

**ANCESTRY TESTING AND DNA:
USES, LIMITS – AND CAVEAT EMPTOR**

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Direct consumer use of DNA tests for ancestry tracing has taken off in the last five years, and we are not just talking about probes for first-generation genetic lineage as in “*Who’s your daddy?*” popularized on daytime “reality” television. Since 2002, nearly a half-million people have purchased tests from at least two dozen companies marketing direct-to-consumer kits (Bolnick et al 2007). The motives for testing range from the desire for ancestral links to those who lived on other continents five-hundred plus years ago – to a more modest interest in reconstructing family histories. For many African- Americans, the quest to find a link to regions and peoples of sub-Saharan Africa can take on a spiritual or even messianic quest, at least partially explained by the fact that the Middle Passage across the Atlantic during the slave trade explicitly and purposefully obliterated linguistic, cultural, religious, political and kinship ties. The 2006 PBS television series, *African American Lives*, brought this quest into sharp relief. First celebrity and later ordinary Blacks were mesmerized by stories of DNA matches that claimed to reveal or refute specific ancestral links to Africa, to Native American heritage, and surprising to some, East Asian or European populations.

In sharp contrast, CBS’ *60 minutes* aired a dramatic segment in the fall of 2007 (October 7) that portrayed a direct and sharp challenge to the claims-making about such ancestry testing. The segment began with Vy Higgensen, an African-American woman from New York’s Harlem triumphantly affirming her connection to “new kin” (one of whom was a white male cattle rancher from Missouri). But as the program unfolds, we see a disturbing cloud of doubt drift over the last part of the segment that ends with a less than subtle hint at specious claims. A first test from the company African Ancestry, claims that Higgensen is linked to ancestors in the Sierra Leone, the Mende people. She rejoices. “I am thrilled! It puts a name, a place, a location, a people!” But then she is shown the results of a second test, from another company, Relative Genetics, which claims that she instead has a genetic match to the Wobe tribe of the Ivory Coast. She seems philosophical. Yet a third test, from still another company, Trace Genetics, claims

that her ancestors are from Senegal, the Mendenka. Now she seems agitated, visibly concerned, confused – and most certainly disappointed that what began as a definitive match to a particular group or region of Africa has now turned into a “you pick which one you want to believe” game.

The very next month, serious questions about the tests were revisited when Henry Louis Gates, who had hosted the aforementioned *African American Lives*, said that the same thing had happened to him. Here is how the *New York Times* (Nov. 25, 2007) cast the story:

[HENRY LOUIS GATES JR.](#), whose [PBS](#) special “African American Lives” explores the ancestry of famous African-Americans using DNA testing, has done more than anyone to help popularize such tests and companies that offer them. But recently this Harvard professor has become one of the industry’s critics.

Mr. Gates says his concerns date back to 2000, when a company told him his maternal ancestry could most likely be traced back to Egypt, probably to the Nubian ethnic group. Five years later, however, a test by a second company startled him. It concluded that his maternal ancestors were not Nubian or even African, but most likely European.

Why the completely different results? Mr. Gates said the first company never told him he had multiple genetic matches, most of them in Europe. **“They told me what they thought I wanted to hear,”** Mr. Gates said.

Here we have the first sally into a combined definitional and epistemological conundrum – beginning with the meaning of “ancestry.” While this is typically used to refer to geographic areas where one’s biological ancestors lived, with just a few minutes of reflection, we can see an enormous problem to which even common sense will alert us: *Which ancestors?* Easy enough if we are only dealing with mom and dad, or four grandparents – or we can even handle three generations back with eight great- grandparents. But if we go back six generations, that means we all have 64 direct biological ancestors. Since each of these 64 could be said to have made an equal biological contribution to our makeup, why would we choose to represent any one or two as our “real” biological lineage? (Eight generations gives us 256 such ancestors, and twenty generations places the figure at 1,048,576.)

The capacities and limits of using DNA to test for ancestry

What can DNA tell us about our genetic lineage, and where does it fall short? What explains Vy Higgensen's multiple results from different testing sites? Flawed methodology? Partial truths hyped as definitive findings? Did the testing companies use different methods, or deploy different reference populations – or both?

