

# **The Dangers in Editing Human History to Fit Methodological Constraints in the Present**

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This paper contrasts two different theoretical approaches to the reconstruction of human evolution: multiregional continuity and genetic marker fission-replacement. In considering these two models it is critical to distinguish among the data, the assumptions of the interpretive framework within which the data are ordered, the conclusions that are offered on the basis of the work, and the significance that is attached to these conclusions. The strategy followed here is to begin with the more recent work, first examining the significance claimed for it and then working back through the conclusions and assumptions to the data. A comparable analysis is then offered of the antecedent alternative model. Finally, some reasons are suggested for the widespread misunderstanding of a multiregional model.

## **Multiregional Continuity**

The interpretive framework for human evolution now generally referred to as multiregional continuity was introduced conceptually by Franz Weidenreich as early as 1936, when he illustrated his views on geographic sequences in fossil hominid lineages. Two years later he formally introduced his Polycentric Theory (Weidenreich 1938). Although neither of these publications ever was widely available, he reiterated these views in more accessible forums. For example, in the same year one paper in *Nature* (1937a:272) concluded with the phrase: “the line linking Pithecanthropus and Sinanthropus, respectively through . . . Neanderthal man, to recent man is continuous,” while a second one in *Man* (1937b:51) opens with a specific reference to his first paper on polycentric origins: “The fact that there is a relationship between Sinanthropus, Pithecanthropus and Javanthropus was asserted for the first time in (1936) in my statement to the effect that: ‘I came to the conviction that Javanthropus approaches in some regard Sinanthropus, or more correctly Pithecanthropus.’ ” He published a popularized version in 1946, which contains the classic figure (1946b:30, Fig. 30) showing Weidenreich’s views on genetic continuity through time and space.

The base established by Weidenreich subsequently has been updated and elaborated (Wolpoff 1992; Thorne and Wolpoff 1992; Frayer et al. 1993; Frayer et al. 1994; Frayer 1997) to incorporate the enormous strides that have been made in genetic theory since Weidenreich’s time, as well as to recognize the extraordinary expansion in numbers of hominid fossil specimens available for study. Because models of regional continuity are persistently misrepresented (e.g., Stringer 1989; Howells 1993; Cavalli-Sforza et al. 1993, 1994; Tishkoff et al. 1996a,b), scientists who wish to

understand these models should consult the publications by Weidenreich as well as Wolpoff and his colleagues to alleviate the need for redaction (Eckhardt et al. 1993).

To many human population biologists today, the multiregional theory is appealing because it offers the possibility for integrating a broad range of data on discrete and continuous heritable characters in present and past populations within a framework that is explicitly uniformitarian in its assumptions. Indeed, the framework offered by Weidenreich is a signal example of anthropological originality.

From a multiregional perspective, human evolution is seen as largely continuous in time and space over a period that could exceed fifty thousand generations, without any need for postulating massive but as yet undocumented waves of Paleolithic population replacement and extinction. All forces of evolution observable at present are assumed to have operated in the past, although almost certainly not at constant rates. Gene flow among adjacent populations is accepted as a basic mechanism that has maintained continuity across the vast territories gradually populated and for the most part continuously occupied by expanding hominid populations. But, in strong contrast to various population replacement scenarios, in multiregional models adaptive processes are admitted as well; in fact, they are seen as essential elements. As humans expanded their habitats from tropical savannas to environments as diverse as temperate woodlands, wind-swept steppes and tropical rain forests, ancestral gene pools would have been subject to substantial repatterning. Against the background of stochastic factors such as genetic drift, natural selection in all probability would have functioned as a highly complex deterministic element that facilitated local adaptation. These and other features of a multiregional model make it a fair candidate for recognition as one of the overlooked conceptual triumphs of anthropology. Its recognition of probable complexity in patterns of genetic adaptation among populations linked as nodes in a network stretching across vast reaches of space and time has made it difficult to test quantitatively on a global scale. Takahata (1993) represents one of the better attempts, though still failing to deal adequately with selection.

The major advantage of a multiregional model is that it is consistent with a large-scale research agenda for studying the potential functional value of human biological diversity. This would be a desirable alternative to the paradox employed by many geneticists (and some anthropologists) at present, invoking the possibility of genetic knowledge to help us to understand and perhaps alleviate human diseases (Cavalli-Sforza et al. 1991), while at the same time assuming analytically that most human genetic variation is selectively neutral or has selective differentials that are impossible to measure (Cavalli-Sforza et al. 1994:13). If it is reasonable to argue that some human genetic variation has been shaped by exposure to different patterns of infectious diseases or other selective agents in the past, then it would seem logical to accept the likelihood that different alleles or genomes are associated with different

selective coefficients. Thus, it would be desirable to employ models that allow for selective influences. Contemporary multiregional models of human variation fit this criterion far better than do various replacement models—despite the widespread use of the latter by human molecular population geneticists. This peculiar situation requires an attempt at explanation.

