNP profiles if these can be used to suggest increasing likelihood of a person's ancestry and appearance, for example. As we shall see, forensic studies that attempt to provide the criminal justice system with strong leads to probable suspects are now being developed. Because phenotypically stereotypes of "race" have played a large role in such identification, we must first turn to the literature that sets the stage for the re-emergence of "race" in molecular biological clothing.

Context and Content for Feed-back Loops: Setting the Empirical Problem

By the mid 1970s, it had become abundantly clear that there is more genetic variation *within* the most current common socially used categories of race than *between* these

categories (Polednak, 1989; Bittles and Roberts, 1992; Chapman, 1993; Shipman, 1994). The consensus is a recent development. For example, in the early part of this century, scientists in several countries tried to link up a study of the major blood groups in the ABO system to racial and ethnic groups.[10] They had learned that Blood Type B was more common in certain ethnic and racial groups -- which some believed to be more inclined to criminality and mental illness (Gundel, 1926; Schusterov, 1927). They kept running up against a brick wall, because there was nothing in the ABO system that could predict behavior. While *that* strategy ended a full half-century ago, there is a contemporary arena in which hematology, the study of blood, has had to resuscitate a concern with "race."

In the United States, there has been an increasing awareness developed over the last two decades of the problem that blood from Americans of European ancestry (read mainly white) tends to contain a greater number of antigens than blood from Americans of African or Asian ancestry (Vichinsky, et al, 1990). This means that *there is a greater chance* for hemolytic reactions for blacks and Asians receiving blood from whites, but *a lower risk for whites* receiving blood from Asians or Blacks. Here we come to a fascinating intersection between the biological and social sciences. In the United States, not only do whites comprise approximately eighty per cent of the population, proportionally fewer blacks and fewer Asian Americans donate blood than do whites. This social fact has some biological consequences, which in turn has some social consequences.

Approximately 400 red blood cell group antigens have been identified. The

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[10]For the discussion in this paragraph, and for the references to the German literature which are used here, I am indebted to William H. Schneider (1996).

antigens have been classed into a number of fairly well-defined systems: the most well known are the ABO and Rh systems, but there are other systems such as P, Lewis, MN, and Kell (standard hematology texts note 10 systems including ABO and Rh). The clinical significance of blood groups is that in the case of a blood transfusion, individuals who lack a particular blood-group antigen may produce antibodies reacting with that antigen in the transfused blood. This immune response to alloantigens (non-self antigens) may produce hemolytic reactions, the most serious being complete hemolysis (destruction of all red blood cells) which can be life threatening. Once generated, the capacity to respond to a particular antigen is more or less permanent because the immune system generates "memory cells" which can be activated by future exposures to the antigen. For those who have chronic conditions, which require routine blood transfusion, this aspect of the immune response is critical, because it increases the likelihood of future transfusion incompatibility. The clinical goal is to minimize immune responses to antigens in transfused blood, in part because a crisis (such as trauma surgery) may require transfusion of whatever blood is available, regardless of its antigen composition.

Most blood banks only test for ABO and Rh -- the most common systems. Testing for the other systems is considered inefficient and will increase the cost of blood. It is essential to minimize the antibodies against blood group antigens for everyone. However, the way in which blood typing is done puts members of racial and ethnic minorities at greater risk for the negative consequences of frequent transfusions. The term *phenotypically matched blood* -- basically means that it is possible to use the social appearances of race as a rough approximation (of likely antigens) to screen to minimize antibodies (along with ABO and Rh).

Transfusion therapy for sickle cell anemia is limited by the development of antibodies to foreign red cells (Vichinsky, et al, 1990). In one important study, the researchers evaluated the frequency and risk factors associated with such alloimmunization, and obtained the transfusion history, red-cell phenotype, and development of alloantibodies in 107 Black patients with sickle cell anemia who received transfusions. They then compared the results with those from similar studies in 51 black patients with sickle cell disease who had not received transfusions and in 19 non-Black patients who received transfusions for other forms of chronic anemia.

