

HUMAN EVOLUTIONARY BIOLOGY

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15 Ten Facts about Human Variation

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INTRODUCTION

The idea of race, so intrinsic a part of American social life, is a surprisingly ephemeral one. The ancient world conceptualized human diversity in purely local terms, and the idea that the human species could be naturally partitioned into a reasonably small number of reasonably discrete kinds of people does not seem to have been seriously entertained until the late seventeenth century (Hannaford, 1996; Hudson, 1996; Jahoda, 1999; Stuurman, 2000). The term “race” was introduced into biological discourse by Buffon in the eighteenth century, but he used the term in an entirely colloquial, not taxonomic, way. In this sense the term meant the equivalent of a “strain” or “variety” – a group of organisms linked by the possession of familial features. Buffon’s rival Linnaeus, the founder of modern taxonomy, divided humans into four geographical subspecies – although he did not call them “races.” The succeeding generation fused Buffon’s word with Linnaeus’s concept, and thus created the scientific term “race,” used well into the twentieth century.

The Linnaean concept of race, however, was a Platonic or essentialist idea – describing not a reality (how organisms are), but a hyper-reality (the imaginary form they represent). Thus, Linnaeus (1758, p. 21) defined “*Homo sapiens Europaeus albus*” – that is to say, white European *Homo sapiens* – as having “long flowing blond hair” and “blue eyes” (*Pilis flavescens prolaxis. Oculis caeruleis*). Even taking account of the fact that Linnaeus did not travel much outside of his native Sweden, it is difficult to imagine him being that naïve. Linnaeus clearly was describing an ideal type, a metaphysical form, not the actual indigenous inhabitants of Europe.

The essentialized race was not necessarily limited to the continents. Since it was not an empirical concept to begin with, it could be easily extended to any group of people with a distinct identity. Thus, one could just as readily talk about the “Aryan race,” the “French race,” or the “Jewish race,” even though the terms technically applied to a linguistic group, national

group, and religious group, respectively. Race was taken to inhere in an individual, as a group quality producing a specific identifiable form and expression in different people. Even so recent a scholar as the Harvard physical anthropologist Earnest Hooton (1926) could think of race as something to be diagnosed, on a medical analogy.

By the early 1930s, partly in response to the rise of racist ideologies in Europe, the concept of race underwent a revision. It became a group of people, a population, rather than an inner quality or spirit. This reversed the locus of race; instead of a race residing within a person, a person would now be a part of a race. Further, the laws of genetics did not seem to permit anything to be transmitted as race was thought to be. What would be “passing” to the previous generation – pretending to be a race you really were not – would be merely the facts of complex ancestry, or euphemistically, “gene flow,” under the new concept. Finally, an appreciation for the significance of cultural distinctions in maintaining boundaries between human groups made it necessary to distinguish between ostensibly biological units of the human species, and culturally constituted group differences, and to juxtapose the latter category of human diversity against the study of race; it would come to be known as “ethnicity.”

Physical anthropology, like human genetics, had to reinvent itself after World War II, since it was in fact not terribly easy to distinguish the good American science of race from its evil Nazi counterpart. Hooton had tried to do so as early as 1936, publishing an indignant review article in *Science* as “a physical anthropologist, who . . . desires emphatically to dissociate the finding of his science from the acts of human injustice which masquerade as ‘racial measures’ or ‘racial movements’” (Hooton, 1936, p. 512).

Hooton, however, was unsuccessful. A “new” physical anthropology (Washburn, 1951) would study human adaptation and microevolution, which was local, not continental. The human species would now be seen “as constituting a widespread network of

more-or-less interrelated, ecologically adapted and functional entities" (Weiner, 1957, p. 80).

The Civil Rights movement precipitated a second revision of the ontology of race for physical anthropology. If the units of the human species were indeed local populations, then higher-order clusters of populations could now be recognized as arbitrary and ephemeral (Thieme, 1952; Hulse, 1962; Johnston, 1966). Thus Frank Livingstone could epigrammatically declare, "There are no races, there are only clines" (1962, p. 279).

Of course, there was the embarrassment of having the President of the American Association of Physical Anthropologists (Carleton Coon of the University of Pennsylvania, Earnest Hooton's second doctoral student at Harvard) colluding with the segregationists in 1962, but Coon stood alone in defending the segregationist literature from censure by the American Association of Physical Anthropologists (Coon, 1981; Lasker, 1999). The "new physical anthropology" gave practitioners leeway to abandon race to the cultural anthropologists and sociologists on one side (as ethnicity), and to the population geneticists (as science) on the other. Thus, widely used biological anthropology texts, such as Frank Johnston's (1973) *Microevolution of Human Populations* and Jane Underwood's (1979) *Human Variation and Human Microevolution* could get by without even mentioning race in the index.