Let's begin with what DNA testing *can* tell us about biological ancestry. There are two different tests – one for males and another for females, and each can provide relatively definitive results along one particular line of our genetic ancestry.

Males inherit the Y-Chromosome from their biological fathers. The markers are sufficiently distinctive so that the test can not only identify the father, but also the father's father, and if the data were available, the father's father's father. This path to ancestry identification can go on for as many generations as data are available – which is how Thomas Jefferson (or one of his brothers) was linked to Sally Hemmings' offspring. For more than 150 years, historians argued and debated as to whether Jefferson had children with one of his slaves, Sally Hemmings. Only in the last decade has Y-Chromosome analysis settled the debate in favor of those who have claimed that the historical record pointed to Thomas Jefferson.

The test for female ancestry has an interesting parallel. We can definitively answer "Who's your mommy?"! All of a mother's children inherit her mitochondrial DNA (mtDNA). Located within the cell but outside the nucleus, mtDNA serve as the cell's energy producers but only the daughters pass it on. Thus, for a female, it is possible to trace and identify her mother, her mother's mother, etc., (along the same line as just noted for males using Y-chromosome analysis). This was the way that granddaughters were linked to their grandmothers in the aftermath of Argentina's "Dirty War" (1976-83). Thousands of young fathers and mothers "disappeared" by acts of the ruling junta, and their orphaned small children were given to couples who wished to adopt (Penchaszadeh 1992). It was through mitochondrial DNA testing that the grandmothers were reunited with the children of their (murdered/disappeared) daughters.

These two tales reveal not only the power of DNA ancestry testing, but their significant and consequential social and political uses as well.

But it is also vital to re-state the limitations -- that these two tests can identify, for example, only two of the 64 great great great great grandparents. Indeed, only two of the next generation further back, of 128, can be so identified, only two of 256, and so on. Yet each of the other (62 or 126 or 254) contributed equally to our genetic makeup as the two we can trace by the sex-linked paternal or maternal lines. The Genographic Project of the *National Geographic Magazine* uses these two tests, supplemented by a selection of 22 additional markers. The researchers correctly inform participants who send in their DNA that there are limitations to what can be claimed. Nonetheless, people who receive the results are often led to believe that if their test does NOT match the archival sample of a particular Native American or Eskimo group, then they are NOT genetically linked to that group. Several years ago, when Genographic scientists sampled people in the Arctic North, Lorianne Rawson, a 42 year-old woman who had strong social ties to, and who believed that she was descended from, the Aleuts of Alaska, submitted her DNA to the Genographic project. She was informed by the testers that results linked her instead to the Yup'ik Eskimos, the enemies of the Aleuts (Harmon 2006:1). Personal and political trauma can understandably ensue from such seemingly authoritative reassignments. This kind of "result", however problematic in terms of disclaimers or caveats, happens when the technology inevitably limits the analysis to particular corridors or silos of the ancestry tree, and locks in on that limited corridor. While the results are presented as an authoritative claim, the laity are not provided with the tools to understand how the many other ancestral links noted above are excluded by the limits of ancestry tracing through DNA analysis.

Sometimes these putative links (or lack of same) have significant financial repercussions. The Black Seminoles have been struggling with this very question of whether to use DNA analysis to "authenticate" their relationship to the Seminole Indian Tribe. The reason is straightforward and serious: money. The federal government, pursuant to a land-settlement claim, made an award to Seminole Indians in 1976, poised to distribute upward of \$60 million. In 2000, the Seminole Nation of Oklahoma amended its constitution so that members needed to show "one-eighth Seminole blood" (Johnston 2003). The Black Seminoles could use either Y-

chromosome analysis or mitochondrial DNA (mtDNA) to link themselves through very thin chains back on two edges of the genealogical axis (mother's mother's mother, etc.; or father's father's father, etc.), but that would miss all other grandparents (14 of 16, 30 of 32, 62 of 64). The stakes are even higher for the Florida Seminoles. In 2006, the tribe purchased the entire Hard Rock Café chain for approximately one billion dollars. If you were offered a genetic ancestry test of either Y-Chromosome or mtDNA analysis, would you really want to engage the probabilistic Russian-roulette type gamble?

