



## **The Persistence of Racial Thinking and the Myth of Racial Divergence**

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# The Persistence of Racial Thinking and the Myth of Racial Divergence

THE CONCEPT OF RACE, racial thinking, and approaches using received racial schema are a part of a theoretical worldview deemed by most anthropologists to be incorrect and passé (Lieberman et al. 1989). But Leonard Lieberman and Fatimah Linda C. Jackson (1995) indicate that racial thinking and the use of racial terms or categories still exist and are seen in the sampling strategies used in studies addressing the origin of modern humans.

Racial thinking rests on the belief that visible human variation connotes fundamental deep differences within the species, which can be packaged into units of near-uniform individuals. This belief leads to the construction of types that by definition must have certain traits. Racial thinking in its classical form requires the explanation of certain kinds of variation as necessarily the result of gene flow between entities conceptualized as having different traits. The origins of these traits may be explained as the result of natural selection (or even drift) in their homelands. But when traits that are predefined as belonging to different groups are found in combination, admixture is invoked as explanation. One example is the epicanthic eyefold of some Khoisan speakers. In the past it was sometimes explained by ancient admixture of migrating "Mongoloids" with "Negroes."<sup>1</sup> Another example is the narrow nasal form of some eastern and western Africans, which was and sometimes still is explained as the result of gene flow from "Caucasians" instead of drift or selection.<sup>2</sup> A related issue is that of groups having "intermediate" trait frequencies or values on continuous variables; these groups in racial models are necessarily hybrids and could not have an autonomous origin. These examples

raise a number of issues, and several questions may be asked. Is there a good fit between the concept of raciation, or racial divergence, which strictly speaking implies the emergence of morphologies said to define the races, and the results of evolutionary genetic studies? Does the phrase *racial divergence* actually describe the process of diversification in *Homo sapiens sapiens*? Or does it represent the imposition of inappropriate constructs onto the biohistorical record?

In exploring the implications of racial terminology and thinking and their persistence, our intention is to encourage dialogue on these issues. We stress that racial thinking is not necessarily synonymous with *racist* thinking. The interest here is in the vestiges of typological or categorical thinking as applied to humans. Conceptually it is important to recall that the classical race concept implies the existence of several collections of uniform individuals who comprise relatively distinct units. Individuals by definition are more similar to each other in each unit in all measurable parameters and any individual can serve as a representative of the whole group. Races in this conception conform to Platonic types; they exist by definition and are bounded distinct entities that are viewed as fundamental units. This type concept is not to be considered in isolation from the actual racial schema that were created. The racial categories found in textbooks cannot be extricated from the conceptual universe of their origins which postulated distinct cradles, widely separated from each other. These categories also cannot be separated from stereotyped notions of which set of traits most authentically represents each continent. Racial thinking is not usually found today in its "pure" form. Nevertheless, this form of categorical thinking influences research design and data interpretation.

The recent single-origin hypothesis for modern humans is a theoretical bias here, although this orientation

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is not a requirement to validate most of the ensuing discussion. Taxonomically, “race” for some investigators is the same as subspecies, officially designated by the trinomen, which raises another issue of systematics since all living humans are usually designated *Homo sapiens sapiens* (Klein 1989:348).

In defense of the race concept, Theodosius Dobzhansky (1970:268) is often cited as stating that a race is a breeding population, containing individuals who are not genetically uniform. The emphasis on the uniqueness of the individual is important. Close reading, however, also indicates that Dobzhansky has simply declared the received racial groups to be Mendelian populations, which they are not. He contradicted himself when he stated that “a race is a cluster of local populations” (1970:310), because a local population best approximates the Mendelian population concept. It is noteworthy that the received racial schemes, which sort people by externally observed traits (morphotypes), are still the basis of most studies.

Although it might be claimed that the term *race* is only used today by geneticists to refer to bona fide breeding units, a brief perusal of the literature indicates that the old racial categories and concepts are still in use. Sometimes they are treated as though they were breeding units, especially when they are called (incorrectly) ethnic groups or macroethnic groups. Sometimes local populations or even single individuals are used as surrogates or putative “core populations” for the old “great divisions of mankind,” in what can only be construed as the typological tradition.<sup>3</sup> In a limited survey of recent literature the authors have been unable to identify an instance in which a local breeding population, which would often correspond to a proper ethnic group (for example, the highland Amhara or Gonja), has been called a race.