Population geneticists, however, were actually multivocal about race. On the one hand, Lewontin's (1972) famous "apportionment of human diversity" was able to quantify what fieldworkers had long known: there are all kinds of people, everywhere. Lewontin's discovery that there is approximately six times more within-group variation than between-group variation detectable in the human species seemed to put the lie to any possibility that the human species could be naturally divided into a small number of relatively discrete gene pools. On the other hand, other population geneticists would use races as natural categories quite unproblematically and unreflectively (Cavalli-Sforza, 1974; Nei and Roychoudhury, 1974).

By the 1990s, race was undergoing yet another transformation at the hands of population geneticists, from a geographically localized gene pool or population to the small amount of difference detectable among the most geographically separated peoples, after overlooking the major patterns of human variation – the cultural, polymorphic, clinal, and local. This is a new concept of race as a genetic residual, a successor to the race as population and the race as essence, and it is the idea of race employed by most contemporary defenders of race in physical anthropology and population genetics. Nevertheless, it would be largely unintelligible to scholars of earlier generations, who might otherwise be inclined to agree with the proposition that race is "real."

To understand race properly, however, we must appreciate that it is a biocultural category, the result of a negotiation between patterns of difference and perceptions of otherness. Old categories of identity are obliterated, or are relegated to "ethnicities" rather than to "races" (Ignatiev, 1996; Brodtkin, 1999) and newer, more politically salient categories become racialized. Notably, the 2000 US Census separated the question of "Spanish/Hispanic/Latino" from that of "race" on the quite sensible grounds that "Spanish/Hispanic/Latino" designates a linguistic category, and thus cross-cuts race. One could, after all, reasonably fall within that category with mostly Native American Ancestry, mostly Filipino ancestry, mostly southern European ancestry, mostly Afro-Caribbean ancestry, and most especially, a mixture of several of those. Then the Census provided the familiar choices in the "race" question (White, Black, Native American, Asian, and Pacific Islander), but also included the option "Some other race." That choice, "Some other race," was checked by 42% of self-identified Hispanics, but by only a negligible amount of non-Hispanics. It seems that the Census Bureau over thought the matter: Hispanic has effectively become "some other race" – the cultural basis of its demarcation notwithstanding (Mays et al., 2003).

Population geneticists have not been able to resolve race because it is not a genetic category (Graves, 2004). Race is a human group which, like all human groups down to "family," is a coproduction of historical/cultural processes and of microevolutionary biological processes. It is not a question of whether humans differ, but of how they do so, and of how we concurrently make sense of it. And any scientific sense we make of human variation must ultimately be consistent with 10 empirical generalizations produced by anthropology and genetics over the last century and a half.

1. HUMAN GROUPS DISTINGUISH THEMSELVES PRINCIPALLY CULTURALLY

This is the singular discovery of anthropology. When E. B. Tylor (1871) separated biology or race from "culture," he described it as "that complex whole which includes knowledge, belief, art, morals, law, custom, and any other capabilities and habits acquired by man as a member of society" (Tylor, 1871, p. 1) – in other words, as the myriad things that we key on to differentiate "us" from our neighbors, "them." Today we would certainly expand the list to include the things that give us the earliest and most basic signals of who we are and who we're not: language, mode of dress or personal grooming, food preferences, body movement. This seems to be what humans evolved doing, and may well precede the emergence of our species itself.

In distinguishing our group from others, in these socially transmitted, historically constructed, and symbolically powerful ways, we structure most of our daily lives. What makes us group members also renders all of our sensory input and experience meaningful. We think and communicate using the metaphors and symbols of our group. We groom and dress ourselves according to the conventions of our group; indeed, the decisions we actually make during the course of our lives are rigidly constrained by the relatively meager options culturally available. In other words, the vast bulk of human behavioral and mental diversity is culturally constituted.¹

It is of some significance that the strongest cultural distinctions are maintained between neighboring groups, who are nevertheless very closely related genetically to one another. This would constitute a paradox if there were a close and deterministic relationship between genetics and human behavior. Rather, however, if the bulk of human behavioral and cognitive diversity is of the sort that differentiates one group from another (culture), and this variation is social and historical in origin, then genetic variation can be invoked to explain at best a tiny part of human difference in thought and deed – presumably some of the differences identifiable among members of the same group.

Considered another way, an imaginary neuropeptide whose variant allele made someone a bit more aggressive, say, might be found both in a wealthy Parisian and in a poor Sri Lankan (and in many others). The variant allele might make its possessor slightly more aggressive, but a Sri Lankan sharing the allele with a Parisian would hardly have their lives thereby rendered significantly more similar. Their different lives would be shaped by their different cultural traditions and practices. Even the (culturally mediated) responses to their aggressive behavior would cause their personal experiences and perceptions to diverge. If the question, then, is to understand the major features of human behavioral diversity, a focus on behavioral genetics is manifestly a case of the tail wagging the dog.

