

Racing Around, Getting Nowhere

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Arguments about race recycle endlessly because the truths we think we're chasing are always chasing us. Maybe we're getting nowhere because we're already there.

What are we supposed to teach our students about "race"? That there are no races, only clines? Or no—that human variation falls naturally into a few major categories? That race has no biological meaning, so racial profiling in medicine is discriminatory and more harmful than healing? Or no—that races are biologically different so that profiling is invaluable in daily practice? Since anyone can easily find articles taking any of these positions, perhaps we should just teach whatever suits our personal politics. Isn't that what most of us actually do?

Whether the term be "race," "ethnicity," "geographic ancestry," or some other favorite euphemism the subject swirls about today as it has for at least three centuries. But anthropologists are the experts. This is our field! We understand human biological and cultural diversity better than anyone else; we develop the facts on this subject. The United Nations trusted prominent anthropologists like Ashley Montagu and Sol Tax for classical pronouncements¹ and a younger generation recently did the same for the Census Bureau.^{2,3} They

basically state the famous position closely associated with the late Frank Livingstone, that "there are no races, only clines,"⁴ a view and history recently recounted in *Evolutionary Anthropology* as well.⁵ Every news story on the subject quotes anthropologists and every symposium includes us. Race has a chapter in our texts. Yet with the same facts available to us all, we the experts can't seem to agree on what race means or why it matters.

The issue of race continues to cycle endlessly, like blinkered horses in old country fair merry-go-rounds, which seemed oblivious to the fact that they are just going 'round and 'round (Fig. 1). The subject takes the headlines episodically and major journals devote reviews or even whole issues to the subject (for example, a special issue of *Nature Genetics*, vol. 36(11), Nov. 2004).^{6–10} But we still cannot manage to move forward or lay the matter to rest. Why?

A TOUCH OF HISTORY

From the earliest moments of the Western Enlightenment's attention to the problem of human variation, it has been clear that humans are not sorted into discrete, clear-cut categories like items in a mail-order catalog.⁷ In 1795, for example, Blumenbach,¹¹ a founding taxonomist in this area, said "innumerable varieties of mankind run into one another by insensible degrees" and that "no variety exists, whether of color, countenance, or stature, etc., so singular as not to be connected with the others of the same kind by such an imperceptible transition, that it is very clear they are all

related, or only differ from each other by degree."

Leaping forward a century-and-a-half into the modern genetic age, the first systematic anthropology book to deal with this subject was Boyd's *Genetics and the Races of Man*.¹² While he drew categorical distinctions between populations in his text, he quoted Blumenbach and just as clearly acknowledged the gradual evolutionary process that generated our noncategorically distributed variation.

The urge to cut and classify persists, despite a huge increase in the genetic data clearly confirming that populations are not discretely differentiated by genes. Moreover, these new data have not yielded any major new insights. Before many readers of this column were even born, trees of genetic relationships among populations based on protein and blood group data (Fig. 2A) showed the same relationships, and for the same genetic reasons, as do the most high-tech analyses, using the latest molecular genetic markers, that are pouring forth today. Even earlier (1950), similar data were presented to show continuous geographic variation on a global scale (Fig. 2B). Despite vehement arguments to the contrary, there's nothing inherent in the data, old or new, to suggest that one presentation format should be preferred over the other. The choice is in the eye of the portrayer, but the eye of the beholder just needs to understand the underlying realities. This is, of course, much easier said than done, even for professionals.

ONLY SKIN DEEP, OR CUTTING ALL THE WAY TO THE BONE?