## Racial Terminology and Paradigm

The terms commonly used to identify race are *Caucasian/Caucasoid*, *Mongoloid*, and *Negro/Negroid*. It is important to note that the term *Negro* is not based on a geographic region. In J. F. Blumenbach’s (1969[1775]) schema the term *Ethiopian* is used instead of *Negro*. The racial categories are based on morphology and to a degree geography, although this has varied. It was long recognized that some groups would not fit. Other racial schema had and have more divisions, usually in order to categorize Native Americans, Native Australians, and heavily pigmented Oceanians as separate groups. All of the schema have as a fundamental corollary that the racial types and their defining traits have original homes, or places of origin. Associated with this is the idea that the homes of the traits are essentially unique. Thus, by

definition, a given trait or complex used in defining a race had to have arisen in a particular racial homeland. This logically leads to the practice of assuming that pre-defined trait complexes found outside of their homes must have gotten there by colonization or gene flow. Parallel microevolution is not seen as a possible or partial explanation in a strict racial approach, a form of categorical thinking.

Culture was sometimes added to biology. Earlier in this century there were assumed a priori associations of races (actually phena) with specific languages or language families. This led some scholars to classify languages such as Fulani (as noted by Greenberg 1966) on the basis of the phenotype of their speakers! A racialized worldview can be detrimental even in the absence of racism. An example would be the physician who misses the diagnosis of sickle-cell anemia in a Central American “mestizo” because of assumptions about race and his or her ignorance of the role of enslaved West and Central Africans in Central American history.<sup>4</sup>

In the racial paradigm, races are the fundamental units and generically may be called ideal types. These types are the units of interaction. Variation is primarily explained by gene flow, and in an earlier time groups conceived as admixed were sometimes called secondary races. This model is well illustrated in the writings of Carleton Coon (1962, 1965), who envisioned five primordial races with unique origins in distinct geographical populations of *Homo erectus*. In his schema the original Africans were those he called Congoid (unfortunately labeled *Pygmies*) and Capoid (Khoisan, sometimes improperly designated *Bushmen*). All other continental African types and populations were said to be the products of colonization, or admixture, between either of these originals and outsiders, groups usually called Caucasian, ultimately from Europe. Hence ancient and modern Nile Valley populations were said to “look like what they are”: ancient hybrids (Coon 1965:119) between an indigenous African population and Caucasian immigrants. As noted, some also believed that there had been an ancient invasion of Mongol-related folk. This nonevolutionary perspective of African variation still persists to some degree. Yet the fact that there is evidence for a long presence of modern humans in Africa (Clark 1989; Stringer 1993) would suggest that diversification by selection and drift would better explain the bulk of variation from Cairo to the Cape and from Algeria to Zimbabwe.

Comparative genetic studies on geographically diverse human populations provide evidence of high levels of diversity in continental Africa. Sarah Tishkoff and her colleagues (1996) find an intermediate pattern of genetic variation for the CD4 locus in northeastern (actually Horn) African populations. They explain this by local evolution and not by admixture with Eurasians. In

essence they are describing a gradient of differentiation. The Horn, largely at the latitude of Nigeria, contains a subset of the diversity seen in other African regions. Tishkoff and her colleagues suggest that the Horn's inhabitants are the local descendants of those who left Africa to people the world. Whether this is true or not, the Horn of Africa certainly contributed more recently to the Near East, because based on linguistic reconstruction and the principles of "least moves" and "greatest diversity," it is the geographical home of the ancestor of Afro-Asiatic languages, spoken primarily in Africa with one member in the Near East (Semitic) (Ehret 1984, 1995; Ruhlen 1987). Early Afro-Asiatic spread out from the Horn and did not come into Africa from Asia (brought by "Caucasians") as was believed at one time, and as is occasionally assumed by nonlinguists (e.g., Barbujani and Pilastro 1993; Cavalli-Sforza and Cavalli-Sforza 1995).<sup>5</sup> In fact, there is evidence for movement out of Africa at the very time when some claim in-migration (Bar-Yosef 1987). By the time of the radiation of Afro-Asiatic speakers there was already genetic differentiation in Africa due to African biohistorical processes.

There is no need to postulate massive European settler colonization of Africa or genetic swamping and/or settler colonization by Eurasians, as is implied or stated in some contemporary genetic work (Cavalli-Sforza et al. 1994), echoing the now defunct Hamitic hypothesis.<sup>6</sup> Continental African variation may be interpreted largely without external mass invasions (Armstrong 1990). The antiquity of modern humans in Africa means that there has been time to accumulate a large amount of random genetic variation (Cavalli-Sforza et al. 1993), which has been shaped by great ecological diversity in the continent (Hiernaux 1975). Genetic drift would also contribute to variability due to fluctuations in population size as founder effects and population expansion events occurred throughout the continent. Therefore it is far more accurate to speak of a range of *biohistorical African* variants than different *races* of Africans. Northern Africans are more accurately conceptualized as primarily the products of differentiation than of hybridization.