¹ Biologized theories of human history have been put forward periodically from Arthur de Gobineau's (1853–1855) *The Inequality of Human Races* through C. D. Darlington's (1969) *The Evolution of Man and Society*. It is in this narrow historical sense, where (as Émile Durkheim famously noted) social facts are only explicable by prior social facts, that the analytic separation between biological (microevolutionary) and cultural phenomena has been most useful. In a broader sense, the interaction between the "natural" and the "cultural" is more complex and problematic. At very least, historical events often have biological consequences, which in turn engender different responses – as evidenced in the well-known relationships among agriculture, malaria, the human gene pool, and modern medicine.

2. HUMAN BIOLOGICAL VARIATION IS CONTINUOUS, NOT DISCRETE

In his 1749 discussion of human variation from *Natural History, General and Particular*, Buffon wrote, "On close examination of the peoples who compose each of these black races, we will find as many varieties as in the white races, and we will find all the shades from brown to black, as we have found in the white races all the shades from brown to white" (Buffon, 1749, p. 454).

That would seem, on the face of it, to preclude the possibility of taxonomically dividing people neatly into black and white; or even into black, brown, and white. Buffon's empiricism, unfortunately, had already lost the day to Linnaean idealism in the area of human taxonomy. Linnaeus's rigorous hierarchical approach to biological systematics was so obviously right in permitting us to understand the relationships among species, that it stood to reason that Linnaeus was correct in applying his ideas below the level of the human species as well. This created a paradox in the writings of Johann Friedrich Blumenbach a generation later.

Blumenbach was, like Buffon, an empiricist in matters of human variation; but he was also, like Linnaeus, a taxonomist. Thus, he famously wrote in 1775, "One variety of mankind does so sensibly pass into the other, that you cannot mark out the limits between them" (Bendyshe, 1865, pp. 98–99), and yet nevertheless proceeded to do just that. The same paradox inheres in the work of population geneticists over two centuries later (e.g., Cavalli-Sforza et al., 1994).

An alternative to the taxonomic approach in microevolutionary studies was suggested by Julian Huxley in 1938. Since a large component of the variation that exists within a species is structured as geographical gradients, he suggested, why not simply describe them that way, rather than trying to shoehorn the populations into taxonomic categories? In fact, Huxley did not mention humans among his examples; nor did he reject the establishment of subspecific taxa. In the 1950s other zoologists began to suggest rejecting the subspecies altogether (Wilson and Brown, 1953), and Livingstone (1962) was extending the argument to humans when he denied the very biological existence of human races.

Trying to explain clinal variation in human physical form from northern to southern Europe in taxonomic terms is what compelled William Z. Ripley (1899) to introduce a subdivision of "the races of Europe" into Teutonic (Nordic), Alpine, and Mediterranean. (Today, even the simple use of a plural in his title seems foreign to us.) Carleton Coon's (1939) revision of *The Races of Europe* identified over a dozen of them. Where no criteria exist other than "difference,"

certainly a broad cline of physical form could be subdivided in a pseudo-taxonomic fashion effectively without limit. It is simply a classic square-peg/round-hole problem.

This clinal pattern is evident for most human traits, extending from lactose persistence through to skin color. The reason for this pattern is two-fold: (1) natural selection, with environmental conditions varying gradually over space; and (2) gene flow, culturally mediated in humans. There are very few systems that do not show much in the way of geographical gradients. Yet even the genetic markers that permit full differentiation of disparate groups (almost all one allele in West Africans and almost all another allele in East Asia at the Duffy blood group locus on chromosome 2 exhibit clines of differing intensities in different regions (East Africa, West and South Asia).

It seems, then, that a division of the world into human races – reasonably discrete from one another and relatively few in number – was an aberration, derived from a peculiar view of human variation adopted by scientists from the seventeenth to the twentieth century. Scholars have differentiated the peoples they encounter according to diverse criteria, but human variation in nearly all times and places has been perceived on a local, not a continental/global, scale. This is because fundamental patterns of human difference are principally gradational, not discrete.

3. CLUSTERING POPULATIONS IS ARBITRARY

Human identities are culturally produced, and can assume a wide range of forms. Those that are principally geographic can be extensively subdivided; one can be Caucasian, Nordic, Slavic, Baltic, and Latvian simultaneously. All have been racialized by someone or another.

Approaching the issue from the bottom, so to speak, where the most basic human populations are local, how do they fit together into more inclusive entities?

We could try to cluster them genealogically, but as Frederick Hulse (1962) pointed out, there is no reason to think human populations are actually genealogically structured entities, and every reason to think they are not. Gene flow (both small-scale and long-term, and large-scale and short-term) is a pervasive feature of human history, and the horizontal modes of genetic transmission it produces are complementary to the vertical modes of genetic transmission depicted in genealogical trees (Fix, 2005). Consequently, the more accurate mode of representation of human populations is not as a tree, but as a trellis, capillary system, or rhizome (Moore, 1994; Pálsson, 2007; Arnold, 2009).