To supplement the limitation of Y-Chromosome and Mitochondrial DNA testing, a group of researchers has come up with a procedure to discern the frequency of certain markers that are hypothesized as belonging, selectively, to our ancestors. However, there are several blind assumptions that have to be accepted in order to have confidence in the links to ancestral populations so defined.

Ancestral Informative Markers (AIMS) – The new proxy for Race

Unlike Y DNA or mtDNA tests, this technology examines a group's relative share of genetic markers found on the autosomes – the non-gender chromosomes inherited from both parents.

Since Ancestry-Informative Markers (AIMs) are overwhelmingly shared across all human groups, it is therefore not their absolute presence or absence, but their rate of incidence, or frequency, that is usually being analyzed, and this is especially true when it comes to claims about continental populations. How did these markers come to represent ancestral populations of Africa, Europe, and Native America? The vast majority of these markers are NOT 'population specific,' as the inventor of Ancestry Informative Markers (AIMs) originally claimed (Shriver et al. 1997). Because the companies marketing ancestry tests hold proprietary interests in their techniques, most do not make them available for possible scientific replication, and their modeling constructs are therefore undisclosed. Thus, we are left to speculate about the threshold level of frequency that is used to determine the grounds for inclusion or exclusion, as well as what counts as a "pure" referent population.

In one lab that permitted its procedures to be studied by a medical anthropologist, ancestry percentages were generated by formulas that compare the relative frequency of markers (44 in total) between selected populations of recent European, African, and Native American descent (Fullwiley 2008). All those in the defined group were tested for the frequency of markers that the researchers hoped would provide *relative* distinguishability. Recall that the frequency at which each marker appears in each group is noted – and whole continents are never sampled. Finally, the researchers compare marker frequencies between the three groups to come up with values which, when taken together, yield a probability result about ancestral percentages. This procedure generates the baseline for the statistically-based notion of a 100 per cent pure European (or African, etc.), so that when you send in your DNA from the saliva swab, and it turns out that you have one-third of the markers that have been designated as “European” – you are told that you are 33 per cent European. It is by this statistical legerdemain that we have come to the molecular reinscription of race in contemporary human genetics (Fullwiley 2007; Duster 2006).

There are a number of deeply problematic, even flawed assumptions behind that percentage claim. What is this “reference population” that has become the measuring stick by which we inform people of their “per cent ancestry to a putatively pure continental population” (read “race” here). Let’s re-examine such a result if reported back to someone of recent African descent. First, more than 700 million people currently inhabit the African Continent – and human geneticists have known for decades that this is the continent with the greatest amount of genetic variation on the globe. The reason for this variation was noted by Pilar Ossorio: “For many regions of the human genome, there are more variants found among people of Africa than found among people in the rest of the world. This is probably because humans have resided in Africa for much longer than we have resided any place else in the world, so our species had time to accumulate genetic changes within the people in Africa.” (Ossorio 2009).

A scientifically valid random sampling of even one percent of this population would require a prohibitively expensive research program – a database of seven million. So instead researchers have settled for “opportunity samples” – namely, a few hundred here or there, or even thousands that have been collected for a variety of reasons. No attempt has ever been made

to take theoretically driven or random samples from African tribes such as the Lua, Kikuyu, Ibo, Hauser, Bantu, Zulu (with all the linguistic, cultural and political complexities of defining the boundaries of such groups), not to mention the thousands of language groups spread across the continent. How then, can we have any sense of reliability or validity for a claim that says someone is 80 per cent African – when the baseline for that claim is based upon the transparent scaffolding of chance – not purposive sampling?

Yet, when taken together, we are told that these markers appear to yield sufficiently distinctive patterns in those continental populations tested. So now we see how a specific pattern of genetic markers on each of a set of chromosomes that have a *higher frequency* in the "Native Americans" sampled becomes established as a "Native American" ancestry reference. (The fact that there are more than 480 different populations of the Tribal Council – the vast majority of which have never been sampled – is no small matter here, but that is not the focus of the critique I am about to make.) The problem is that millions of people around the globe will have a similar pattern -- that is, they'll share similar base-pair changes at the genomic points under scrutiny. This means that someone from Bulgaria whose ancestors go back to the 15th century could (and sometime does) map as partly "Native American," although no direct ancestry is responsible for the shared genetic material. There is an overwhelming tendency for those who do AIMS analysis with the purpose of claims about ancestry to arbitrarily reduce all such possibilities of shared genotypes to "inherited direct ancestry." In so doing, the process relies excessively on the idea of 100-percent purity, a condition that could never have existed in human populations.