It is curious that, although the race concept has largely been rejected, even those in the no-race school have not developed working alternative concepts (other than the cline) and schema that effectively eliminate racial thinking when populations, biohistory, and gradients of differentiation are the subjects (Lieberman and Jackson 1995). Instead, the received racial models and terms are used, sometimes apologetically. Sometimes they are used in an unknowing fashion, while at other times names of continents are used, but the populations or physiognomies deemed representative, or the "true" originals, by various investigators, merely con-

form to Coon's (1962, 1965) or C. G. Seligman's (1930) ideas of original races. This is especially true in the case of Africa. This situation is puzzling. Are these practices due to methodologies that are inherently typological or to the cultural context of anthropological genetic studies?

The persistence of the racial paradigm (and not just names) is further illustrated by investigators who use dendrograms (trees) to assess group similarities or dissimilarities, usually in quest of intraspecific phylogenies. The groups utilized usually conform to the old racial schema. Dendrograms are also used to illustrate the divergence of entities called human races or of populations used as their surrogates. This is problematic since few human populations, even authentic breeding populations, are so well differentiated (and independent) from each other as to support the distinctness implied by tree branches. The degree of drift has not been necessarily equal across space and time. The ubiquity and complexity of human migration patterns guarantee that branching points in trees will always be suspect (Jorde 1985). Also, strictly speaking, studies can only inform about the groups used in the analysis. Therefore a study using Mbuti, a clan of Saame speakers, a Swedish village, and Vedda can only tell us about each of them. These groups should not be reified into other entities.

## Racial Divergence

The phrase *racial divergence* is used by several scholars to describe the fissioning of presumably generalized mid- (to late) Pleistocene *Homo sapiens sapiens* into essentially discrete units. The genetic profiles are said to categorize certain groups defined by morphology and geography.<sup>7</sup> Some studies utilize classic genetic markers such as blood-group antigens and serum-protein polymorphisms. Others use restriction-site polymorphisms (RSPs) and nuclear or mitochondrial DNA (mtDNA). Generally, these investigations assess the amount of genetic difference between the studied groups and estimate their divergence times. Sometimes the term *race* is not used to describe the units. On close scrutiny, however, these groups are conceived as the traditional races or are taken to denote those races and hence all other groups within those races. Strictly speaking, the divergence times can *only* apply to the specific groups studied, which are hopefully real breeding units, and not to any others. The phrase *racial divergence*, in a strict sense, must first imply the appearance of the morphologies used to define races. This is inherent in the conceptual model and the terminology. But few studies address this issue of the assumed correlation between bony/soft-part phenotypes and genotypes

**Table 1**

Published estimates of "racial" divergence times. Dates are averages or rounded figures. "Kya" means thousands of years ago.

Caucasoid/ Negroid	Caucasoid/ Mongoloid	Mongoloid/ Negroid	Genetic data	Reference
15 Kya–20 Kya	15 Kya–60 Kya	25 Kya–100 Kya	blood groups	Cavalli-Sforza 1969
53 Kya–106 Kya	20 Kya–40 Kya	45 Kya–90 Kya	serum proteins	Nei 1982
113 Kya	41 Kya	116 Kya	serum proteins	Nei and Roychoudhury 1982
104 Kya	104 Kya	104 Kya	mitochondrial DNA	Johnson et al. 1983
35 Kya–75 Kya	13 Kya	31 Kya–61 Kya	mitochondrial DNA <sup>a</sup>	Nei 1985
115 Kya	55 Kya	120 Kya	various data sets <sup>b</sup>	Nei and Ohta 1991

<sup>a</sup> Data used were from Brown 1980.<sup>b</sup> Gene frequency data collected from serum protein, blood-group loci, and nuclear DNA restriction data.

conjured by the term *racial divergence*, and *when* these became associated.