Further, the relationship between processes of human demographic history, and the products they have yielded at different times, is often far from clear. Patterns of relative genetic distinctiveness might be expected from several different demographic processes. Consequently, different clustering analyses applied to human populations by different researchers have often yielded different results. Clusters of populations may be produced as well simply by sampling discontinuously (Serre and Pääbo, 2004).

The idea that human populations fall naturally into genealogical clusters is itself the result of a gloss on the Biblical theory of human biogeography. Genesis 10 tells us that Noah's three sons (Ham, Shem, and Japheth) went out and populated the world after surviving the Deluge. Ham has sons named Cush, Mizraim, Phut, and Canaan – and is the ancestor of both the Babylonians (Babel) and the Egyptians (Mizraim). Shem has sons named Elam, Asshur, Arphaxad, Lud, and Aram – and is an ancestor of other local city-states. And Japheth sires Gomer, Magog, Madai, Javan, Tubal, Meshech, and Tiras – and once again, is an ancestor of a group of city-states. "These are the families of the sons of Noah," the Bible tells us, "after their generations, in their nations: and by these were the nations divided in the earth after the flood."

By the first century, the Jews understood this to explain the peopling of the three known continents. According to *The Antiquities of the Jews* by Flavius Josephus (Book I, Chapter 6), Ham heads south to beget the Egyptians, Ethiopians, and other Africans; Shem begets the Asians as far east as India (including the Hebrews themselves, through his son Heber); and Japheth is the ancestor of the European peoples, as far west as Spain.

In the nineteenth century, this story was embellished even further, as Noah curses his grandson Canaan for an ambiguous sexual deed perpetrated by his father Ham. Josephus had interpreted the curse in the context of Jewish origins, and the political/religious/military transformation of "Canaan" into "Judea." But to American physical anthropologists in the era of slavery, that curse became the Biblical justification for the modern enslavement of Africans.

Nevertheless, there was very little change in the biohistorical model explaining the human race. The three sons of Noah emigrate to the corners of the earth and populate it, becoming the pure progenitors of the people living there; and where their remote descendants encounter one another, impure races are found. The power of this model is such that it even underlies some genetic studies of the modern era. Thus, prominent population geneticists can casually write, as recently as 1993:

[H]uman populations can be subdivided into five major groups: (A) negroid (Africans), (B) Caucasoid (Europeans and their related populations), (C) mongoloid (East Asians and Pacific Islanders), (D) Amerindian (including Eskimos), and (E) australoid (Australians and Papuans). (There are intermediate populations, which are apparently products of gene admixture of these major groups, but they are ignored here.) (Nei and Roychoudhury, 1993, pp. 936–937)

Of course, there was never a time when people lived only in Lagos, Oslo, and Seoul; indeed, the most ancient representatives of *Homo sapiens sapiens* are right there in the middle. That raises a crucial question about the statistical clustering of populations: What do the clusters actually represent? What is their connection to human history? While most population geneticists readily acknowledge that the clusters are statistical reifications (Templeton, 1998), it is not too difficult to find them naïvely interpreted as cladogenetic events, with that occasional rare admixture. And indeed, philosopher Robin Andreasen (2000, 2004) misunderstands the evolutionary meanings of those trees in precisely that fashion, as a series of literal, historical bifurcations that produced – you guessed it – races.

4. POPULATIONS ARE BIOLOGICALLY REAL, NOT RACES

Gilmour and Gregor (1939) coined the word “deme” to refer to the local population that exists as an ecological and social unit in nature. The focus on the population genetics of human demes is what permitted biological anthropologists of the 1970s to avoid “race” altogether.

The application of this concept to human diversity revolutionized the study of physical anthropology in the years following World War II. The genetical processes described in the evolutionary synthesis were measurable and meaningful at the local level; Sewall Wright’s work showed that local populations were effectively the units of general microevolution. That is consequently where the study of human population genetics would have to focus.

Larger units than the deme lack cohesion or time depth. Their evolutionary meaning is consequently not obvious. To adopt a unit of analysis of human biology larger than that of the local population or deme, then, is what requires some justification today. Perhaps the most interesting question in this vein is that of representation: Can local populations “stand for” anything other than themselves? In one famous study, geneticists used 94 African pygmies, 64 “Chinese . . . living in the San Francisco Bay Area,” 110 samples from “individuals of European origin from ongoing studies in our laboratories or reported in the literature,” and concluded sweepingly that “ancestral Europeans are

estimated to be an admixture of 65% ancestral Chinese and 35% ancestral Africans” (Bowcock et al., 1991, p. 839). That is, the samples were intended to represent larger categories assumed to be natural and separate.

5. POPULATIONS ALSO HAVE A CONSTRUCTED COMPONENT

“Population” is a term that is notoriously difficult to define rigorously. The usage above is intended to juxtapose the “local” against the “global” – or ontologically real “demes” against reified human megapopulations. And yet, local human populations, as previously noted, tend to distinguish themselves by features such as language, dress, religion, and dietary prohibitions or preferences. These are not biological attributes, but they help circumscribe an entity that is to some extent biological, namely the local human population or deme.