While this is a huge problem, yet another issue looms even larger. If a computer program produces an outcome indicating that 35 per cent or more of a particular genetic marker exists in population A (let's call them East Asian), while 35 per cent or less occur in population B (let's call them European), the researcher may use that marker to say that someone is from East Asian ancestry. To make matters even more complicated, claims about how a test subject's patterns of genetic variation map to continents of origin and to populations where particular genetic variants arose, require that the researchers have "reference populations." The public needs to understand that these reference populations comprise relatively small groups of *contemporary* people. Those groups sampled may have migrated over several centuries, and thus these researchers must make

many untested assumptions in using these contemporary groups to stand as proxies for populations from centuries ago, whether putatively representing a continent, a region, or a linguistic, ethnic or tribal group. To construct tractable mathematical models and computer programs, researchers bracket these assumptions about ancient migrations, reproductive practices, and the demographic effects of historical events such as plagues and famines. Given these intractable barriers to even low-level probabilistic reliability, geneticists are on thin ice telling people that they do or don't have ancestors from a particular people.

Thus, instead of asserting that someone has no Native American ancestry, the most truthful statement would be: *It is possible that while the Native American groups we sampled did not share your pattern of markers, others might since these markers do not exclusively belong to any one group of our existing racial, ethnic, linguistic, or tribal typologies.* But computer-generated data provide an *appearance* of precision that is dangerously seductive and equally misleading. Now we come to one part of the answer as to why different companies come to different results. We cannot conclude that an individual has a close affinity to a particular ethnic or racial group or local geographical population simply because their DNA markers match that population. “Such a conclusion would require demonstrating that the DNA sequence is not present in other places, it would require demonstrating that the gene pool of that ethnic group or local population had been close and immobile for centuries and millennia...” (Weiss and Long, 2009, forthcoming).

Be especially wary of applications of these claims

There is a yet more ominous and troubling element of the reliance upon DNA analysis to determine who we are in terms of lineage, identity, and identification. The very technology that tells us what proportion of our ancestry can be linked, proportionately, to sub-Saharan Africa (ancestry-informative markers) is the same being offered to police stations around the country to "predict" or "estimate" whether the DNA left at a crime scene belongs to a white or black person. This "ethnic estimation" using DNA relies on a social definition of the phenotype (phenotype being the observable physical or biochemical characteristics of an organism, determined by both genetic makeup and environmental influences). That is, in order to say that someone is 85

percent African, we must know who is 100 percent African. **Any molecular, population, or behavioral geneticist who uses the term “per cent European” or “per cent Native American” is obliged to disclose that the measuring point of this "purity" (100 per cent) is a statistical artifact that begins not with the DNA, but with a researcher's adopting the folk categories of race and ethnicity.**

The Segue to Forensics and Criminal Justice and “Molecular Race”

It is possible to make arbitrary groupings of populations (geographic, linguistic, self-identified by faith, identified by others by physiognomy, etc.) and still find statistically significant genetic markers between those groupings. For example, we could simply pick all of the people in Chicago, and in Los Angeles, and find statistically significant differences in DNA marker frequency at *some* loci. Of course, at many loci, even most loci, we would not find statistically significant differences. When researchers claim to be able to assign people to groups based on marker frequency at a certain number of loci, they have chosen loci that show differences between the groups they are trying to distinguish.

The work of Evett et al (1993, 1996), Lowe et al (2001) and others suggest that there are only about ten per cent of sites in the DNA that are "useful" for making distinctions. This means that at the other ninety per cent of the sites, the allele (one member of a pair or series of genes that occupy a specific position on a specific chromosome) 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 we cannot find a single site where allele frequency matches some phenotype that we are trying to identify (for forensic purposes, we should be reminded), that there are not several (four, six, seven) that will not be effective, for the purposes of aiding the FBI, Scotland Yard, or the criminal justice systems around the globe in highly probabilistic statements about suspects, and the likely ethnic, racial, or cultural populations from which they can be identified – statistically.