An examination of the results of studies that implicitly or explicitly use racial categories and evaluate racial divergence indicates inconsistency. In one study, racial divergence is said to have occurred at about 115,000 B.P. for Negroid and Caucasoid, at 120,000 B.P. for Negroid and Mongoloid, and at 55,000 B.P. for Caucasoid and Mongoloid (Nei and Ohta 1991). Other studies yielded different results (see Table 1). For example, a much later estimate—between 15,000 and 20,000 years ago—was given for Negroid and Caucasoid divergence (Cavalli-Sforza 1969). The inconsistencies are difficult to reconcile, although blood substances are stated to be nonneutral and therefore not as reliable for this kind of enterprise; this means that results based on certain kinds of data could be theoretically eliminated. Different data sets and methods give contradictory results. Deciding which results accurately reflect biohistory is also difficult. The use of genetic systems not responsible for morphology in order to study groups that are defined by morphophenotype is theoretically unsound, especially when divergence times are the subject. Furthermore, the notion of diverging into discrete units is inherently problematic. Groups of humans, whether real breeding populations or aggregates of individuals assembled at the whim of investigators, cannot be treated as species or conceptualized as closed systems. The problem in retrospect is obvious: there is a weighted interest in differences.

### Implications of Genetic Studies

It cannot be overstated that the classical race concept and received schema imply discrete and nonoverlapping groups. This discreteness, as noted, is a property of the ideal type. Genetic studies effectively show that the received racial schema, which are ultimately based on typological thinking and categories, are misleading. Several classical polymorphism studies indi-

cate that for the received racial categories the within-group variation is greater than the between-group variation.<sup>8</sup> Therefore group boundaries are not sharp or "real." Mitochondrial DNA studies indicate that sequences of individuals from the received racial groups do not form exclusive clusters of mtDNA types. Put another way, it has been shown that individuals from geographically separate and morphologically different "racial" groups sometimes possess mtDNA sequences more similar to each other's than to those of members of their assigned group.<sup>9</sup> Given that mtDNA may be viewed as representing maternal lineages, this is not insignificant. This pattern has been interpreted as being the result of gene flow between populations (Cann et al. 1987). But it would also be seen if the ancestral *Homo sapiens sapiens* population was highly polymorphic and subsequent migrants were samples of this diversity. Curiously, the converse is also observed. Eastern and western short-statured peoples from Central Africa are similar in gross morphological phenotype; that is, they belong to the same "race" but are as different from each other in some loci as they are from peoples from the other side of the world (Chen et al. 1995). Not surprisingly, the lack of exclusive "racial" clustering is also seen when haplotype phylogenies were constructed using Y-chromosome polymorphisms. A. Ruiz Linares and his colleagues (1996) believe that clear evidence exists for geographic (continental) clustering of Y-chromosome haplotypes. Their phylogeny, however, does not support this. Their purported African cluster contains only 63 percent African haplotypes, while other haplotypes identified as European and Asian are intermingled in the same cluster. Furthermore the Africans used were scattered throughout the non-African cluster. These studies render the races as discrete units invalid, because they illustrate that races are not bounded, genetically homogeneous entities when numerous systems are considered. There is a lack of concordance between morphophenotypic and other traits; different groupings emerge from the use of different systems.

Genetic studies may be said to have helped demolish one racial construct: that of the Oceanic Negro. This entity's name suggests that certain Pacific/Indian Ocean peoples were recent or ancient extensions of narrowly defined Africans, those called Negroids, especially so-called True Negroes (Seligman 1930). The Oceanic peoples are more genetically similar and genealogically related to mainland East Asians than to any Africans with the so-called Negroid phenotype (Bowcock et al. 1991). Curiously, there seem to be attempts to revive the idea that aspects of the morphophenotypes of Oceanians (and sometimes Dravidians of India) are retentions from early African (modern human) migrants.<sup>10</sup> This idea is problematic, not least because it implies that Africans (stereotypically defined) have remained nearly unchanged since the emergence and redistribution of modern humans. It would also imply a model that would require explaining variation in continental Africa primarily by back migration into Africa, especially Saharan and supra-Saharan Africa.

Nuclear DNA studies also contribute to the deconstruction of the received racial entities. Ann Bowcock and her colleagues' interpretation (Bowcock et al. 1991; Bowcock et al. 1994) of analyses of restriction-site polymorphisms and microsatellite polymorphisms (STRPs) suggests that Europeans, the defining Caucasians, are descendants of a population that arose as a consequence of admixture between already differentiated populations ancestral to (some) Africans and Asians.<sup>11</sup> Therefore, Caucasian would be a secondary type or race due to its hybrid origin and not a primary race. This compromises the racial schema and also invalidates the metaphysical underpinnings of the persisting race construct, which implies deep and fundamental differences between its units. In this case, if the interpretation of Bowcock and her colleagues (1991) is correct, then one of the units is not fundamental, because its genesis is qualitatively different from the other units and even connects them.