A new allele (mutation in our DNA) always arises in one new baby some-

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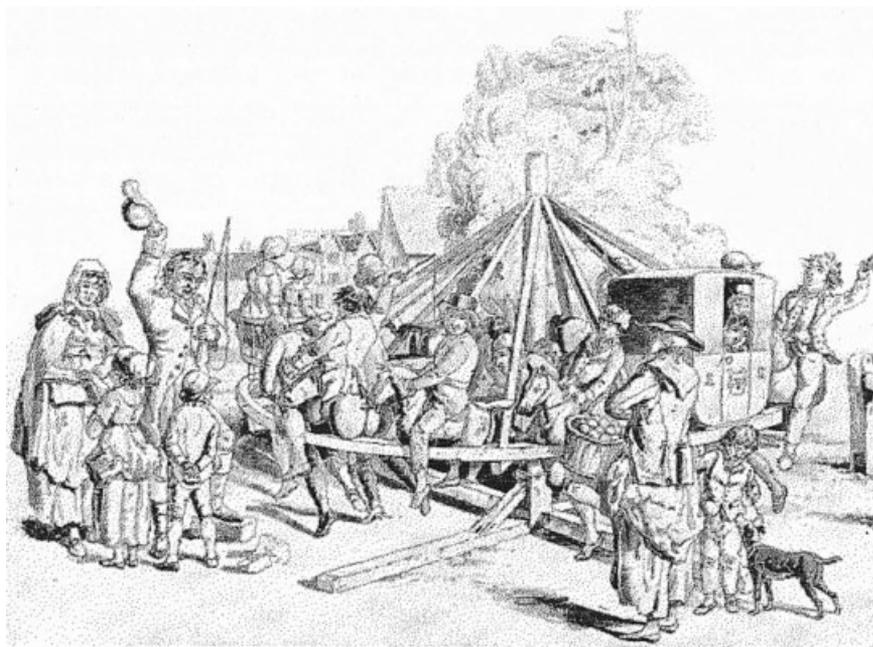


Figure 1. Merry-go-round horses, 1810, W.H. Pyne (courtesy Henry Churchyard; See <http://www.crossmyf.com/hc/index.html>).

where. In our slow-breeding species it takes many generations for the number of descendant copies of that unique new variant to increase. For those copies to spread geographically far from their infant of origin took similarly long because our hunter-gatherer ancestors typically married someone from a nearby village and stayed around. This is why common variants today are likely to be older and geographically more widespread,

while rare variants are usually recent and local. Natural selection speeds the spread of favorable variants, but only somewhat, because not even selection can override our slow reproduction and limited mobility.

New mutations occur every generation in all people in the world. Different mutations that arise in the same geographic region and time will have independent transmission histories, but the new alleles will share the same

overall demographic history of that region, arising and diffusing, for example, within Africa or India. This shared history generates statistical associations of the geographic dispersions of such variants, which make it possible to identify peoples' geographic origin with high probability, if enough genes are examined.^{9,14} Of course geographic origin has to do with place and history, not "race," a problematic, culturally imposed notion.

Statistical similarity doesn't imply that individuals with similar ancestry are genetically identical. While many alleles are generally found only in a given geographic region, very few are found in everybody in that region. The more localized or isolated the group, the more alleles one might expect to be "private" to that group. But being found only in, say, a local village means that it must be rare. Because of the exogamy rules that characterized human culture when our present variation was largely being established, if an allele is common in any local village it is likely to be found in kin living in neighboring villages. In fact, what we find in most people and in most regions are the common alleles that predominate in most of our genome. At most sites in the genome, there is an allele that was present in the most recent common human ancestor somewhere in Africa and that is still shared by the vast majority of us.