So when it comes to molecular biologists asserting that “race has no validity as a scientific concept,” there is an apparent contradiction with the practical applicability of research

on allele frequencies in specific populations. 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. All this is true. However, when Scotland Yard or the Birmingham, England police force, or the New York City police force, wants to narrow the list of suspects in a crime, they are not primarily concerned with tight taxonomic systems of classification with no overlapping categories. That is the stuff of theoretical physics and logic in philosophy, not the practical stuff of helping to solve crime or the practical application of molecular genetics to health delivery via genetic screening -- and all the messy overlapping categories that will inevitably be involved with such enterprises. That is, some African- Americans have Cystic Fibrosis even though the likelihood is far greater among Americans of North European descent, and in a parallel if not symmetrical way some American whites have Sickle Cell Anemia even though the likelihood is far greater among Americans of West African descent. But in the world of cost-effective decision-making, genetic screening for these disorders is routinely done based on common-sense versions of the phenotype. The same is true for the quite practical matter of naming suspects.

Searching for Racial and Ethnic markers in Forensic DNA

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 cases.

Evetts's work (1993), 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, 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.

The legal and social uses of these technologies are already in considerable use by the *cognoscenti*, and they are poised to "take off." Here are some examples:

More than a decade ago, several states began keeping DNA database files for sexual offenders. Three factors converged to make this a popular decision by criminal justice officials that would be backed by politicians and the public: 1) sex offenders are those most likely to leave body tissue and fluids at the crime scene, 2) they rank among the most likely repeat offenders, and 3) their crimes are often particularly reprehensible in that they violate persons, from rape to molestation and abuse of the young and most vulnerable. Today, all fifty states store DNA samples of sex offenders, and most states do the same for convicted murderers. But now thirty-four states store DNA samples of all felons (Simoncelli 2006:1).

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. Thus, civil privacy protection, which in the default mode would place the burden on the state, is reversed. In other words, instead of "innocent until proven guilty" it has become "criminally suspect until proven innocent" so to speak. Twenty states now authorize the use of databanks for research to develop new forensic techniques. Based on the statutory language in several of those states, this could easily mean assaying genes or loci that contain predictive information – even though current usage is supposed to be restricted to analyzing portions of the DNA which are only useful as

identifying markers. Since most states retain the full DNA (and every cell contains all the DNA information), it is a small step to using these DNA banks for other purposes. The original purpose has long been pushed to the background, and the “creep” expands not only to other crimes besides sexual offenses, but to misdemeanors and even those merely arrested as well, California being a case in point.

On January 5, 2006, the president of the United States signed into law HR 3402, the Department of Justice Reauthorization bill of the Violence Against Women Act of 2005. This legislation for the first time permits state and federal law enforcement officials the right to transfer DNA profiles of those merely arrested for federal crimes into the federal Combined DNA Index System (CODIS) database. Previously, only convicted felons could be included. Those DNA profiles will remain in the database unless and until those who are exonerated or never charged with the crime request that their DNA be expunged. Thus the default will be to store these profiles, and expunging requires the proactive agency (and resources) of those arrested.

This announcement was the source of celebration by one of the leading providers of DNA testing services, Orchid Cellmak, Inc, of Princeton, New Jersey. The president and chief executive officer of Cellmak, Paul J. Kelly, immediately issued a statement applauding this development, stating:

This is landmark legislation that we believe has the potential to greatly expand the utility of DNA testing to help prevent as well as solve crime... It has been shown that many perpetrators of minor offenses graduate to more violent crimes, and we believe that this new legislation is a critical step in further harnessing the power of DNA to apprehend criminals much sooner and far more effectively than is possible today.” (Orchid Press Release, January 6, 2006: 1).

But there is yet another reason why we must be much more wary of these developments. Criminologists and statisticians have provided enough convincing evidence that reliability may be a systemic issue with regard to “exact matches”, leading to false “hits” with traditional STR

approaches (Thompson 2008). As for the possibility of using full DNA samples for forensic research, attempts to determine physical features, such as skin color, hair texture, and eye pigment, have already been made (Fullwiley 2008b). These techniques, as they rely on “admixture estimates” discussed earlier, are also rife with reliability issues despite their veneer of exact precision with regard to continental genetic affinity, or, put bluntly, racial diagnosis. This kind of categorizing of subjects and patients is occurring in medical and health journals, often with the idea that pharmaceuticals could be tailored to patients based on putative notions of their ancestral genetic “admixture.” Researchers are also finding new ways to identify genetic variants related to “admixed” populations that they believe may be “linked” to variable complex disease conditions, such as end-stage renal disease (Kao et al 2008). Here whole areas of the genome are assumed to be ancestrally “African” or “European” with very little discussion of how such prior determinations of purity are--or are not-- relevant for all self-identified Africans and Europeans.