> We assessed the effect that racial differences might have in the frequency of alloimmunization by comparing the red-cell phenotypes of patients and blood-bank donors (n=200, 90 percent white). Although they received transfusions less frequently, 30 percent of the patients with sickle cell anemia became alloimmunized, in contrast to 5 percent of the comparison-group patients with other forms of anemia (P less than 0.001). Of the 32 alloimmunized patients with sickle cell anemia, 17 had multiple antibodies and 14 had delayed transfusion reactions. Antibodies against the K, E, C, and Jkb antigens accounted for 82 percent of the alloantibodies.

They then go on to conclude:

> These differences are most likely racial. We conclude that alloimmunization is a common, clinically serious problem in sickle cell anemia and that it is partly due to racial differences between the blood-donor and recipient populations (Vichinsky, et al., 1990).

Note that Vichinsky and his colleagues conclude "that it is partly due to racial differences between the blood-donor and recipient populations." True enough, this may not be "race" in any essentialist conception, but that is precisely the point. A full eighty years ago, Hirschfeld and Hirschfeld (1919:675) posited that when introducing the blood of one

species into that of the same species "those antigen properties which are common to the giver and receiver of blood can not give rise to antibodies, since they are not felt as foreign by the immunized animal." While the Hirschfelds were talking about dogs, they were drawing a straight line towards humans, human classification, and racial taxonomy:

> If we inject into dogs the blood of other dogs it is in many cases possible to produce antibodies. By means of these antibodies we have been able to show that there are in dogs two antigen types. These antigen types, which we recognize by means of the iso-antibodies, may designate two biochemical races (Hirschfeld and Hirschfeld, 1919:675-76).

Using this hypothesis, they went on to perform the first systematic and comprehensive serological study of a variety of ethnic and racial groups. As I indicated above, their classification system did not survive the test of time, but "a way of thinking" persists (Marks, 1995). Moreover, with the data reported in the Vichinsky study (given that the increased blood donations from "Blacks" is a key policy goal for those suffering from a relatively common genetic disease -- sickle-cell anemia), the resuscitation of "race" through blood antigen theorizing and empirical research can not be far behind. That persons who are phenotypically "white" can and do have sickle-cell anemia complicates any essentialized racial theorizing, to be sure – but for the purposes of further action (blood donation requests and transfusion direction), racial phenotyping as a "short-hand" is back with us at the end of the twentieth century.

This provides a remarkably interesting intersection. While the full range of analysts, commentators and scientists -- from post-modern essayists to molecular geneticists to social anthropologists – have been busily pronouncing "the death of race," for practical clinical purposes the concept is resurrected in the conflation of blood donation

frequencies, by "race." I now want to make it clear that I am not merely trying to resurrect "race" as a social construct (with no biological meaning) – no more than I am trying to resurrect "race" as a biological construct with no social meaning. Rather, I am arguing that when "race" is used as a stratifying practice (which can be apprehended empirically and systematically) there is often a reciprocal interplay of a biological outcomes that make it impossible to completely disentangle the biological from the social. While that may be obvious to some, it is completely alien to others, and some of those "others" are key players in current debates about the biology of race.

The American Anthropological Association Statement on "Race"

In May, 1998 the American Anthropological Association issued its own statement on "Race".[11] It attempts to address the myths and misconceptions, and in so doing takes a "corrective" stance towards the folk beliefs about race. The statement strongly states the position that "physical variations in the human species have no meaning except the social ones that humans put on them." But in casting "the problem" in this fashion, it gives the impression that the biological meanings that scientists attribute to race are biological facts, while the social meanings that lay persons give to race are 1) either errors or mere artificial social constructions, and 2) not themselves capable of feed-back loops into the biochemical, neurophysiological, and cellular aspects of our bodies – that, in turn, can be studied, scientifically. The statement of the Anthropological Association is consistent with that of the UNESCO statement on race. However, by formulating the matter so that

[11] This statement, approved by the Executive Board on May 17, 1998, can be retrieved at http://www/ameranthassn.org/racepp.htm. Copies will be made available to conference participants.