### Multiregional Model Misunderstood

The widespread present rejection of Weidenreich's scientific viewpoints, as well as the multiregional theory of evolution derived from them, is somewhat puzzling. After all, at least this theory is consistent with all of the data on past as well as present human population variation and does not require acceptance of assumptions that are strongly counter to reality (e.g., that evolution occurs principally by splitting, that selection can be ignored, and that genetically complex traits contribute no useful phylogenetic information). The puzzle disappears, however, once it is realized that in all probability very few geneticists are familiar with Weidenreich's views firsthand, having instead gotten their information about his ideas from secondhand sources that manifestly have distorted them. Foremost among these sources is a book by Carleton Coon, *The Origin of Races* (1962).

In his introduction to *The Origin of Races*, Coon described an intellectual debt to Weidenreich, and he cited several of Weidenreich's publications in the book's bibliography. But Coon's views really departed sharply from Weidenreich's. Where Weidenreich inferred from morphological features of fossils that there must have been continuous inter-regional gene flow *as well as* regional continuity, Coon (1962:36) expressed his hope that "acquaintance with the principles of genetics may also help us to solve the central problem of this book—that is, to discover how long ago the ancestors of the human subspecies parted company." In fact the only debt explicitly acknowledged by Coon to Weidenreich lies in the assignment of Peking Man to the Mongoloid race; and although *The Origin of Races* is ostentatiously dedicated to Weidenreich's memory, the anatomist receives scarcely a mention in Coon's autobiography. Coon's views resemble far more those of his Harvard mentor Earnest Hooton (1946) on the one hand, and Reginald Ruggles Gates, Emeritus Professor of Botany at University of London and Research Fellow in Biology at Harvard in the 1940s, on the other.

We are fortunate in having a critique of a paper by Gates (1937) in which Weidenreich (1946a:415) noted disapprovingly that "the author distinguishes five 'species' of living man: *Homo australicus*, *Homo capensis* (Bushman type), *Homo africanus* (Negro), *Homo mongoloideus* and *Homo caucasicus*. All other human races are considered subspecies of the five primary 'species.' " Gates believed that "the span of time a group has needed to differentiate and the duration of its isolation, but not the degree of their morphological differences, are the criteria for their ranging in

certain categories.” Significantly, not only are Coon’s expressions about importance of isolation congruent with those of Gates, but additionally Coon’s (1962) subdivisions of the human species are precisely those of Gates (1937), five for five.

Far from anticipating Coon’s construct of ancient, separate subdivisions of a temporally continuous human species, Weidenreich excepted to it. This disagreement about the fundamental bio-historical unity or diversity of the human species is underscored by a brief and intense exchange between Weidenreich and Gates in the pages of the *American Journal of Physical Anthropology*. Although Weidenreich had studied nearly all of the specimens firsthand and Gates (1944) had not, Gates criticized as “naïve” Weidenreich’s (1943) inference that all hominids from the middle Pleistocene to now represent a single species. Polemics aside, there was an important contrast between their views. In maintaining that “not a single individual in bisexually reproducing animals is known that is not heterozygous in many of its genetic characteristics,” the physical anthropologist Weidenreich articulated a grasp of population genetic diversity that was prescient, and far from widespread at a time when a classical model of the genome still was generally accepted. In contrast, Gates, a botanical geneticist who aspired to be an authority on human heredity, interpreted human heterozygosity as “racial and due to crossing, while many others are mutational in origin” (1947:29). The idea that a single human species could be variable over most of its range in time and space was as inconceivable to Gates as to Coon.

This leaves us with a question: Why didn’t Coon simply acknowledge Gates rather than Weidenreich? The answer appears to be that Weidenreich was respected by many anthropologists as a scholar and paleontologist, while Gates’ extreme views on race and eugenics made him a more peripheral figure, particularly in the immediately post-WWII era (Washburn 1947; see also Boyd 1948 and McCown 1948). Coon and Gates were further linked through Carleton Putnam’s notorious *Race and Reason* (1961), to which Gates co-authored an introduction, and which Coon ignominiously defended from the podium of the American Association of Physical Anthropologists. Indeed, Coon’s intellectual debt to Gates is much clearer in the companion volume, *The Living Races of Man* (Coon 1965), in which Weidenreich is neither cited nor mentioned yet no less than 12 publications by Gates are. In Gates’ 1948 book expressing the same ideas of five deep and different species of humans, he acknowledges “the benefit of a critical reading of the whole book with valuable suggestions by Dr. Carleton S. Coon. . . .”