An Unregulated No-Man’s Land – No oversight, no guidelines

Much like the industry of assisted reproduction in the United States, there is a complete absence of regulation or quality control with genetic ancestry testing. There is no requirement for transparency in the construction and use of reference populations. Any company can claim that their laboratories can analyze your DNA to provide accurate information about your ancestry. If three different companies provide three different answers (as in the *60 Minutes* report noted at the outset), what is a consumer to do? Which company is correct, or more to the point, which one is more likely to be correct? There is no way of knowing, since we have no “gold standard” for excellence or professional self-policing. This was pointed out in *Science* two years ago (Bolnick et al 2007), and in November 2008, the American Society of Human Genetics (ASHG) issued a statement on ancestry testing that included five recommendations emphasizing the need for greater responsibility, research, explanatory clarity, collaboration and accountability by these direct-to-consumer companies.ⁱ The statement also pointedly warned of several important limitations to the scientific approaches used to infer genetic ancestry, including the false assumption that contemporary groups are reliable substitutes for ancestral populations, and

most significantly, the lack of transparency regarding the statistical methods that companies use to determine test results. (Lee et al forthcoming 2009).

But while the ASHG statement calls for greater transparency, we have seen that private sector providers of ancestry testing have proprietary reasons for keeping secret their own particular combinations of key technology, software and population sampling procedures. Most are unwilling to disclose the size and composition of their reference populations. Without mechanisms to enforce transparency, there is no way of assessing the scientific basis for specific assertions of “percent ancestry”. For example, until and unless there is a publicly available version of what constitutes a 10 percent European or a 100 percent African, etc., claims about 80 percent ancestry cannot be fully understood or tested, much less replicated.

Building on the ASHG recommendations for transparency, there is a need for specific policies enforced by federal agencies. For example, the Federal Trade Commission and the Centers for Disease Prevention and Control can and should play pivotal roles in setting industry standards for what constitutes responsible and accountable practices. These agencies can promote the research necessary to identify minimal guidelines for presenting the fair uses and clear limitations of current genomic technologies. Guidelines for transparency would also include clear statements spelling out the risks associated with over-extrapolating or misinterpreting genetic ancestry results. The active involvement of regulatory agencies would provide infrastructure for the interdisciplinary dialogue necessary to create effective policies and for maintaining industry standards (Lee et al, forthcoming 2009). While supporting such measures, we should not be naïve about their effectiveness, since the demands on these companies to generate profits are strong and insistent. It is difficult to exaggerate the role that money plays in this whole process, whether for ancestry testing companies trying to stay in business or members of groups seeking to cash in on casino gambling by being designated an Indian tribe by the U.S. Interior Department’s Bureau of Indian Affairs (BIA). For example, the Mashantucket Pequot (largely African-Americans) and the Mohegan Tribal Nation (largely whites) of Connecticut have established the largest casinos in the world, generating billions of dollars in profits.