"it is *only* the social meanings that humans provide" implies that mere lay notions of race provide a rationale for domination, but have no other utility.

There is profound misunderstanding of the implications of a "social contructivist" notion of social phenomena. How humans identify themselves, whether in religious or ethnic or racial or aesthetic terms all matter for their subsequent behavior. Places of worship are socially constructed with human variations of meaning and interpretation and use very much in mind. Whether a cathedral or mosque, a Synagogue or Shinto Temple, those "constructions" are no less "real" because one has accounted for and documented the social forces at play that resulted in such a wide variety "socially constructed" places of worship (Fujimura, 1998). "Race" as social construction can and does have a substantial effect on how people behave. One important arena for further scientific exploration and investigation is the feed-back between that behavior and the biological functioning of the body. It is now appropriate to re-state the well-known social analytic aphorism of W. I. Thomas, but to re-focus it on human taxonomies of other humans: *If humans define situations as real, they can and often do have real biological and social consequences.*

Molecular Genetics and the New Conflation of Race and Forensics

If "race" is 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 seven years, 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.*

> 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 (figs. 2-4). p. 540

> …it 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 approximate biases, see fig. 9). 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)

When researchers try to make probabilistic statements about which group a person belongs to, they look at variation at several different locations in the DNA -- usually from three to seven loci.[12] For any particular locus, there is an examination of the frequency of that allele *at that locus, and for that population*. In other words, what is being assessed is the frequency of genetic variation at a particular spot in the DNA in each population.

In the July 8, 1995 issue of the *New Scientist* entitled, "Genes in Black and White," some extraordinary claims are 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 work, published in the *Journal of Forensic Science Society,* draws on 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, say the researchers, it is possible to estimate the probability that someone belongs to a particular racial group. The implications of this for determining, for legal purposes, who is and who is not "officially" a member of some racial or ethnic category are profound.

Two years after the publication of the UNESCO statement purportedly burying the concept of "race" for the purposes of scientific inquiry and analysis, and during the same time period that the American Anthropological Association was deliberating and generating a parallel statement, an article appeared in the *American Journal of Human Genetics,* authored by Ian Evett and his associates, summarized thusly:

> Before the introduction of a four-locus multiplex short-tandem-repeat (STR) system into casework, an extensive series of tests were carried out to determine robust procedures for assessing the evidential value of a match between crime and suspect samples. Twelve databases were analyzed from the three main ethnic groups encountered in casework in the United Kingdom; Caucasians, Afro-Caribbeans, and Asians from the Indian subcontinent. Independence tests resulted in a number of significant results, and the impact that these might have on forensic casework was investigated.

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[12] Each location is called a locus, and the plural, or several in combination are called "loci."

> It is demonstrated that previously published methods provide a similar procedure for correcting allele frequencies – and that this leads to conservative casework estimates of evidential value. (Evett, et al., 1996:398)

These new technologies have some not-so-hidden potential to be used for a variety of forensic purposes in the development and "authentication" of typologies of human ethnicity and race. A contemporary up-date of an old idea of the idea of deciding upon "degree of whiteness" or "degree of Indianness" is possibly upon us, anew, with the aid of molecular genetics. The Congress of the United States passed the Allotment Act of 1887, denying land rights to those Native Americans who were "less than half-blood." The US Government still requires American Indians to produce "Certificates with Degree of Indian Blood" in order to qualify for a number of entitlements, including being able to have one's art so labeled. The Indian Arts and Crafts Act of 1990 made it a crime to identify oneself as a Native American when selling artwork without federal certification authorizing one to make the legitimate claim that one was, indeed, an authentic ("one-quarter blood" even in 1990s) American Indian.

As noted above, it is not art, but law and forensics that ultimately will impel the genetic technologies to be employed in behalf of attempts to identify who is "authentically" in one category or another. Geneticists in Ottawa, Canada have been trying to set up a system "to distinguish between 'Caucasian Americans' and 'Native Americans' on the basis of a variable DNA region used in DNA fingerprinting" (*New Scientist*, 1995:37).