Overall, if we choose to focus on

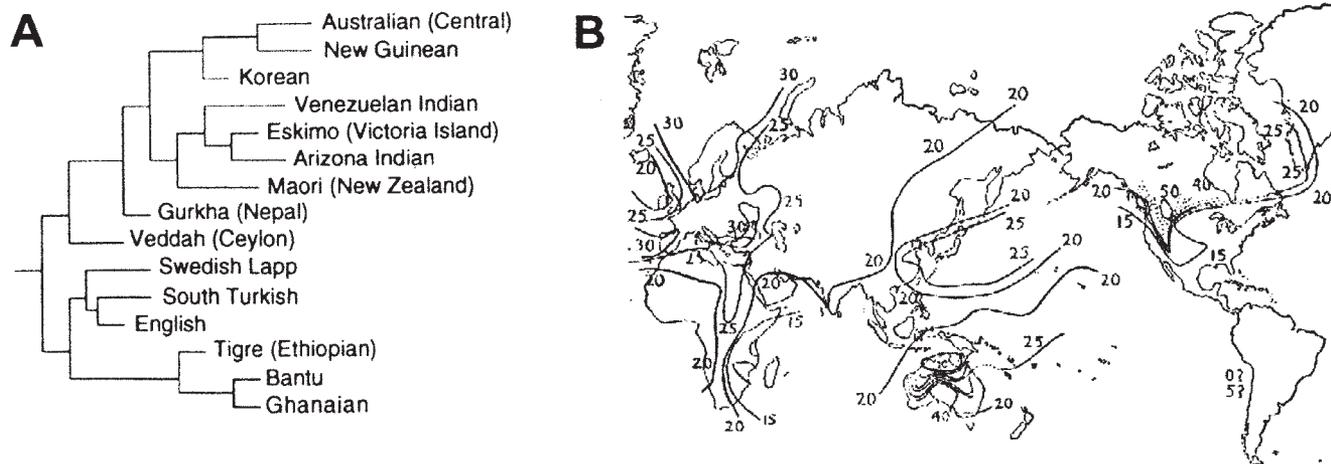


Figure 2. Not much has changed since the early days of anthropological genetics. Variation can be portrayed as either: A. A tree of relative differences among populations treated as sampling units¹³; or B. A continuous geographic pattern interpolating among sample units, numbers indicating allele frequency for the A allele of the ABO locus.¹²

allelic differences rather than this common genetic patrimony, we find that populations or individuals differ roughly in proportion to the geographic distance between their “indigenous” locations, a pattern sometimes generally described as isolation by distance. This pattern is not perfectly smooth because chance aspects of reproduction and population growth, plus factors like mountains, deserts, bodies of water, long-range migration, and religion and other cultural prescriptions produce deviation from simple gradual variation over space (Jeffrey Long, personal communication). Of course our usual definition of ‘indigenous’ today implicitly reconstructs history in a particular way, as if to reconstitute a pristine human state that ended when Columbus bit the Caribbean apple. Thus, for analytic purposes, Navajos in Arizona, but not African Americans, are “native” Americans, while African Americans are Africans, and even the Navajos, Na Dene speakers who not so long ago immigrated into Arizona, are relocated toward the Arctic. This kind of genetic relocation makes legitimate scientific sense in terms of reconstructing more distant history. But when there has been postmigration admixture among formerly distant peoples (as, for example, African and European Americans or Navajos and the Amerind-speaking Hopis), things become more complicated.

These simple nontechnical facts explain the global pattern of variation in our species, a pattern affirmed again and again by population genetic investigation. Because history applies to all genes in our genome, the same facts show why human variation isn’t just skin deep, but goes all the way to the bone, including variation with no direct effect on gene expression or biological function. The presence of patterned variation is an indisputable biological fact, resistant to the forces of analytical deconstruction or empirical reconsideration. That such variation can cut to the bone is, however, a very different sort of fact; a cultural fact. People’s imposition of racial categories on, not to mention racist treatment, of each other is a culturally determined and ultimately somewhat arbitrary attempt to make sense of our

species’ variation in categorical terms. Troubles arise when social predilections lead us to mistake cultural facts for biological ones and vice-versa.

LOADING THE DICE?

The choice of sample and analytic method affects or even determines what we know or don’t know about race. For practical reasons, a sample of humans has to be obtained from units selected by the investigator. If those units are populations, “races,” language groups, or phenotypes like skin color, they can be treated as if they were biologically discrete entities, so a tree of relationships that looks like a phylogenetic tree can be drawn (Fig. 2A). But a tree presentation of a set of samples has a branch for each population you decided to sample, and thus inevitably reflects your prior decisions (and, perhaps, your world view). This is very different from representing the same samples as a continuous distribution because you do this by interpolating values between your actual samples (Fig. 2B). To do this, you have to make the assumption that your samples are from an underlying continuous pattern of variation.

