

NEW ENCYCLOPEDIA OF  
**AFRICA**

**Volume 2**

Dakar–Hydrology

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however, that such a practice does not afford an optimal description of human biodiversity.

It is obvious that human beings differ from one another, that local human populations differ from one another, and that such differences are patterned geographically. This does not indicate, however, that the human species is naturally partitionable into a fairly small group of reasonably discrete races, nor how such entities might be distinguished from one another. What is clear, rather, is that populations of humans are each variable, and are generally more similar to populations nearby than to populations far away. Not only are local populations the most natural units of the human species, but they are also bioculturally constituted—the result of marriage patterns, migrations, wars, trade, and adoption. The human species is best understood biologically “as constituting a widespread network of more-or-less interrelated, ecologically adapted and functional entities” (Weiner 1957).

Further, the identification of significant clusters of human populations is not itself a strictly biological enterprise, for many areas are biologically heterogeneous, and cultural classifications (especially linguistic) are commonly imposed upon human populations as well. Sub-Saharan Africa contains an extraordinary amount of human biological diversity—by some measures, more than the rest of the human species. The distribution of these human populations is the result of biological, demographic, and historical forces, and has resulted in a complex geographical pattern.

In 1758 a Swedish naturalist formalized the classification of the human species into subspecies (later made equivalent to races), grouping all Africans together and juxtaposing them against Europeans, Asians, and Americans. The criteria were often nonbiological, however, using stereotypes of dress, law, and personality. Although subsequent generations of anthropologists invoked more obviously constitutionally based features when attempting to formalize natural divisions of the species, they nevertheless generally ignored the real extent of African biological diversity and presented Africans as a homogeneous biological entity, often derived from a stereotype.

Explorers and anthropologists undermined the idea that the diverse aboriginal peoples of Africa could readily be subsumed under a single biological

#### HUMAN BIOLOGICAL DIVERSITY

The distribution of biological variation in the human species is among the most contentious issues in contemporary science because of its abuse throughout modern history as a rationalization for social injustice. Though the concept of race was never clearly defined, anthropologists traditionally grouped people into hierarchically organized clusters of populations, or races. It is presently clear,

category. Africa contains both the shortest and the tallest peoples of the world, as well as the greatest breadth of skin color and body build. The diverse biological populations of Africa can be grossly contrasted, although the specific number of groups is not intended to be significant, and it must be borne in mind that considerable heterogeneity exists within each of these categories and in each of these areas: 1) The North Africans generally resemble other Mediterranean peoples; 2) West-Central Africans are most deeply pigmented; 3) Peoples of eastern Africa range from resembling other populations of the Middle East to the tall, thin, dark peoples of the Nile Valley, and encompass peoples of varying complexion, facial features, and body builds; 4) Pygmy denotes the short-statured people of the central African rainforest; and 5) Khoesan designates the lighter-skinned and small-jawed aboriginal peoples of southern Africa. It should be noted when making these distinctions that these may not be biologically equivalent categories. They are neither qualitative identifiers of individuals nor representations of distinct differences among primordial populations. These categories are simply constructs to help visualize the contrasts among indigenous Africans drawn from different parts of the continent, and to highlight the considerable biological diversity present.

Some populations tend to be characterized by particular anatomical or genetic variations, but these are generally neither universal within a given area nor distinct from populations in other areas. Rather, biological traits are found to be distributed as clines, or gradients. This is true regardless of whether the feature under study is a complex phenotype or a specific allele.

Skin color is clinally distributed, such that aboriginal populations far from the equator tend to be more lightly pigmented than those close to the equator. Likewise, specific alleles, such as that for sickle-cell anemia, reach frequencies of up to 25 percent in malarial regions of western Africa, gradually descending as one proceeds outward.

#### MICROEVOLUTIONARY PROCESSES IN HUMAN POPULATIONS

The detectable patterns of biological variation across human populations are due to the operation of four forces, each of which has different effects upon the human biological landscape. The first is

natural selection, the more efficient survival or proliferation of people with particular inherited qualities. If such a bias in survival or reproduction is consistent over many generations, the composition of the population will gradually reflect the preponderance of those favored qualities. Ultimately, this is the way that biological populations evolve adaptively and come to track the demands of their environment. This is also a manner by which populations come to differ from other populations, adapting to other local conditions. Natural selection is generally invoked to explain the stature of pygmies, the linear body build of Nilotics, and the clinal variation in skin color. Recent studies have also shown that the ability to digest milk through adulthood, or lactase persistence, is caused by a genetic change that is far more common in East African dairying peoples than in other African populations.