The boundaries being nonbiological, they are consequently porous to biological input, in the form of gene flow (e.g., Hunley and Long, 2005). This can take place through social practices, such as exogamy and adoption; economic practices, such as trade and subsistence; and political practices, such as warfare, slave raids, and forced migrations.

Unfortunately, a large class of population genetics models have tended to work best for populations in isolation from one another, which in turn necessitates a high degree of “purity” for the populations under study. This assumption was raised during the public discussion over the Human Genome Diversity Project in the 1990s, as the Project itself continually talked of “isolated” populations. But this had in fact been highlighted as a problem half-a-century earlier, as Boston University’s anthropological geneticist William C. Boyd had proclaimed the purity of the Navajo group he was studying. But cultural anthropologist Clyde Kluckhohn knew the specific community and its ethnohistory, and knew of its extensive interbreeding, with Walapai, Apache, Laguna, and Anglo/Spanish contributions. “In spite of all this, [they] conclude from their blood group data that the Ramah Navaho represent an ‘unusually pure’ Indian group” (Kluckhohn and Griffith, 1950, p. 401). The implication was clear that the population in question would actually have their complex history erased by the geneticists, and would be falsely simplified and reified into one in which they were more-or-less “pure.”

The myth that non-European peoples are “pure” and “unmixed,” and have more or less always been where (and as) we find them today, was comprehensively refuted by Eric Wolf (1982) in *Europe and the People without History*. That it complicates some population genetic analyses is unfortunate (Moore, 1994;

Templeton, 1998), but human populations are biocultural units, connected economically, socially, and genetically; and with complex histories intertwined with those of their neighbors (Lasker and Crews, 1996).

6. THERE IS MUCH MORE VARIATION WITHIN GROUPS (POLYMORPHISM) THAN BETWEEN GROUPS (POLYTYPOY)

Lewontin's (1972) calculation that there is six times more within-group variation than between-group variation in the gene pool of *Homo sapiens* has been the subject of periodic criticism, but the results have proved remarkably robust to the kinds of genetic data analyzed. Barbujani et al. (1997) found a similar result for nuclear DNA, as did Rosenberg et al. (2002).

Indeed, the recognition that variation within human groups vastly exceeds that between human groups was noted explicitly in the second (1951) UNESCO statement on race. Now, however, with genetic data, the observation could be quantified. The most obvious conclusion is that the human species does not come naturally partitioned into reasonably discrete gene pools, which had been the predominant theory of race for most of the twentieth century.

A. W. F. Edwards (2003) has recently criticized the invocation of these numbers against the race concept as "Lewontin's fallacy," on the grounds that a proportion of the diversity detectable in the human gene pool is indeed correlated with geography, and thus can be used to sort people into large groups, if one focuses upon it closely enough. The argument here is not with the data, but with the meaning of the data and its relation to human races. Geographical correlations are far weaker hypotheses than genetically discrete races, and they obviously exist in the human species (whether studied somatically or genetically). What is unclear is what this has to do with "race" as that term has been used through much of the twentieth century – the mere fact that we can find groups to be different and can reliably allot people to them is trivial. Again, the point of the theory of race was to discover large clusters of people that are principally homogeneous within, and heterogeneous between, contrasting groups. Lewontin's analysis shows that such groups do not exist in the human species, and Edwards's critique does not contradict that interpretation.

Moreover, the Lewontin numbers show that patterns of human genetic diversity simply do not map well onto the patterns of human behavioral or cognitive diversity. The latter kinds of differences tend to be localized at the borders of human groups, as noted above, and are of the sort we call cultural (Peregrine et al., 2003; Bell et al., 2009). To the extent that genetic diversity is structured quite differently (mostly polymorphism and

clines), it seems unlikely that genetic differences could play a significant role in understanding the major patterns of human behavior, unless variation in the hypothetical genes involved were structured quite differently from the rest of the known human gene pool.

7. PEOPLE ARE SIMILAR TO THOSE NEARBY AND DIFFERENT FROM THOSE FAR AWAY

The primary factor governing between-group variation in our species is geography, a fact known even to the ancients. This allows us grossly to predict patterns of relatedness: a Dane will tend to be more similar to an Italian than to a Hopi. This, however, only allows us to classify the Dane and the Italian *in relation to the Hopi*; it does not tell us whether Danes and Italians themselves belong to the same group or to different ones. There are indeed geographical patterns in the human gene pool, and they can indeed be used to allot people into groups (Witherspoon et al., 2007); the groups simply do not correspond to "races," in any previously or generally understood sense of that term. The ability to discriminate Swedes from Nigerians genetically does not tell you what to do with Moroccans. The existence of genetic variation over space is thus disconnected from race as theory of human groups and their classification – a point sufficiently important, yet subtle, as to be lost on some geneticists! In fact, one needs neither statistics nor genetics to tell an Inca from a Dinka.