Anthropologists have suggested that to escape sample-choice bias we should entirely abandon any prior notion of populations and simply collect a random sample of individuals in a grid-like fashion from around the world. This appears, on the surface, to be a culturally neutral way to reveal the distribution of human variation. But the North American part of a truly grid-based sample would barely capture any Amerindians. Moreover, it would yield a chaotic geographic genetic map, with the Navajos looking very different from their African American neighbors in Phoenix, for example, yet the latter looking closer to people sampled 10,000 miles away in Africa. How do you make any sense of that unless you correct for known population history, which is exactly what advocates of grid sampling criticize population samples for doing? In fact, if you take the grid-sampled data and do a clustering analysis of the individuals, they will end up falling into the usual geographically coherent patterns reflecting the individuals’ histo-

ries. Here is where individuals with recent-admixed ancestry from different continents would distort the evolutionary interpretation if you didn’t take into account what is known of history. For example, African Americans, who have roughly 20% European ancestry on average, might appear to represent descendants of a place 20% of the way across the Mediterranean between Africa and Europe—remnants of a lost Atlantis!

There is a substantial amount of irregularity in the landscape of human genetic variation because of natural selection, drift, and social disequilibrium due to major population changes like those since the development of agriculture. If you take the current distribution of sociopolitical power and scientific influence as measures of what counts, a set of samples from Central Africa, Japan, and Europe might justifiably be interpreted as representing the “major” human taxa (though they might not have seemed so influential to scholars 10,000 years ago). Suppose, instead, that you chose Icelanders, New Zealand Maoris, and Mayans as your major ancestral populations. They would form three nice clusters and you’d be free to call them “major” or “races” if you wanted to. But ask yourself why you’re more likely to prefer the first choice of samples to the second.

These are not inherent features of the data, but choices investigators make for a host of reasons, some so taken for granted that we may not recognize them as choices at all. To make the point in a slightly different way, let’s go back to the notion of admixed ancestry. To Americans this may seem straightforward, as in the average ancestral mix of African Americans. But for any set of cardinal populations you might choose, you can analyze the genotype of any person as if it were the product of admixture from those populations by estimating what set of fractions from the gene pools of your chosen ancestral populations would be closest to the person’s genotype.¹⁵ A native of India with no outside ancestry might, for instance, be told that s/he is a mix of European, East Asian, and African ancestors. But that same person could be assigned parentage fractions from Iceland, New Zealand,

and Central America. Both would be fictions resulting from inaccurate assumptions.

The concept of race is as slippery as an eel, and so elusive that it even eludes itself. In 1951, Sherwood Washburn, a leading physical anthropologist, coined the phrase, “the new physical anthropology,” in what quickly became a landmark paper.¹⁶ He said anthropology should move from a static classificatory view to one that used population, evolutionary genetic thinking. He acknowledged Boyd’s influence but could not shake the categories. Even in this position paper, while he was in the process of making his main point, he violated that point, essentially saying that the only real races are the real ones: “There is no way to justify the division of a breeding population into a series of racial types. It is not enough to state that races should be based on genetic traits; races which cannot be reconciled with genetics should be removed from consideration.”¹⁶ And a few pages later, he named names (the usual cast, including Mongoloid and Negro).

Race is irresistibly juicy for professors and journalists alike, and recent genetic data are more detailed than those we’ve previously had. But it’s important to understand that nothing conceptual is new: Authors of new genetic studies of human variation (and media stories about them) often suggest that they are, for the first time, revealing that human variation is not discretely packaged among groups. That might suggest that social ills associated with the subject of race can be attributed to our previously innocent but benighted lack of genetic knowledge. But it’s not so. New studies are only fleshing out the details of a picture that has long been well known.

RACE-NEUTRAL STUDY DESIGN: TAY SACHS IN LAPLAND, SICKLE CELL IN JAPAN?