Genetic studies also have implications for the notion of race as related to the concept of racial divergence. As noted previously, in the studies of groups in which times are given for divergence, the oldest split is between groups labeled *Negroid* and other racial categories. Other studies that do not use racial terminology (but usually use the same groups, because the underlying thinking is the same) find the first split to be between Africans, typically restricted to Coon's Congoids or Capoids, and others, generally called Eurasians.<sup>12</sup> The times given for the earliest divergence between Africans and all others, range from 156,000 years ago (Goldstein et al. 1995) to 115,000 years ago (Nei and Ohta 1991). At and between these times (in the mid- to late Pleistocene), there is no evidence for modern humans outside of Africa. Therefore so-called (molecular)

racial divergence is really mid- to late Pleistocene genetic differentiation taking place in a population or populations in Africa. The range of body morphologies and external phenotypes of the population(s) in which this differentiation is taking place are unknown. Calling this differentiation "raciation" is misleading and is analogous to the medieval idea that sperm contained fully formed humans in miniature, which only needed to be incubated.<sup>13</sup>

By definition, the chronology and geography of this biohistory renders these genetic variants as also African. Failure to understand this creates the illusion of highly admixed African populations or those said even to be biohistorically non-African! There is no evidence that a monomorphic population left Africa, differentiated outside, and then returned en masse in the late Pleistocene or early Holocene to populate empty regions of Africa, especially supra-Saharan or Saharan Africa, as is implied by most racial schemes. Genetic variants whose origins are dated to before 90,000 B.P. (the estimated time of modern humans outside of Africa [Valladas et al. 1988]) are actually biohistorically African (in origin) whether they are currently found in high frequencies within Africa or not. This is because the next major intraspecific fission seems to occur well after 90,000 B.P. based on nuclear DNA polymorphisms (Bowcock et al. 1991; Cavalli-Sforza and Cavalli-Sforza 1995) and separates select Pacific peoples from a cluster of Far East Asians and Europeans, or just from Asians if Europeans are interpreted as later hybrids. These extra-African events may be said to mark the beginning of incipient non-African biohistorical variation, if the recent-African-origin hypothesis is accepted in a form that minimizes gene flow between moderns and archaics. This examination also reveals that the range of indigenous biological African variation cannot be restricted to the genomes of those having the morphology of the preconceived stereotyped African. Either way, uniquely African biohistory commences after the appearance of modern *Homo sapiens* outside of Africa.

The dates alone indicate that the genetic variation that is the antecedent baseline (or part of it) from which the Eurasian fissioning occurs would also be shared by some Africans. Obviously, in time unique variants appear in Asia (and Oceania) and Europe, although private alleles are rare. Only in a racial model would invasion, settler colonization, or gene flow into Africa be necessary to explain the genetic overlap of various African groups with non-Africans. The evolutionary perspective described here is more parsimonious. Of course there is documented historical migration into Africa, and it is postulated that a small amount of gene flow per generation into a regional population can radically alter gene frequencies in a few thousand years (Cavalli-Sforza et al. 1994). But such biocultural

assimilation of outsiders by indigenous Africans is not the same as wholesale population replacement as occurred in some places (for example, Tasmania) in the era of European expansion. In the case of supra-Saharan Africa, it is obvious that statistically removing the known historical movements and presumed genetic influences would not produce a picture of genetic identity between the various regions of Africa, because diversification began there early. In other words, there was substructure in early African genetic variation.

This synthesis of time, genetics, and geography more parsimoniously explains another case where typological thinking has been the mode of explanation. The Khoisan have been stated to have ancient Caucasian admixture, and in no small quantity.<sup>14</sup> This leads to having to find a way to place the ancestral African population (proto-Khoisan?) in proximity to Caucasians (or Eurasians?). This is done by extending the geographical range of the ancestors of the Khoisan into at least the Sudanese Nile Valley, if not further. This then allows a geographical situation that facilitates gene flow. Incidentally, Coon (1962, 1965) postulated that Saharan and supra-Saharan Africa were once inhabited by Capoid (Khoisan) or similar groups. Hence the idea is not new. But if the genes (genetic variants) being called Caucasian date to before 70,000 B.P. (or even 40,000 B.P.), it is more likely that they came from a biohistorical resident African population (with an unknown phenotype), or else that some of the ancestors of the Khoisan were highly polymorphic, irrespective of their geographic range. The term *Caucasian* is clearly misleading in the interpretation of these data. Lynn Schepartz (1987) has suggested that the range of Khoisan speakers never extended beyond subequatorial Africa. The racial paradigm requires migration into Africa. The evolutionary model acknowledges the in situ differentiation suggested by current work and privileges the locale of biohistory and time.