References

- American Society of Human Genetics Ancestry Testing Statement. November 13, 2008.
available at <http://www.ashg.org/>
- Bolnick, Deborah A., Duana Fullwiley, Troy Duster, Richard S. Cooper, Joan H. Fujimura, Jonathan Kahn, Jay S. Kaufman, Jonathan Marks, Ann Morning, Alondra Nelson, Pilar Ossorio, Jenny Reardon, Susan M. Reverby, and Kimberly TallBear, "The Science and Business of Genetic Ancestry Testing," *Science*, 18, (19 October 2007) 399-400.
- Duster, Troy "The Molecular Reinscription of Race: Unanticipated Issues in Biotechnology and Forensic Science" *Patterns of Prejudice*, 40, Nos. 4/5, 2006
- Evet, I.W., I.S. Buckleton, A. Raymond, and H. Roberts, (1993) "The Evidential Value of DNA Profiles," *Journal of the Forensic Science Society*, 33 (4): 243-244, 1993
- Evet, I.W., P.D. Gill, J.K. Scrannage, and B.S. Wier, "Establishing the Robustness of Short-Tandem-Repeat Statistics for Forensic Application," (1996) *American Journal of Human Genetics*, 58: 398-407,
- Evet, I.W., "Criminalistics: The Future of Expertise," *Journal of the Forensic Science Society*, 33 (3):173-178, 1993
- Fullwiley, Duana "The Molecularization of Race: Institutionalizing Human Difference in Pharmacogenetics Practice," *Science as Culture*, 16, No. 1, 1-30, (March 2007)
- Fullwiley, Duana, (2008a) "The Biological Construction of Race: Admixture Technology and the New Genetic Medicine," *Social Studies of Science*, 38, 5, 695-735
- Fullwiley, Duana, (2008b) "Can DNA 'Witness' Race: Forensic Uses of an Imperfect Ancestry Technology," Council for Responsible Genetics national conference, *Forensic DNA Databases and Race: Issues, Abuses and Actions*, June 19-20, 2008, New York University. Available at www.gene-watch.org.
- Harmon, Amy, "DNA Gatherers Hit a Snag: The Tribes Don't Trust Them" *New York Times*, Dec. 10, 2006 (p. 1), Section 1
- Johnston, Josephine "Resisting a Genetic Identity: The Black Seminoles and Genetic Tests of Ancestry," *Journal of Law, Medicine and Ethics*, (November 2003) 31, 262-271

- Kao WH et al. *Nat Genet.* Oct; 40(10): 1185-92. (2008)
- Lee, Sandra Soo-Jin, Deborah Bolnick, Troy Duster, Pilar Ossorio and Kimberle Tallbear, "Moving Beyond Quality Assurance: The Ethics of Genetic Ancestry Testing" (forthcoming, 2009)
- Lowe, Alex L., Andrew Urquhart, Lindsey A. Foreman, Ian Evett, "Inferring Ethnic Origin by Means of an STR Profile," *Forensic Science International*, 2001, 119:17-22
- Olson, S., *Mapping Human History: Discovering the Past Through Our Genes.* Anonymous, Ed. (Houghton Mifflin Company, New York, 2002). Pp.292.
- Ossorio, Pilar N., "Race, Genes and Intelligence," Council for Responsible Genetics briefing paper series *Genetics and Race: Past Abuses, Present Prospects and Future Solutions* (forthcoming June 2009).
- Penchaszadeh, Victor B. "Abduction of Children of Political Dissidents in Argentina and the Role of Human Genetics in Their Restitution," *Journal of Public Health Policy*, 13, 3 (Autumn), 1992), 291-305
- Simoncelli, Tania, "Dangerous Excursions: The Case Against Expanding Forensic DNA Databases to Innocent Persons," JLME, 2006 (full reference to be supplied)
- Shriver, Mark D., Michael W. Smith, Li Jin, Amy Marcini, Joshua M. Akey, Ranjan Deka, and Robert E. Ferrell, "Ethnic-Affiliation Estimation by Use of Population-Specific DNA Markers," *American Journal of Human Genetics*, 1997, 60:957-964.
- Thompson, William C., "The Potential for Error in Forensic DNA Testing (and How That Complicates the Use of DNA Databases for Criminal Identification)" Council for Responsible Genetics national conference, *Forensic DNA Databases and Race: Issues, Abuses and Actions*, June 19-20, 2008, New York University. Available at www.genewatch.org.
- Tishkoff, S.A., K.K. Kidd, *Nature Genetics* 36, S21 (November 2004).
- Tracy, Paul and Vincent Morgan. (2000) "Big Brother and His Science Kit: DNA Databases for 21st Century Crime Control," 90, *J of Criminal Law and Criminology* 635, 682
- Weiss, Kenneth M. and Jeffrey C. Long, "Non-Darwinian Estimation: My Ancestors, My Gene's Ancestors," (forthcoming 2009).

Endnote

ⁱ The American Society of Human Genetics Ancestry Testing Statement. November 13, 2008. available at <http://www.ashg.org/>

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