Mapping Ethnic Korean Genomics

In late June, 2001, the *Korea Times* published an article in which it reported the work of a biotechnology company completed preliminary research "on mapping the genetic details of what it defines as an ethnic Korean." The company took 96,768 bacterial artificial chromosomes from DNA from those that they claimed to be "pure Korean" – then compared those with the genetic

map produced by Celera. The Korean-based company, Macrogen, then claimed to have "successfully deciphered the genetic information of an ethnic Korean." The president of the company, Suh Jung-seon told a news briefing that the long-term plan was to move from gene-sequencing to drug discovery, but that the genetic map was the first step. The company is now working on identifying genetic markers for four forms of cancer – breast, colon, lung and pancreatic. And here is the tell-tale line from the story: "The research was kicked off in 1999 as a means of developing personalized medical treatment for diseases commonly confronting ethnic Koreans."

Haplotype Map issue

Pharmacogenomics as the harbinger of germline intervention

In the last few years, the field of pharmacogenomics has begun to develop around the delivery of pharmaceuticals to population specific groups. The new pharmacogenomics asserts unequivocally that there are racial differences in the way "different races" respond to certain drugs. Writing in *Science* in mid-October, 1999, Evans and Relling claim that "all pharmacogenetic polymorphisms studied to date differ in frequency among ethnic and racial groups."[i] Whether or not this is based on thoughtfully controlled subject populations, this helps explain the recent announcement that the Food and Drug Administration has just given a provisional green light for a pharmaceutical company (NitroMed) to proceed to try to market "the first ethnic drug", BiDil. It is drug for heart disease specifically designed for the African American population. Blacks are reported clinically to have higher blood pressure rates than whites, and are twice as likely as whites to suffer heart failure. This opened the door to biotechnology companies seeking to develop and market drugs to ethnically and even "racially" specific. In early 2001, NitroMed developed a drug designed specifically for African Americans.

It is not much of a conceptual leap from a pharmaceutical designed for a particular "population group" and a germline intervention designed for such a group. Yet, since economic profit will drive the engine of biotechnology (unashamedly, proudly pronounced as the sine qua non of good business in a capitalist society), a germline intervention for the Zuni is not in the cards – or perhaps, more realistically, not in the profit margin.

International Journal of Forensic Science, reference

In 1989, Virginia was the first state to pass legislation requiring all convicted felons (not just sex offenders) to provide blood samples for use in a state DNA data base. In the next three years, several states followed the lead of Virginia, and in 1993, the FBI, initiated a national DNA databank to link the DNA profiles of convicts across state jurisdictions. The Omnibus Crime Control Act of 1994 included a provision for coordinating DNA databank systems nationwide. Soon thereafter, the Department of Justice awarded nearly nine million dollars to state and city agencies to improve their DNA testing capacities and to encourage uniform standards (Butterfield, 1996). As a direct result, all fifty states have adopted laws requiring "specified offenders to provide blood samples for forensic DNA testing (Nelkin and Andrews, 1999).

For practical purposes, the issue of the authentication of persons' membership in a group (racial/ethnic/cultural) can be brought to the level of DNA analysis. The efficaciousness of testing and screening for genetic disorders in risk populations that are ethnically and racially designated poses a related set of vexing concerns for the "separation" of the biological and cultural taxonomies of race.[13] The technology to use "SNPs on Chips" to group, identify, categorize, and

[13] In New York City, Mayor Guiliani has been an advocate for the use of DNA testing of those arrested by the police. He has been joined by others, who have convinced Attorney General Janet

marginalize is with us, but it is still at a relatively early stage. The Department of Energy awarded a contract to IBM in early 1998 to produce a chip that can hold more than eight times the amount of information available and permit analysis at more than ten times the speed now possible with current chip technology. That technology is currently available, and capable of 7.5 trillion calculations per second.