If intentional racism can find no support in the biological data, it can be just as misleading and even pernicious to assume that none of the known genetic variation is important. Why else is it that those who make



Figure 3. Satchel Paige helped erase problems in baseball, but nobody’s gaining in the race race. See www.satchelpaige.com/index.html

some of the most nihilistic statements about the existence of “races” don’t also complain about studies of, say, sickle cell anemia in Africans, or Tay Sachs disease in Ashkenazi Jews, or phenylketonuria in Europeans? There would be a huge outcry if a director of the NIH with a well-meaning social conscience were to ban funding of population-specific studies because such studies were inherently racist. Many who object to racial profiling in medicine nevertheless regard such studies of disease genetics as good research design. It would be counterproductive and downright harmful to suggest that such human has no biological meaning. Similar statements apply to anthropological studies of genetic adaptation. You wouldn’t study Amerindian adaptation to high altitude using a random sample of the European-American population currently living in Lima, Peru.

The desirability of race-neutral approaches might make more sense for understanding the genetic basis of common complex traits and diseases that do not occur at appreciably higher frequency in any one specific population or ethnic group. To the extent that such globally common diseases are caused by shared common genetic variants, associations between common polymorphism and common diseases might be identified. Yet even here the correlated character of geographic variation can confound anal-

yses that do not control for population structure, generating spurious associations that might be avoided if some measure of genetic identity (often approximated, however imperfectly, by self-described race) is taken into account.¹⁷ There are also puzzling differences in associations between diseases and genetic variants across populations and racial groups as usually defined. These inconsistencies suggest that additional genetic and social correlates of group identity and/or ancestry modify disease risk but remain unidentified in our focus on common genetic variation alone. These are the sorts of questions anthropologists should be attending to rather than simply continuing to demonstrate for the umpteenth time that sampling and analyzing human variation by population categories is a cultural decision.

COMING TO RESOLUTION

The merry-go-round of race in popular and scientific culture alike remains riotous, but not so merry, though it does keep going ‘round and ‘round. The problem is not the facts. We cannot avoid them, no matter how we might try. The facts include the manifest geographic variation in our species, variation we can see with our eyes and with our DNA sequencers. Another set of facts has to do with the way culture divides largely quantitative variation into categories. It sorts out the world and provides opportunity to make sense of it all, and to classify who’s who. A third set of facts demonstrates that these same facts lead to both ethnic cohesion and to ethnic strife.

We already know the facts. In that sense, the endless cycling could stop, because we’re already there. But people stubbornly continue to see what they want to see in the facts—either that or what they want to see determines which facts count. Most articles on the subject are rather predictable, transparently reflecting the authors’ social politics,^{5,6,8–10,18,19} which is understandable but usually not helpful in terms of understanding the facts and mainly serves to heat up ever-recycling stances. Can there be a way that we, at least those of us in anthropology, might get past this? Is race

“real”? Does it have “biological meaning”? These are not scientific questions because their meaning hinges entirely on definitions and implicit but unclear connotations.

Perhaps we should simply recognize that getting past this is really about the dead hand of our cultural past, of vested social and material interests correlated with categorical concepts that did have some biohistorical basis (for example, black slaves were from Africa, white citizens from Europe). We waste our expertise endlessly attempting to adjudicate cultural mores with biological data, debating whether “race” is “real” when we know that the social reality of race, whatever race is, is mediated by the distribution of genetic variation but not determined by it.

Race is a conceptual construct with historical, biological, and anthropological elements. Its mix differs for each person, probably in ways he or she is not even fully aware of. None of these thoughts is new or secret, but for similar sociocultural reasons they seem hard for people, even anthropologists, to accept. The legendary baseball great, Satchel Paige (1906–1982) (Fig. 3), veteran of the Negro Leagues, once quipped “Don’t look back. Something might be gaining on you!” In the study of race, it’s a shame that even scientists rarely seem to look back, to

realize that we are not putting any distance between ourselves and our past. Paige finally made it to the Major Leagues and never had to look back. Maybe it’s time for us to move forward in our race, too.

NOTES

Comments on this column are welcome: kenweiss@psu.edu. There is a feedback and supplemental material page at http://www.anthro.psu.edu/weiss_lab/index.html. We thank Anne Buchanan, Debra Mathews, Steven Orzack, and John Fleagle for critically reading this manuscript. S.M.F. was supported by an NRSA fellowship HG002629 from the National Human Genome Research Institute.

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