In general, the most geographically proximate peoples are the most genetically similar. In rare cases, a (permeable) barrier of language, politics, or ethnicity might serve to reinforce a genetic distinction between one people and their neighbors (Hulse, 1957); these differences are nevertheless often genetically subtle, arbitrary, and discordant. If the Ainu of Hokkaido are more hirsute than other Japanese, can one be a glabrous Ainu? Likewise, can one be an Rh⁺ Basque, or a tall pygmy?

The answer is presumably "yes" to all of those, although perhaps with varying degrees of aspersion cast upon one's ancestry, in proportion to the degree of purity ascribed to the group itself. Once again, however, this is hardly meaningful in the context of races; but rather, only in the context of local populations.

Perhaps the most celebrated confusion of geographic difference for race followed the publication of Genetic Structure of Human Populations (Rosenberg et al., 2002). The authors studied genetic variation in 1052 people from 52 populations and then asked a computer program called Structure to group the samples. When they asked it to produce two groups, Structure gave them EurAfrica and East Asia–Oceania–America. When asked for three groups, Structure gave Europe, Africa, and East Asia–Oceania–America. When asked for four, it gave Europe, Africa,

East Asia–Oceania, and America. When asked for five, it gave roughly the continents. And when asked for six, it gave the continents and the Kalash people of Pakistan. When asked for more (up to twenty groups), it gave more (Bolnick, 2008).

This was more or less what population geneticists had been doing with the human gene pool since the pioneering work of Cavalli-Sforza and Edwards (1965). On the face of it, once again, this would seem to have little relevance for race. The user specifies the number of groups, and geographic proximity is the strongest predictor of similarity, so asking the computer to break the human species into five groups might reasonably be expected to yield groups roughly corresponding to the continents. And the Kalash people of Pakistan certainly do not have green skin and square heads; nor do they constitute a “natural” contrast against Europeans or Africans.

Nevertheless, a headline in the *New York Times* announced, “Gene study identifies five main human populations, linking them to geography” and quoted Marcus Feldman², the principal author of the study, to the effect that “the finding essentially confirmed the popular conception of race” (Wade, 2002).

Of course the popular conception of race as a classification system applies not just to the more-or-less indigenous peoples surveyed by the geneticists, but as well to the entire admixed urban populations of the modern world, especially the Americas. This raises an important criticism of genetic “racial” studies: their focus on a mythological past rather than on a real present (Cartmill, 1998). What biological relevance does an exercise like this have, after all, for the peoples of New York, Chicago, Los Angeles, Mexico City, Rio de Janeiro, or Johannesburg? It is indeed an odd and perverse approach to history, geography, and genetics that would cast a blind eye to the centuries of colonial contact and demographic reconfiguration that have constructed the human gene pool.

In modern American populations, it is certainly reasonable to expect people who look “black” to tend to cluster genetically with Africans when examined with carefully selected genetic markers (Bamshad et al., 2003), but the vagaries of Mendelian genetics and the complexities of human history will combine to place an increasing amount of weight on the phrase “tend to.” Further, given nontrivial amounts of polymorphism and admixture, there is always a nontrivial possibility that a particular person may have the “wrong” racial marker at a specific locus. That is ultimately why a racialized pharmacopoeia is a very poor and risky substitute for an individualized one, which will have to be predicated on the direct assessment of individual genotypes.

8. RACIAL CLASSIFICATION IS HISTORICAL AND POLITICAL, AND DOES NOT REFLECT NATURAL BIOLOGICAL PATTERNS

The contemporary racialization of Hispanics in the United States (see above) is certainly *prima facie* evidence for the political embeddedness of racial classifications. In classic anthropological fashion, the cultural aspects of race are revealed most clearly when we contrast the classifications and their uses from place to place and time to time. Thus, while “Black” in the United States has effectively meant “possessing any recent African ancestry,” that category in the United Kingdom traditionally referred to South Asian ancestry (meaningful in the context of the colonial relationships between Britain and India), and only recently has the category “Afro-Caribbean” emerged there to designate what Americans mean by “Black.” People of South Asian ancestry in the United Kingdom are now commonly regarded as “Asian” in the United Kingdom, but in the United States the term instead tends to connote people of East Asian ancestry.

Central and South American classifications have tended to incorporate more categories, based on actual variation in skin shade, in contrast to the “one drop of blood” rule prevalent in the United States. While there is commonly status differential associated with skin color, it is nevertheless quite different from the binary racial system of the United States.

The point is that biological or genetic difference can be studied and quantified, but it is not race. Race is a sense-making system imposed upon the facts of difference. Races are not merely human divisions, they are *politically salient* human divisions. All classifications exist to serve a purpose; the purpose of a racial classification is to naturalize human differences – that is, to establish important categories and make their distinctions appear to be rooted in nature, rather than in history or politics.