In more recent years, the technology has moved along, and forensic scientists are now using VNTR loci, and investigating 12-15 segments of the DNA, not just the earlier 3-7.[14] The forensic research reported above occurred before the current computer chip revolution, which will 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 correlation of markers, and it is far from anything but a spurious correlation that will explain nothing – while it will have the seductive imprimatur of molecular genetic precision.

The dangerous intersection of "allele frequencies in special populations" and "police profiling via phenotype"

The conventional wisdom is that DNA fingerprint is just a better way of getting a fingerprint. That is wrong. The traditional physical imprint of your finger or thumb provided only that specific identifying mark, and it is attached to you and you alone.[15] Quite unlike the actual

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Reno that she should appoint a commission to bring back recommendations on this matter. A report is due in 2000, but a preliminary draft has already concluded that such data collection would pass constitutional muster. Critics have pointed to the fact that who the police stop and arrest is not a neutral matter, but heavily politically biased, and in particular, "racially" biased. Indeed, the American Civil Liberties Union has filed a lawsuit to stop the police from targeting primarily African Americans.

[14] The pilot program of the New York Police Department attempts to locate13 loci for identification purposes. (Kevin Flynn, "Police Gadgets Aim to Fight Crime with 007-Style Ingenuity," New York Times, March 7, 2000)

[15] Simon Cole (2001) has just published a book challenging some of the long-held beliefs about the

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 CODIS system. Moreover, there has been rapid change in the inter-linking of state data bases. 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

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infallibility of the physical fingerprint, but that is another story.

"nearly 400,000 offender profiles, and close to 20,000 forensic profiles." States are now uploading an average of 3,000 offender profiles every month. If this sounds daunting, recall that the computer technology is increasingly efficient and extraordinarily fast. It takes only 500 microseconds to search a database of 100,000 profiles (Barry Brown, Harvard DNA conference, December 8, 2000).

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. Based on the statutory language in several of those states, this could easily mean assaying genes or loci that contain predictive information. Tom Callaghan, Program Manager of the FBI's Federal Convicted Offender Program, refused to rule out such possible uses by behavioral geneticists seeking a possible profile for a particular allele among specific offender populations, including especially violent offenders and sexual offenders (Kimmelman, 2000). It is useful to note here that this is the wedge, and then the expansion via "function creep" to other crimes and even misdemeanors. Indeed, Louisiana is the first state to pass a law permitting the taking of a DNA sample for all merely arrested for a felony.

Seven states now require DNA databanking on *all* felons, including white-collar felonies. In the fall of 1998, Governor Pataki proposed that New York state include white collar convicts into the DNA database, but the state legislative assembly balked and forced him to jettison the idea. Perhaps they were concerned that some saliva might be left on the cigars in those backrooms where price-fixing and security-exchange fraud occur. Today, nearly half the states include some misdemeanors in the DNA databank. So we can now see that what started as "sex offenders" has now graduated to misdemeanants and arrestees. While 39 states permit expungement of samples

if charges are dropped, almost all of those states place the burden on the individual to initiate expungement.

Population-Wide DNA Database

It is now relatively common for scholars to acknowledge the considerable and documented racial and ethnic bias in police procedures, prosecutorial discretion, jury selection, and sentencing practices -- of which racial profiling is but the tip of an iceberg. (Mauer, 1999) Indeed, racial disparities penetrate the whole system and are suffused throughout it, all the way up to and through racial disparities in seeking the death penalty for the same crime. If the DNA database is primarily composed of those who have been touched by the criminal justice system, and that system has provided practices that routinely select more from one group, there will be an obvious skew or bias towards this group. Some have taken the position that the way to handle the racial bias in the DNA data-base is to include everyone. But this does not address the far more fundamental problem of the bias that generates the configuration and content of the criminal (or suspect) database. If the lens of the criminal justice system is focused almost entirely on one part of the population for a certain kind of activity (drug-related, street-crime), and ignores a parallel kind of crime (fraternity cocaine sales a few miles away), then even if the fraternity members' DNA are in the data bank, they will not be subject to the same level of matching, or of subsequent allele frequency profiling research to "help explain" their behavior. *That behavior will not have been recorded.* That is, if the police are not stopping to arrest the fraternity members, it does not matter whether their DNA is in a national database or not, because they are not *criminalized* by the selective aim of the artillery of the criminal justice system.