There is evidence that the putative African-Eurasian split, as claimed in various studies and touted as a fundamental fact, is misleading. A recent study of mtDNA from various human populations shows that the world does not divide into Africans and Eurasians (Penny et al. 1995). Rather it divides into a *select group* of sub-Saharan Africans (the group of 49) and others. These others also include (sub-Saharan) Africans. Unfortunately, this and other microphyletic studies are not as information rich as they might be because all of the regions of Africa are not well represented in sampling. This is due to typological preconceptions about what traits or which groups are to be considered biohistorically African. The definition of African is clearly socially constructed and not developed logically from biogeography.

Evidence from the mid- to late Pleistocene for the commonly understood and defining racial morphologies is also lacking in the geographic areas traditionally viewed as racial homelands. This is even true in East Asia, where regional continuity is claimed; but fossils from this time period are not modern. The Neanderthals resident in Europe and the Near East at this time possessed limb proportions indicative of cold adaptation (Trinkaus 1981). Upper-Paleolithic European remains have limb ratio values of ancient and extant tropical populations (Jacobs 1985, 1987), suggesting that they or their immediate ancestors had come from tropical regions. Paleontological studies suggest Africa is a likely place of origin for these early Europeans or, more properly, their immediate ancestors (Brauer and Rimbach 1990; Stringer 1993).

It is clear that the racial terminology and its conceptual associations are misleading when the genetic data are viewed in the context of geography, time, and fossil data.

## The Persistence of Raciotypological Thinking

Even a casual review of the literature reveals that raciotypological thinking persists. Geneticists and anthropologists still frequently interpret data in terms of interacting discrete groups when this is not the only or even the more plausible interpretation. Alternative models or explanations for variation which might be more powerful are rarely considered. Although the cline concept is useful for understanding individual traits, it is less helpful for understanding the totality of local population processes. While analytical technology and types of data have changed, the sampling and interpretation of human variation continues under the influence of Coonian descriptions and models. The old races (morphophenotypic units) are simply described with new data, although the new data shatter the unity of the anatomically defined categories at the individual level.

The problematic nature of genetic sampling is illustrated by the persistence of stereotyped ideas about continental populations or by practices that minimize the reality of variation. This seems especially true in the case of Africa. An example is the particular use of Khoisan and the short-statured groups of Central Africa. These populations are used as the archetypal African in many studies.<sup>15</sup> This notion is clearly traceable to Coon (1962, 1965) and Seligman (1930). More recently, other scholars have stated that "contrary to many earlier opinions, modern Pygmies [Biaka and Mbuti] and Khoisans are not good candidates for a proto-African population" (Cavalli-Sforza et al. 1994:194). The belief that any living population could be proto-African is fundamentally unsound. The implication of some recent



work is that new paradigms and new approaches are needed (see, for example, Penny et al. 1995). But it is still anticipated that it will be some time before the fact of indigenous African diversity (from Cairo to the Cape) is successfully integrated into historical genetic analyses. Jean Hiernaux (1975:54) has noted the existence of a stereotyped idea of what constitutes a "real African," held by many investigators. His work has long supported the recognition of indigenous African diversity, although it failed to incorporate supra-Saharan into its evolutionary perspective; this is easily remedied. Another example of the use of a socially constructed typological paradigm is in studies of the Nile Valley populations in which the concept of a biological African is restricted to those with a particular craniometric pattern (called in the past "True Negro," although no "True White" was ever defined).<sup>16</sup> Early Nubians, Egyptians, and even Somalians are viewed essentially as non-Africans, when in fact numerous lines of evidence and an evolutionary model make them a part of African biocultural/biogeographical history.<sup>17</sup> The diversity of "authentic" Africans is a reality. This diversity prevents biogeographical/biohistorical Africans from clustering into a single unit, no matter the kind of data.

Many investigators still use dendrograms to represent the phylogenetic history of human "races." These representations imply bifurcations or splitting of ancestral populations, and *complete* genetic isolation of the daughter populations. They suggest an absolute distinctness or discreteness that is not a flaw of ordinate methods. This is problematic. Dendrograms cannot accurately depict evolutionary gradients of differentiation or distinguish similarity due to gene flow. They can also be unreliable in their depictions of population relationships when demographic factors such as population size are not constant or equal between populations. Their very structure may obscure affinities of significance and interest. Different tree-building methods may yield conflicting results. For example, dendrograms based on serogenetic data are different from those based on craniometrics (Howells 1973). It is sometimes claimed that craniometric traits are DNA equivalents (Brace et al. 1993) and that trees should be the same when generated from both types of data. But a comparison of studies indicates that in trees based on serogenetics or DNA, New Guineans/Melanesians cluster with mainland Asia, whereas in craniometric analyses they group with some Africans. In a word, dendrograms are ambiguous in their apparent depiction of certainty.