The pervasive tendency for racial classifications to see sub-Saharan Africans as a single group, for example, has far more to do with the politics and history of slavery than with the gene pool of Africans. After all, fieldworkers like Seligman (1930) and Hiernaux (1975) consistently emphasized the physical diversity of Africans. Julian Huxley could write, “It is a commonplace of anthropology that many single territories of tropical Africa, such as Nigeria or Kenya, contain a much greater diversity of racial type than all Europe” (Huxley, 1931, p. 379). Today, their genetic diversity is generally considered to harbor the ancestral gene pool of the rest of the world. Sub-Saharan Africans thus encompass more genetic diversity than other “races,” and more significantly, constitute a paraphyletic category, and are thus not even

² Feldman (personal communication) said it was a misquotation.

taxonomically comparable to other “races” (Marks, 1995). So if the empirical data have long been known to contradict it, how then do we account for the presentation of sub-Saharan Africans as consistently monolithic in racial classifications as late as those of Campbell (1962) and Boyd (1963)?³

9. HUMANS HAVE LITTLE GENETIC VARIATION

Ferris et al. (1981) found a much greater degree of heterogeneity in the mitochondrial DNA of chimpanzees and gorillas than in humans. This finding was soon extended to nuclear DNA by Deinard (1997) and Kaessmann et al. (2001). Stone et al. (2002) found very different patterns of diversity in chimpanzees and humans as well, chimpanzees having deeper coalescences, and more between-group variation (which is especially striking, given their considerably more restricted range), than humans. At some loci where humans are variable, apes turn out to be less variable, but this is the result of a statistical bias – if we try to identify variation in apes where humans are already known to vary, then we miss the many loci at which apes vary but humans do not.

Although it must be noted that there is a conservation-driven push towards “taxonomic inflation” in the apes, the levels and degrees of genetic differentiation in our closest relatives seem to be considerably different from our own. Ape subspecies appear to cluster strongly together with mitochondrial DNA, for example, while human races do not. To the extent that they have traditionally been divided into subspecies, then, these great ape taxa represent very different entities than human races.

One interesting consequence of finding such high levels of genetic diversity in the apes is the difficulty it imposes upon phylogenetic reconstruction (Ruano et al., 1992; O’Higin et al., 2002). Very high levels of homoplasy and ancestral polymorphism undermine the assumption of parsimony in molecular phylogenetics (Marks, 1994; Satta et al., 2000; Chen and Li, 2001), and contribute to the relatively large statistical errors associated with the calculation of divergence times of human and ape species (Stauffer et al., 2001; Glazko and Nei, 2003; Kumar et al., 2005). This in turn suggests the need for models of ape-human ancestry more complex than just a sequence of simple bifurcations (Chaline et al., 1991; Deinard, 1997; Barbulescu et al., 2001; Marks, 2002; Patterson et al., 2006; Arnold, 2009).

³ Coon’s (1962) *The Origin of Races* followed Gates’ (1948) *Human Ancestry* in splitting the Khoisan peoples of southern Africa off from other Africans, thus doubling the number of African races.

Thus, the temptation to represent evolutionary history as a series of cladogenetic events seems to be nearly as problematic just above the human species as just below it. Clearly, the demographic histories of these populations made the patterns of genetic difference we see today more difficult to interpret than earlier generations of scholars appreciated.

10. RACIAL ISSUES ARE SOCIAL-POLITICAL-ECONOMIC, NOT BIOLOGICAL

The most important aspect of the study of race is its connection to racism, a political ideology in which humans are ranked according to group membership. It has occasionally been argued that the absence of taxa equivalent to zoological subspecies in humans invalidates racism, as if all we had to do to disband the Ku Klux Klan would be to teach them some population genetics.

This view, however, misrepresents the basis of racism, for it takes racism to be predicated on science. In fact racism is independent of science, and is simply one of many anti-democratic political discourses that function to rationalize social inequalities. Sexism, anti-Semitism, and homophobia are quite real, in spite of the fact that the groups constituted by women, Jews, and homosexuals possess varying degrees of “naturalness.” In other words, it is the social ranking and prejudice, not the biology, which comprise the salient features of racism.

Race is thus paradoxically of minor relevance to racism. The “race” in “racism” is the first – the essentialist – version of race, in which any group can possess its own innate qualities, and individual people can be relied upon to embody those qualities. The categories are still real and experienced, however, despite how little they may correspond to biology (Smedley and Smedley, 2005).

If “white” and “black” denote intractably large, highly heterogeneous, extensively overlapping populations, then, as Lewontin (1972) recognized, there can be little justification for ascribing great biological meaning to the perceived discontinuities between them. On the other hand, if: (1) considerable social inequality is mapped onto the categories; and (2) phenotypes are coconstructions of genotypes and the cultural conditions under which the genotypes are expressed, then it follows that; (3) significant perceived differences between the two groups, particularly etiologically complex ones like odor (Classen, 1995), body form (Bogin, 1988), or intelligence (Lewontin et al., 1984), are simply more likely to be attributable to their different social statuses (especially class and ethnicity) than to their gene pools.