Thus, it is imperative that we separate arguments about bias in the criminal justice system at the point of contact with select parts of the population from "solutions" to bias about "cold hits." It is certainly true that if a member of that fraternity committed a rape, left tissue samples at the scene, and – because he was in a national DNA database – the police could nab him with a "cold hit," that would be the source of the justifiable applause with which I opened this paper. But my point here is that by ignoring powder cocaine and emphasizing street sales of cocaine in the African American community, the mark of criminality thereby generated, and this is not altered by having a population-wide DNA database. However, the surface fiction of objectivity will lead to a research agenda on the DNA database about which I would now like to issue a warning.

There is a serious threat of how these new technologies are about to be deployed that is masked by the apparent global objectivity of a population-wide DNA database. I am referring to the prospects for SNP profiling of offenders. As noted, even if everyone were in the national database, this would not deter the impulse to do specific and focused research on the select population that has been convicted.

An article appeared in the *American Journal of Human Genetic*s in 1997 that made the following claim:

> …we have identified a panel of population-specific genetic markers that enable robust ethnic-affiliation estimation for major U.S. resident populations. In this report, we identify these loci and present their levels of allele-frequency differential between ethnically defined samples, and we demonstrate, using log-likelihood analysis, that this panel of markers provides significant statistical power for ethnic-affiliation estimation (Shriver, et al, 1997:957).

As in the earlier work by Devlin and Rich (1992a), one of the expressed purposes of this research is its "use in forensic ethnic affiliation estimation" (Shriver, et al, 1997:957). This research agenda is likely to produce a significant challenge to the communitarian claim of a

common public safety interest.

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Epilogue: The New and Emerging Relationship Between Behavioral and Molecular Genetics

July 2003

Up until the middle of the 1990s, the fields of behavioral genetics and molecular genetics had very little in common. Behavioral geneticists rarely worked at the molecular level, and their methodology could be characterized as overwhelmingly committed to the use of correlations between a) outcome data of some complex behavioral "phenotype" – such as intelligence, criminality, violence, risk-seeking, alcoholism, manic-depression, schizophrenia, or homosexuality – and b) frequency-of-occurrence of these behaviors or attributes[i] in different populations,[i] often ethnic and racial groups.

In contrast, molecular geneticists were rarely concerned with complex behavior. During its first three decades, the field was riveted to the search for coding regions or DNA markers for such single-gene disorders such as Tay-Sachs disease, hemachromatosis, cystic fibrosis, Huntington's, sickle-cell anemia, and alpha-antitrypsin deficiency, to name but a few. Molecular geneticists did not concern themselves with such complex subject matter as intelligence, schizophrenia or homosexuality.

All that has begun to change. First, there has been a sharp u-turn in the strategic orientation of the Human Genome Project. Rather than an emphasis upon our "sameness" – the field of molecular genetics has now begun to emphasize the importance of looking for "differences" at the level of the DNA.[i] Second, Behavioral Geneticists are turning quickly to find genetic markers (and sometimes even coding regions) that they can associate with complex behaviors. In the last five years, we have seen claims linking DNA regions to cognitive ability in children (Chorney, et al, 1998:159-166), crime

(Jensen, et al, 1998), violence (Caspi, et al, 2002), and attention-deficit/hyperactivity disorder (Smalley, et al, 2002).