Thus, Coon’s ideas were not Weidenreich’s in spite of Coon’s fictive pedigree. And, not suprisingly, Coon’s ideas proved to be as controversial and ultimately as anathema as those of Gates. Unfortunately, through the rejection of Coon’s ideas, those of Weidenreich came to be swept away as well; a classic case of guilt by association.

And what an association! Cavalli-Sforza et al. (1993a) associate Weidenreich with Coon as co-authors of a book published approximately 15 years after Weidenreich's death, then they (1993b) "correct" the initial error by citing the wrong work by Coon alone. Although this might be taken as unfamiliarity with Weidenreich's ideas in the scientific literature, the geneticists criticize repeatedly an error that does not exist in the original publications: "The major difficulty with this hypothesis is that it requires parallel evolution all over the Old World for a long period" (Cavalli-Sforza et al. 1994:63). In fact, gene flow was so explicit in Weidenreich's (1946b:30, 85-86) formulation that insistence on parallel evolution is at best an absurdity.

Even more recently, Wolpoff (1996) has had to rebut the assertion by geneticists that "parallel evolution" occurring "among regional populations from *H. erectus* to *H. sapiens*" is required by the multiregional origin model descended from Weidenreich, and the attribution to multiregionalism that "non-African populations have been diverging since *H. erectus* emerged from Africa 800,000 or more years ago" (Tishkoff et al. 1996a). All in all, this succession of inaccurate representations would be merely disappointing if its logically unnecessary alternative were not also being used as the basis for structuring large-scale research programs.

### **Genetic Marker Fission-Replacement Theory**

When *The History and Geography of Human Genes* (Cavalli-Sforza et al. 1994) was published, it was met with a level of media attention and effusion uncommonly accorded to scientific reference works. From the outset it was heralded as a unique effort, with a *Time* magazine account (Subramanian 1995) labeling it as "nothing less than the first genetic atlas of the world." Most human population biologists know this is not true, of course. Almost everyone in the field has on their shelves a copy of W. C. Boyd's modest but popular *Genetics and the Races of Man* (1950). Even more immediately comparable are the numerous authoritative compendia of genetic variation produced over the years by A. E. Mourant's group, including *The Distribution of Human Blood Groups* (1954), *The ABO Blood Groups: Comprehensive Tables and Maps of World Distributions* (1958), and *The Distribution of Human Blood Groups and Other Polymorphisms* (1976). The last volume is an atlas that is over twice the length of the book by Cavalli-Sforza's group and similar enough in format that it could have served as a model for the later work, though obviously the vast increment in computational power now available has made certain technical advances possible in *The History and Geography of Human Genes*.

In fact this curious misrepresentation of the literature is derived from the work itself. Thus we are told that "The first attempt at reconstructing human evolution on the basis of genetic data from living populations was undertaken in 1964 by Cavalli-Sforza and Edwards" (Cavalli-Sforza et al. 1994:68). That work indeed attempted to

use new statistical methods, but to sweep away all previous attempts to use genetic data to answer questions about human historical biology results in considerable distortion of the record. Thus, there are two relatively brief paragraphs (Cavalli-Sforza et al. 1994:18) mentioning earlier attempts indeed to use genetic data to reconstruct human evolution, ranging from the Hirszfelds (1919) through Mourant (1954) to Nei and Roychoudhury (1988). However, these efforts are lumped together with the speculations of Lucretius and Pliny the Elder in a section titled "Classical Attempts to Distinguish Human 'Races' " and followed immediately by another section titled "Scientific Failure of the Concept of Human Races."

But the book does not offer much that will be seen as conceptually new by most investigators. One might begin by noting the close parallel between the statement of Cavalli-Sforza et al. (1994:19) that "although there is no doubt that there is only one human species, there are clearly no objective reasons for stopping at any particular level of taxonomic splitting" and Blumenbach's (1795) observation that "innumerable varieties of mankind run into each other by insensible degrees." Nevertheless, in his analysis Blumenbach established discrete geographical categories of humans—Ethiopian, Mongolian, Caucasian, American, and Malay—and likewise Cavalli-Sforza et al. (1994) impose a discrete color-code upon the geographical variation of humans—Africans yellow, Australians red, "Mongoloids" blue, and "Caucasoids" green. This consequently has every appearance of neo-classical racial anthropology: the techniques change, but the goal remains the same: imposing qualitative divisions on the human species where none exist in nature.