The second force is genetic drift, the propensity for gene pools to diverge from each other purely at random. Here, populations become biologically differentiated from one another, but in nonadaptive ways, for these genetic changes do not result in the gene pool's being molded to track its environment. These genetic changes are as likely to be harmful as they are to be beneficial, although they are generally benign. Genetic drift operates in inverse proportion to the size of the population, for small populations will have the largest stochastic fluctuations from the mathematical expectations of population genetics. Here, features such as flatness of the face, shape of the nose, and many other qualities that vary without providing a significant advantage for their bearers may be the result of genetic drift.

The third force is gene flow, or the result of intermarriage between populations. Here the net effect is to make neighboring populations genetically similar to one another in adaptive or nonadaptive ways, and to increase the diversity within any particular population.

The last force is cultural selection, by which populations with nongenetic advantages (generally technological) expand demographically at the expense of other indigenous populations. Although the technology responsible for this spread is not a genetic feature, it results in the proliferation of the people bearing it and consequently mimics natural selection in promoting the survival and reproduction of people

possessing certain cultural traits at the expense of other populations. Obviously, the biological peculiarities borne by those peoples will spread along with their technologies.

The clinal pattern of variation is principally the result of two factors: first, the gradual variation in climate and geography to which human populations adapt, and second, gene flow.

#### GENETIC VARIATION IN AFRICA

The study of biological variation is impeded by a general lack of historical knowledge of sufficient depth over most of the world. Without such knowledge it is often difficult to tell whether a particular biological feature found in a particular area requires an adaptive explanation, a nonadaptive explanation, or is simply the result of sociohistorical (nonbiological) processes.

Perhaps the greatest difficulty, however, is the biologically ephemeral nature of the cultural categories in which human groups identify themselves. These categories are continually submerged and reinvented, which creates a sampling problem for the biologist interested in studying intergroup differences: who biologically represents the named group, and what does the group itself represent? Two paradigmatic cases from Africa demonstrate this.

Aboriginal populations of Southern Africa are classically designated by the linguistic category Khoesan subsuming Hottentots (Khoe) and Bushmen (San). Their history prior to the last few centuries is conjectural, and their history in early colonial times is controversial. The Khoe are noteworthy in the classical literature for steatopygia (enlarged buttocks) and lengthening of the labia in females—attributes that were of sufficient interest in the early 1800s to have merited the 1817 dissection of Saartje Baartman (1789–1815), the so-called Hottentot Venus, by Georges Cuvier (1769–1832), the leading anatomist in France. Although the Khoe and San cluster together linguistically, historically high amounts and complex patterns of gene flow result in discovering the Khoe to be more genetically similar to the Bantu speakers to the north than to the San. Thus, the category Khoesan is a construct and not a valid representation of the true patterns of biological similarity of the contemporary peoples.

If the Khoesan exemplify the constructed fusion of cultural groups in contrast to their patterns of biological differentiation, the Hutu and Tutsi of Rwanda exemplify the opposite, the constructed division of peoples in contrast to their biological or genetic identity. Again, generations of gene flow obliterated whatever clear-cut physical distinctions may have once existed between these two Bantu peoples—renowned to be height, body build, and facial features. With a spectrum of physical variation in the peoples, Belgian authorities legally mandated ethnic affiliation in the 1920s, based on economic criteria. Formal and discrete social divisions were consequently imposed upon ambiguous biological distinctions. To some extent, the permeability of these categories in the intervening decades helped to reify the biological distinctions, generating a taller elite and a shorter underclass, but with little relation to the gene pools that had existed a few centuries ago. The social categories are thus real, but there is little if any detectable genetic differentiation between Hutu and Tutsi.

#### THE INTERPRETATION OF GENETIC DATA

Surprisingly, there is little systematic data available on the peoples of Africa. As a result, much of what exists involves unjustifiable generalization. For example, in an ostensibly global study, Pygmies from Democratic Republic of the Congo and the Central African Republic were presented as representing Africa.

Another major problem is typology. The earliest genetic studies were carried out on the classic ABO blood group markers, now known to be coded by a single gene on chromosome 9. The three major alleles are present in all populations of the world, with the exception of some New World populations, which appear to have lost B. Because nonhuman primates possess this polymorphism, and nearly all known human populations do, may easily be inferred that all ancestral human populations were polymorphic as well. This is, however, not the way the work was originally interpreted. Geneticists assumed genetic purity of ancestral populations and consequently imaginatively reconstructed a primordially *O* human species invaded by an *A* race from northern Europe and a *B* race from south Asia.

There seems to be no basis on which to infer the interbreeding of genetically homogeneous archaic races as the cause of present-day polymorphisms. It appears as though many human polymorphisms are ancient (such as ABO) and have been carried through the biohistory of the human species for hundreds of thousands of years. The complex processes of microevolution must be invoked to explain the current distribution of these variations.