This conclusion, obviously, is not value-neutral. The ascription of inequality to biological causes is a political position that minimizes the role of political-economic factors in producing and maintaining that social inequality. The implication is that biological causes require biological remedies, or at least, not remedies involving significant expenditures on social programs. Obviously there is considerable harmony between this ostensibly scientific conclusion and a political agenda of social conservatism, often explicitly so. Indeed, this is what links the reasoning of the social Darwinists, eugenicists, and segregationists of earlier eras with works like *The Bell Curve* (Herrnstein and Murray, 1994) in the modern era. Consequently they necessitate a higher degree of scrutiny than the ordinary run of scientific work, and generally, they do not stand up well to it (Boas, 1911; Hogben, 1931; Merton and Ashley-Montagu, 1940; Dobzhansky, 1962, 1963; Gould, 1981; Lieberman, 2001; Marks, 2005).

In the case of health care, for example, it is quite uncontroversial that identifiers such as ancestry, age, and occupation carry different statistical health risks and that knowledge of them can aid in producing a proper diagnosis. Being born white carries a risk of 1 in 2500 of having cystic fibrosis; being born black carries a risk of 1 in 15000. Nevertheless, one needs to guard carefully against misdiagnosing the presentation of symptoms in a black child, say, on the grounds that cystic fibrosis is a white child's disease, since that act puts lives directly at risk (Garcia, 2003). Further, race itself is a red herring here: being Ashkenazi Jewish, Pennsylvania Amish, "not northern European," a football player, a primary school teacher, or a computer hacker puts one at higher risk for familial dysautonomia, Ellis-van Creveld syndrome, lactose intolerance, knee problems, mild viral infections, and carpal tunnel syndrome, respectively, but those labels do not designate groups we would identify as races. And more importantly, since the social inequality associated with race is a significant variable affecting many aspects of life and health care (Sankar et al., 2004), it should not be surprising that some of the most well-known racialized medical issues – low birthweight and hypertension – also do not stand up well under scrutiny as innate differences (David and Collins, 1997; Kaufman and Hall, 2003).

Most significantly, the modern context of racial science involves another player, in addition to science and politics – the economics of health care, in which "racial pharmacogenomics" is being positioned as a source of new markets for the pharmaceutical industry (Duster, 2005; Bibbins-Domingo and Fernandez, 2007). With such conflicting interests, it becomes harder than ever to evaluate the merits of scientific research on the genetics of race. A broad perspective on what we already know about science and human

difference is consequently often quite valuable. After all, the newest work is hardly carried out in an intellectual, historical, or cultural vacuum.

Earnest Hooton almost understood this, trying to differentiate his own ostensibly benign physical anthropology from that of the Nazis, while nevertheless remaining a eugenicist long after it fell out of fashion in American academia. He warned, somewhat poignantly,

There is a rapidly growing aspect of physical anthropology which is nothing less than a malignancy. Unless it is excised, it will destroy the science. I refer to the perversion of racial studies and of the investigation of human heredity to political uses and to class advantage ... [T]he output of physical anthropology may become so suspect that it is impossible to accept the results of research without looking behind them for a political motive (Hooton, 1937, pp. 217–218).

CONCLUSIONS

Both human beings, and the scientific study of human beings, are coproductions of nature and culture. Human biologists are very familiar with the manifold processes by which "culture" is inscribed upon the human organism, and is ultimately not separable from the biology, or the human phenotype – "nature." It has proven more difficult to accept the idea that science itself – despite being a human activity, taking place in a cultural context, and being subject to conflicting interests of various kinds – produces conclusions about nature that are ultimately also not separable from culture. The idea that you can separate the natural from the cultural with a high degree of confidence, however, is an Aristotelian survival (Goodman et al., 2003).

The most significant aspect of the study of human diversity is that it consists of natural-cultural facts. These facts emanate from the kinds of questions framed, the manner in which categories are envisioned and established, the applications that assign people to the categories, the meanings attributed to group membership, and of course, the program of the investigator. Certainly there is a base of data that can inform us about the patterns of diversity that exist in our species, both somatic and genetic. The problem lies in the presumptions: (1) that the biological data on human variation are fundamentally separable from their cultural context and values, and from the interests of the scientists producing them; and (2) that the data themselves are meaningful independently of a stream of Euro-American ideas about difference, heredity, and hierarchy. That is why the problem of race has never been resolved by genetics; its domain is anthropological, rather than biological.

DISCUSSION POINTS

1. What are the incompatibilities among the three concepts of race discussed in this essay?
2. Why can't we separate facts of nature from culture?
3. Are Hispanics a race?
4. Old anthropology books used to show maps of the races of the world, with, for example, no presence of Europeans, Asians, or Africans in America. What are the merits of, and problems with, that?
5. What are the major patterns of human genetic variation and the major patterns of human cognitive variation, and how do they relate to one another? What implications can be drawn from that?

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