Obviously the book is not a mere bicentennial update of work by Blumenbach and his contemporaries. For example, Blumenbach believed that Europeans, with the exception of Lapps and descendants of the Finns, represented the primeval human population from which all others subsequently were derived. In contrast, Cavalli-Sforza et al. favor Africa as the locus of the original human populations from which others descended, as do virtually all other anthropologists (although there are serious substantive disagreements over timing and continuity). But even here it should be noted that an African hominid origin derives its earliest and strongest support from the fossil record rather than from the distribution of simply-inherited genetic traits.

The specific phylogenetic conclusions of *The History and Geography of Human Genes* run an extraordinary gamut. At one end, we have the mundane inference that Canada Eskimo and Alaskan Eskimo cluster together, and that speakers of Andean Amerindian languages cluster closest to Penutian speakers located principally in Oregon and California. At the other end of the scale, however, is the astonishing announcement publicizing this very work that "all Europeans are thought to be a hybrid population, with 65% Asian and 35% African genes" (Subramanian 1995). Surely, this must be a journalistic misconception—but no, it is from the book itself, for this hypothesis has been "tested" (Cavalli-Sforza et al. 1994:92, referring to

Bowcock et al. 1991), producing the reported results. A Delphically-phrased explanation is provided for the very short branch linking Caucasoids (i.e., Europeans) to the human phylogenetic tree: "One hypothesis is that they might have originated from an admixture between their southwestern and northeastern neighbors, Africans and Mongoloids, between which Europeans are sandwiched. One cannot exclude other hypotheses" (Cavalli-Sforza et al. 1994:155).

Approached straight on, this appears to be a new problem (short branch length linking one major geographic group to the others) with a very old solution: the assumption of a few original human populations, and explaining the biological attributes of other populations in terms of admixture among the hypothetical primordia. In the terminology of Cavalli-Sforza et al. (1994:19) these groups are not "pure" primary races in the sense of nineteenth-century anthropologists but "'core' populations, selected because they presumably underwent less admixture." They conclude (1994:92) that "The only hypothesis compatible with the data is that there was an admixture between African ancestors and Chinese ancestors." Regardless of the details, this approach of explaining the attributes of some groups in terms of admixtures among others can be found explicitly as far back as Genesis (6:4), and more recognizably in the work of Immanuel Kant (1775), and more recently in Gates and Coon. By such means, conceptually archaic frameworks appear to be validated by technologically modern data.

The concept of race is a folk belief that was adopted uncritically by early biologists and anthropologists in an era when taxonomic categories were accepted as fixed and natural. The categories presupposed in earlier eras and reified by early anthropologists represent at best first crude approximations to summaries of the genetic and phenetic patterns observed in populations distributed over time and space. Data collection on the scales undertaken in our own time deserves a far better interpretive framework than those now prevalent in many studies of human molecular population genetics.

A key operating feature in the modern genetic work is that the representation of *relationships* among human populations with dichotomous trees reflects a chiefly branching or fissioning historical *process*. They acknowledge that there are alternative models that employ population networks rather than trees (e.g., Lathrop 1982), but commonly dismiss these as unworkable at present. In fact, however, the structure of these trees is affected by population structure and genetic contact as well as by common ancestry. Thus, there is no guarantee that the tree obtained represents phylogenetic history.

Marker-based approaches have the apparent advantage of being highly quantitative in their structure and technically sophisticated in the analysis and presentation of their limited subsets of single locus genetic traits. However, they

contain a conceptual flaw: they accept biological features of the living as a sufficient empirical basis for inferring prehistoric relationships—as if this were model-free—with as much assurance as did Topinard (1892).

Throughout the work by Cavalli-Sforza et al. (1994), genetic loci are referred to as “markers.” This term is used so commonly and uncritically in population biology that it has become distorted in an Orwellian sense. At one point, markers marked something. Certain alleles, it was believed, were indicators—markers—of ancestry. Thus the hemoglobin S allele, when detected in a blood sample, was accepted straightforwardly as indicative of African ancestry (da Silva 1948). The situation is better understood now and correctly accepted as being vastly more complicated. “All populations or population clusters overlap when single genes are considered, and in almost all populations, all alleles are present but in different frequencies. No single gene is therefore sufficient for classifying human populations into systematic categories” (Cavalli-Sforza et al. 1994:19). Thus genetic markers are generally widespread and acknowledged to be poor at marking—without markedly affecting the folk belief in the reality of geographical “racial” subdivisions (see Fix 1997).