An example of ambiguity is to be found in the work of Luigi Cavalli-Sforza and his colleagues (1988), who studied select world populations, using cluster analysis in an effort to explore the issue of possible congruence between dendrograms based on genetics and those based on language. The resulting dendrogram is inter-

preted as indicating the phylogenetic relationships of the studied populations. As in other studies, a restricted set of African groups form one major cluster and the rest of the world, another. But a Berber-speaking northern African population does not fit. Bootstrapping reveals that the sample of Berber speakers joins a cluster of European populations in 80 percent of the resamplings and joins the African cluster in the other 20 percent. This is noteworthy because the Berber sample is shifting between the two major clusters regarded as denoting the primary bifurcation of modern humans. A bootstrap value less than 95 percent is deemed insignificant if the goal is to show definitive primary relationship. The Berber sample in this example possibly illustrates the low resolution of dendrograms when data are not highly differentiated and the inappropriateness of representing human population differences with dendrograms.

The biohistory of this sample of Berber speakers is not elucidated, let alone that of all Berbers whose geographical range is great. Nor should admixture be invoked to explain the lack of resolution. Much of the genetic variation of Berber speakers no doubt goes back to the time of early genetic differentiation in Africa. Modern humans have been in northwestern supra-Saharan Africa for more than 60,000 years, perhaps in relative isolation due to Saharan hyperaridity (Clark 1989). Neanderthals were in Europe at this time. Modern Berber speakers' similarity to Europeans is not surprising; it does not reflect colonization by Europeans (or Near Easterners) but indicates only that Europeans derive from populations that postdate the early differentiation, probably from supra-Saharan sources. The "intermediate" biological characteristics of supra-Saharan Africans are not easily explained primarily as the result of hybridization. A Dravidian sample from southern India likewise shifts between European and Asian populations, not attaining significance by standard bootstrap criteria. This is to be regarded as a less serious error if this kind of work is accepted in a general sense. But both of these results are devastating to the race paradigm. The Berber and Dravidian examples show shifts between the major *racial* groups as traditionally and currently defined by some scholars. This situation is made more complex when it is considered that some scholars wish to conceptualize some of the soft-part traits of Dravidians as retentions from ancient Africans. This gene-language study is further compromised by poor representation of the members of some language families and the use of the race constructs, which force boundaries onto a seamless biocultural and historical matrix with extensive geographical parameters. Cavalli-Sforza and his colleagues (1988) do not accurately represent the Afro-Asiatic family because they exclude Chadic, Omotic, and Cushitic speakers, thereby



giving the illusion that Ethiopians are an anomaly, being genetically Africans (but mixed) who also speak the languages of Caucasians (Afro-Asiatic!?) (Armstrong 1990). An evolutionary model explains the geographical range of Afro-Asiatic speakers as one overlaying gradients of genetic differentiation, which a racial model breaks into discrete units that cannot be shown to have ever existed.

Another example of ambiguous branching patterns and clusters within inferred phylogenies is seen in the work of Masatoshi Nei and K. Roychoudhury (1993). Their study, which utilized gene-frequency data from samples derived from the traditional racial constructs, revealed poor support from bootstrap tests for a cluster designated Caucasian and consisting of European and Middle Eastern populations. Although this poor support is more reflective of the inadequacy of typological constructs and racial thinking, the investigators excluded the non-European samples and subsequently obtained results more satisfying to them. The data in effect were tailored to fit into the traditional racial schema.

Other examples of the persistence of racial thinking may easily be identified. The examples cited above illustrate this problem in otherwise interesting work. The issue is not simply one of terminology. The racial approach clearly does not contribute to an understanding of biohistorical processes, especially in Africa, which cannot be defined by one trait or cluster of traits, on any level: serogenetic, mtDNA, Y chromosome, nuclear DNA, odontometric, odontomorphological, craniometric, craniomorphological, hair form, or skin color.

## Conclusions

Racial thinking persists in spite of multiple lines of evidence that deconstruct racial schema and their underlying philosophy. These lines of evidence derive from analyses of serogenetic, nuclear DNA, mitochondrial DNA, Y-chromosome polymorphisms, and skeletal data. All show that the received racial categories should not be treated as bounded entities.

Theory also helps in the examination of the racial construct. None of the putative races as generally understood are breeding populations. Hence these entities are collections of various biological phenomena. They are not evolutionary units.