Unfortunately, it is still common to find geneticists naively treating the polymorphic genes in a typological manner. Thus, an allele whose frequency ranges from 30 percent to 80 percent in a small sample of Africans, and 10 percent to 20 percent in a small sample of Europeans, casually becomes an African allele, and one found in 20 percent to 60 percent of Europeans sampled, but in less than 10 percent of Africans sampled, becomes a Caucasoid allele.

From cavalier treatment of such data emerge comparably cavalier conclusions, such as scientifically inferring that Caucasians are the admixed products of 65 percent African and 35 percent Asian genetic contributions. Unfortunately, the technologically most sophisticated data are often bound to the most conceptually primitive interpretations. This is probably the major handicap to biological studies of African populations in the early twenty-first century.

A related set of problems involves the interpretation of patterns in the genetic data. Because the analytic units of population genetics are populations, sampling is commonly done for tribes, which has the consequence of reifying them as stable genetic entities. The odd properties of mitochondrial DNA have made it a valuable commodity for companies marketing recreational genetic services, some of which match an American client's DNA to that of Africans, although the significance of such a match, and its relationship to the client's ancestry, may be far from clear. Finally, the relationship between population genetic patterns and ethnohistory may be far more complex than geneticists commonly assume.

#### **MITOCHONDRIAL EVE**

One of the most influential studies of the 1980s was the genetic survey of the small bit of DNA possessed by a subcellular organelle known as the

mitochondrion. Passed on from mother to child (rather than biparentally, as nuclear or Mendelian genes are), mitochondrial DNA, or mtDNA, has several other significant properties: it accumulates mutations rapidly and thus will detect differences among populations; it is easy to isolate and study; and it is inherited as a single unit. Studies indicated that Africans subsumed more genetic diversity than Europeans or Asians. This was initially interpreted as evidence that the human lineage originated in Africa, but it is also compatible with other interpretations, such as the idea that for most of their existence, human populations in Africa were generally larger than those elsewhere.

Mitochondrial Eve was the name given to the African possessor of the hypothetical ancestral DNA sequence from which all other modern mtDNA sequences have evolved. In its crudest form, a scientific origin myth of the 1980s held that Mitochondrial Eve was the founder of the modern human lineage in Africa, and her descendants spread across Europe and Asia 200,000 years ago, supplanting the archaic aboriginal populations of those continents. The relationship between the ancestral mtDNA sequence and the ancestral population of modern human beings is, however, exceedingly unclear.

#### **BIOLOGICAL IMPLICATIONS OF OUT OF AFRICA**

Contemporary interpretations of genetic diversity acknowledge three things. First, if compared to the genetic diversity encountered in humans to that encountered in their closest relatives, the apes, humans are much more similar genetically to one another than the apes are to their conspecifics. Second, there is more genetic diversity among Africans than among Europeans or Asians. And third, the genetic variation in Europe and Asia appears to be a subset of the African diversity, and thus appears to have originated in Africa.

Nuclear DNA can be analyzed as haplotypes, that is, as a physically contiguous series of variable genetic sites. For example, two genes, A and B, can be imagined to be located nearby one another on a specific human chromosome. Over time, mutations occur and spread throughout the population, so at some later time there might be two variants of A (A1 and A2), and four variants of B (B1, B2, B3, and B4). There are thus eight possible haplotypes:

A1B1, A1B2, A1B3, A1B4, A2B1, A2B2, A2B3, and A2B4. In general, there is a considerably more restricted range of haplotypes in populations outside of Africa, and a fuller range of haplotypes within sub-Saharan Africa. The simplest interpretation is that the restricted range of variation outside Africa is a result of comparatively recent origin of these populations, from a subset of the diversity still found in contemporary Africans, in harmony with the mitochondrial Eve story.

The interpretations of these data, however, are still somewhat primitive, as it is also clear that different processes could account for these patterns. A regimen of strong selection would also reduce genetic variation. The correctness these interpretations hinges on the ability to infer demographic properties of the prehistoric populations of Africa—notably, their size, mobility, and migration rates.

The fossil record suggests the development of modern human features about 200,000 years ago, first in Africa, then elsewhere. Modern human features, however, incorporate a general overall reduction in skeletal robusticity, which may not be entirely genetic in origin and may instead be related to lifestyle. Anatomically, modern humans do not appear to have been so different from archaic humans as to preclude the possibility of interbreeding. Indeed, in some parts of the world a few specific skeletal features of modern populations are arguably found in the archaic fossils. Whether this represents genetic continuity or similar selective pressures acting on different populations in the same place is unclear.

*See also* Archaeology and Prehistory: Historical; Baartman, Sara; Knowledge: Overview; Prehistory; Research.

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