Other geneticists have taken over from anthropology the archaic explanatory mechanism that invokes the existence of a few primary human populations (“races” or “core populations” or the various equivalent terms denoting belief in earlier, less mixed, or “purer” human populations than now exist). An explicit version of this can be seen in the publications by Nei and Roychoudhury (1974, 1982, 1993), which would not have been out of place in any of the classic old-fashioned textbooks of anthropology, including archaic discussion of possible explanations for the presence of “African traits in the mongoloid stock of New Guinea and Australia.”

Although the trees produced by Nei and Roychoudhury have different topologies than those of Cavalli-Sforza’s group, and are thus fundamentally inconsistent with them, the results proceed from the same basic assumptions: that the evolution of modern humans can be explained in terms of a few primary populations that arose (in this case from African ancestors) via splitting, with other human populations resulting from genetic admixture among the “major” groups. In these models natural selection enters chiefly as a source of potential interpretive problems rather than as a dynamic force of evolution.

The final point to be made about these studies is the manner in which they dismiss any fossil evidence for continuity of lineages between living populations and any regional antecedents that are not themselves anatomically modern. As a result, the inference that extant human populations converge in common ancestors who existed about 100,000-200,000 years ago is less an empirical result than an *a priori* postulate (Cavalli-Sforza et al. 1994:ix, 4). Reliance only on supposedly non-adaptive single-locus genetic variation continues not because the concept is realistic but because such



assumptions are necessary for the analysis—as they were for most previous attempts to reconstruct human evolution chiefly on the basis of regular population splitting supplemented by occasional admixture. A less dogmatic approach might be simply to view these characters with caution and to attempt to quantify the extent of environmental influence (as did Boas [1911] and Shapiro [1939], among others).

Any doubts of the primacy of theoretical preconceptions over empirical findings in the advocacy of “Out-of-Africa” models should be dispelled by comparing two well-publicized genetic studies. Mitochondrial DNA was promoted as an ideal system for tracing patterns of human descent because of its high rate of nucleotide substitution. This was the basis for the well-known conclusion of a common ancestry for modern humans in the range of 100,000-200,000 years ago. But recent studies of the ZFY locus on the Y chromosome estimate common ancestry in the same range in spite of detecting *no variation at all* in a sample of 38 modern humans. We should dismiss ZFY for the same reason that we were supposed to believe mtDNA, but paradoxically that is not the message we hear. (For critiques of both of these convoluted arguments, see Eckhardt [1997] and Templeton [1992, 1996].) The mere fact that certain models are widely used and appear to yield congruent conclusions should not in itself be taken as an indication that the findings necessarily support each other. Sometimes in science repetition marks a peak of enthusiasm rather than validation (Byrne 1989, particularly entry for May 25).

### **How Misconceptions of the Past May Shape the Future**

The 1990s have seen the proposal and preliminary funding of an ambitious new project, The Human Genome Diversity Initiative (Cavalli-Sforza et al. 1991). Its major premise is that knowledge of the “genetic history of *Homo sapiens sapiens*” is endangered as the result of rapidly increasing admixture among various human populations, as a consequence of advances in transportation and other aspects of modern life. But this urgency assumes that isolation of populations was the usual circumstance and that gene flow was minimal until recently. Observations on the ubiquity of human variation within and between populations are at odds with this view. In contrast, from the perspective of multiregional continuity it is assumed that there are not now and possibly for millennia never have been human populations that have been materially unaffected by gene flow. Moreover, in this view, gene frequency patterns reflect not only gene flow but also adaptation to various geographic areas, with their different climates, food sources, disease patterns, and so on.

A corollary of this multiregional perspective on the antiquity of human diversity is the realization that the most promising frontier of human genetic research is not phylogeny—which has been done for so long that it is yielding diminishing returns—but a refocus into investigating gene function, expression, and variation in relation to history. Against this conceptual background it is worth bearing in mind that

in any case current patterns of genetic variation may reflect not ancient patterns of variation in relict populations but, to a considerable extent, the impact of infectious diseases that have increased in importance following the widespread adoption of agriculture and its attendant waves of explosive population growth.

Finally, given the tragic history of investigations into human population biology and phylogeny, particular care must be taken not to convey meanings that hopefully are not intended. In this regard, it is late in the day to be referring to certain human populations in Ethiopia as “living fossils” (Cavalli-Sforza et al. 1994:193). Such terms are all too easily confused with the invidious identification of “primitive” as opposed to “progressive” races (e.g., von Eickstedt 1934). In the human sciences, a humanistic perspective would not be out of place.

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