There are numerous populations today that are products of the matings of peoples from two or more of the alleged racial groups. These new populations historically tie these groups together, in one perspective, but may also be seen as smoothing species-level genetic gradients. Interestingly, the race construct is sometimes not consistently used in terms of its own logic by

its adherents. An example is the labeling of groups by a single racial label when the data indicate that the peoples in question are hybrids. This inconsistency is no doubt due to social practice and a racialized worldview that has political trappings. The existence of intermediate groups, whether they are the products of gene flow or reflective of gradients of differentiation, or are the results of other microevolutionary processes, tends to negate the validity of the implicit or explicit practice associated with the concept of race.

It is hoped that the Human Genome Diversity Project (HGDP) (Cavalli-Sforza et al. 1991; Weiss et al. 1992) does not contribute to this practice of racial typological thinking. If anything, the HGDP should help to destroy these myths as long as the researchers do not combine 19th-century thinking with 20th-century data. Although at present this project is only a proposal, specific issues such as criteria for selecting populations and sampling strategies must be fully addressed in the near future.

Why do the concepts of biological race and racial categories continue to exist and be utilized? In part, it is probably due simply to old habits. Categorical thinking is entrenched. Also, methods tend to be reductionist. Furthermore, the practice of science cannot be divorced from a sociocultural context. Group designations still persist from the pregenetic era.

Human geographical variation in external traits is obvious, but the idea that this variation connotes fundamental biological difference does not flow from the available data. Continental stereotypes are nonscientific and do not flow from biogeography. More insight was obtained when single traits were analyzed and their clinal nature discovered. This did not, however, negate typological thinking in the works of many who were interested in *populations*. The study of population variation must be distinguished from single-trait analysis; these represent legitimate but different approaches to the study of human variation. Human diversity cannot be conceptualized as racial variation, because the latter, in addition to being tautological, is also misleading as to the processes of evolution. The term *ethnic group*, which properly speaking describes a sociocultural entity, cannot be substituted as a descriptor of the traditional racial categories, whose basis is morphophenotype. It must also be recognized that there is a problem with the fluidity of the term *population*. Sometimes samples in studies are closer to breeding units and sometimes not. It is advocated that breeding populations be used in model-based approaches that integrate data from different disciplines. There is a need to develop new terminology and concepts that acknowledge the complex nature of human population variation, biohistory, phenetic and genealogical affinities, and gradients of differentiation. The no-race school has so far failed to do this. In this failure one of the major

implications of genetic studies is being ignored: that the received racial categories, concepts, and constructs should *not* be used as starting points in analyses. The ghosts of the pregenetic synthesis era must be exorcised.

## Notes

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1. See discussion in Montagu 1960.
2. See critique in Hiernaux 1975.
3. It has been proposed by L. Cavalli-Sforza and his colleagues (1994:19) that "core" (presumably less admixed) populations be used in order to reconstruct human evolutionary history. This position is the same as that taken by Horai and his colleagues (1995). Using the entire mtDNA sequence, they dated divergence times for the so-called major geographic populations, which were sampled according to racial schema. Their study consisted of mtDNA derived from an African individual from Uganda (who was used to represent all Africans), ten Japanese individuals whose sequences were amalgamated into one consensus sequence (to represent Asians), and the Cambridge sequence (used to represent Europeans). Here a single mtDNA sequence in two of three cases were deemed by the investigators to be representative of entire geographical regions conceptualized as being authentic.
4. See Rogers et al. 1989.
5. On the misconception of the spread of Afro-Asiatic from Asia to Africa, see Seligman 1930. See also Barbujani and Pilastro 1993 and Cavalli-Sforza and Cavalli-Sforza 1995.
6. See Seligman 1930; see also Armstrong 1990 and Sanders 1969.
7. For example, Nei 1982; Nei and Ohta 1991; Nei and Roychoudhury 1982.
8. Latter 1973; Lewontin 1973; Nei and Roychoudhury 1974.
9. Cann et al. 1987; Horai et al. 1986; Merriwether et al. 1991; Penny et al. 1995; Vigilant et al. 1989; Vigilant et al. 1991.
10. See Nei and Ohta 1991.
11. See also Mountain et al. 1992 and Poloni et al. 1995.
12. See, for example, Wainscoat et al. 1986.
13. In this case the prepackaged goods would be discrete anatomical racial types with the serogenetic and molecular profiles now associated with them.
14. See Cavalli-Sforza et al. 1994 and Spurdle et al. 1994.
15. Bowcock et al. 1991; Bowcock et al. 1994; Horai et al. 1995.
16. See Brace et al. 1993.
17. See Brace et al. 1993.

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