The Human Genome Project and the "turn to difference"

In the first decade of the Human Genome Project (*circa* 1988-98), the major focus was on how the mapping and sequencing process could be done on *any one human*, precisely because we are all so alike at the level of our DNA. Any two persons, chosen completely randomly across the globe, share 99.9 per cent of the exact same sequence of nucleotides (the four famous nucleotides –**C**ytosine, **G**uanine **A**denine, and **T**hymine – that are the building blocks of DNA) throughout the genome. That similarity was so overwhelming that it became the rationale for the conclusion that *anyone's genome would do* for generating the map. While there are approximately three billion base pairs of complete overlapping similarity (of c,g,t,a pairs), that recurring figure of 99.9 per cent also means that, with only a .01 difference, there are still approximately *thirty million points of difference* in the DNA between any two people. With the use of new super-computers, it is now possible to take a closer look at these many points of difference. From this perspective, there is suddenly the realization of a considerable amount of differentiation between individuals – and lurking in the corridors of computer-generated correlations and patterns, there will be the inevitable shift to a concern for differences between population groups. Little surprise that this turn to a concern for difference in molecular biology would capture the imaginations and the research agendas of behavioral geneticists. It was inevitable that some among them would attempt to deploy technologies to get at single nucleotides that mark DNA differences – in the hope that these might explain different behaviors.

Armed with this new potential technological development, in the late 1990s

pharmaceutical companies and the biotechnology industry began to change the focus of their attention to "groups of differences" that will permit them to market drugs to select groups (whose DNA indicate a positive reaction). In March, 2001, a company touted as having produced the "first ethnic drug" received a green-letter of approval from the Food and Drug Administration, purposefully aimed at a putative difference of population groups (Winslow, 2001). The drug, BiDil, is being developed by the pharmaceutical company, Nitromed, currently in clinical trials. The company Chief Executive Office, Michael Loberg, explicitly states that the African American population will be the marketing target for the drug, indicating that "BiDil, a heart failure product, reduced mortality in 66% of African Americans, but proved of very little benefit to whites" (*Financial Times*, March 9, 2001:16). This is highly contested terrain, and the fields of pharmacogenomics and pharmacotoxicology are engaged in fierce internal battles as to the appropriate role of race in diagnostics and treatment (Xie, et al 2001; Braun, 2002; Frank, 2001, Lee et al, 2001, Risch et al, 2002). This is not the place to address this dispute. However, it is important to address the serious implications, *for behavioral genetics*, of having race re-enter the scientific and medical literature through the DNA.

The forensic applications of the molecular genetics "turn to difference" are now well-known, converted into household conversations by sensational murder trials and the exculpation of those on death row who have been set free by DNA evidence showing that it was not their DNA that was left at the crime scene (Dwyer et al, 2000). This renewed legitimacy of an emphasis upon both *individual* differences in the DNA, and *group* differences (the Haplotype Maps) has not been lost on behavioral geneticists.

If leading figures in the field of pharmacogenomics could publish, in *Science*, the claim that:

> "All pharmacogenetic polymorphisms studied to date differ in frequency among ethnic and racial groups…" (Evans and Relling 1999:487-91)

and subsequently, in the same article, that:

> "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 1999:487-91)

then it would only be a matter of time before behavioral geneticists would generate correlational data in the attempt to link such behaviors to violence, impulsivity, crime – and lurking in the background, race. It took less then thirty months.

The MAOA gene and predicting violent behavior

In the last half of 2002, *Science* published an article that cemented the new engagement between behavioral genetics and molecular genetics, with a promissory note of an impending marriage. This was a report of research in which the authors claim that their

> … findings provide initial evidence that a functional polymorphism in the MAOA gene moderates the impact of early childhood maltreatment on the development of antisocial behavior in males (Caspi, et al, 2002)

The quotation below is from the last two sentences of this article, and are "pregnant" with policy implications that will re-generate a somewhat dormant social and ethical debate about the advisability of "early identification" of young people at risk for becoming violent and/or "anti-social":

> Moreover, 85% of cohort males having a low activity MAOA genotype who were severely maltreated developed some form of antisocial behavior. Both attributable risk and predictive sensitivity indicate that these findings could

inform the development of future pharmacological treatments. Caspi, et al, 2002).

The notion that one can intercept, and then treat with pharmaceuticals, presumes a much higher "correlation" in subsequent replication studies than this study has reported. In particular, in that very same paragraph (last paragraph in the article) -- those having "the combination of low-activity *MAOA* genotype and maltreatment were only 12% of the male birth cohort, they were 22% of those with multiple antisocial outcomes, yielding an attributable risk fraction (11%)....." (Caspi et al). Isolating, identifying, and "treating" subjects has its own social dynamic. There is a remarkable slippage here, between individual DNA and the attributions of the "operationalization" of the concept of "anti-social" rests entirely upon measures that look at the individual, while both the ideas of "anti-social" and "maltreatment" are interactional. Some substantially greater attention to the *interactional* dynamics needs to be a part of any larger framing of attempts at "early identification" and, even more significant, breaking down the components of "anti-social." Getting in trouble with the criminal justice system is partly about individuals, but it is substantially about individuals with membership in particular social groups, where the criminal justice system has a greater focus of its lens and apparatus. For example, the Drug War, which accounts for more than half of all those incarcerated in US jails and prisons, has been remarkably disproportionately aimed at African Americans and Latinos (Mauer, 1999, Miller, 1996; Cole, 1999; Reinarman and Levine, 1997).

Race and the DNA: Tensions and Current Tendencies Relevant to Behavioral Genetics

Miami, Florida was the scene of the most notorious and widespread DNA dragnet of the last decade. 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 for the purposes of determining a possible DNA match (Pan, 1998). The so-called "Tamiami Strangler" was identified through other means, but this dragnet is of particular interest because 1) almost all of the men who were asked for DNA samples were African Americans, and 2) their DNA samples were stored. 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.

There have been two strongly conflicting voices about the role of the DNA in addressing racial taxonomies. At the White House news conference announcing the completion of the first draft of the complete human genome on June 26, 2000, Francis Collins (director of the Human Genome Project) and Craig Venter (who headed the rival private mapping and sequencing venture at Celera) agreed that human similarities at the DNA level were so dramatic that "race is of no significance" at the level of the DNA (Human Genome News, 2000:1-2). This statement by Collins and Venter echoed assertions in the literatures of physical anthropology, the updated UNESCO statement on race, and a host of other "official positions" by associations of scientists.

However, on the other side, there are practitioners who make use of DNA analysis for the practical task of delivering pharmaceuticals, or of trying to determine from DNA evidence at a crime scene whether there can be an "ethnic estimation" of the suspect's probable identification with some specific population group. As we shall see, this often means "race" or an effective proxy for race. This latter group of researchers have held to the position that race is a meaningful category both for delivering pharmaceuticals and for assessing risk for genetic disorders or for genetic predispositions to complete disorders. (Risch et al, 2002; Lin and Kelsey, 2000; Evans and Relling, 1999). 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). Quite demonstrably, race is still very much alive as a concept, in use, in molecular genetics. It is therefore inevitable that this usage, and this debate, would spill over into behavioral genetics which, as we have seen, has now a formidable branch of its discipline linked to molecular genetics.

We can all celebrate the use of DNA technology to free the nearly one-hundred wrongly convicted prisoners, some who were on death row facing execution, and others who served decades for rapes they did not commit (Dwyer, et al, 2000). Similarly, when law enforcement can score a "cold hit" and catch a rapist because his DNA was on file, there are reasons to applaud. The use of this technology in these 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. 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. The 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.

To provide the context for the discussion of the expanding DNA databases, it is important to point out yet again the systematic bias, by race, of a full range of behaviors displayed across the criminal justice system, from the decisions by police at the point of stop, search, and arrest – through the sentencing guidelines and practices, to incarceration. I have noted the empirical evidence that documents recent developments in the literature of forensic science that claim to be able to predict "ethnic-affiliation" from population-specific allele frequencies. It is the relationship between these two

developments that is the source of easily crafted DNA-based research programs with the consequent misattribution of genetic causes of crime.

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