

## The Great Human Diasporas

This wonderful, fascinating book is a collaboration between a father and son. The father, Luca Cavalli-Sforza, is a geneticist who has spent his career studying human evolution. The son, Francesco Cavalli-Sforza, is a film director. It started out as an interview book but changed into a first-person account.

The author has studied human evolution not only from the biological point of view, but also from that of archaeology, social anthropology, linguistics, and others as well, in order to reduce the uncertainty of his conclusions.

In the 1960s Luca Cavalli-Sforza began studying African pygmies, among the last remaining hunter-gatherers. He gathered blood samples from different pygmy tribes in order to analyze their genetics. Paleolithic society must have been organized much like the pygmies. Other hunter-gatherers in modern times include native North and South Americans.

Looking at the languages that exist today, it would appear that about 5,000 human populations remain, and very few of them are hunter-gatherers. All of today's hunter-gatherers have certain customs in common: living in small groups with no political or social hierarchy. They all have highly developed rules of conduct, and private ownership is rare and unimportant, with the exception of rights regarding hunting territories. This way of life, though, is disappearing rapidly; these societies have no future.

About 2 million years ago, the species *Homo habilis*, which we consider human, lived on the earth, having descended from the same ancestors (who lived about 5 million years ago) as both humans and today's chimpanzees. Anatomically, modern humans appeared only about a hundred thousand years ago—but until a few thousand years ago, all humans lived as *Homo habilis* did, as hunter-gatherers. In the last few thousand years, enormous change has come, but studying the remaining hunter-gatherers provides us with valuable knowledge of ancient humans, especially how they find mates and the differences between the structure of their society and modern society.

### **What we know about the development of humans up to 100,000 years ago**

Agriculture was invented 10,000 years ago; *Homo sapiens* is two to three hundred thousand years old; life has existed on earth for three or three and a half billion years.

In the last few decades, we have developed what is called the molecular clock, a method of establishing similarities between species and dating origins. This technique studies the differences between various complex biological molecules (proteins such as hemoglobin & DNA), based on a reference point that tells us, on average, how many millions of years it takes for a change to occur.

This method has allowed us to improve the precision of our estimates as to when humans and chimpanzees diverged. Current thinking is about 5 million years ago. Gorillas were earlier, and orangutans were earlier still, about 10-15 million years ago.

At least three species of the genus *Homo* have been identified: *Homo habilis*, *Homo erectus*, and *Homo sapiens*.

Australopithecines are the earliest humans after the ancestor we share with apes. The last species of australopithecine died out about 1 million years ago.

Coming about 1 million years after the first australopithecines (about 2-2 \_ million years ago), *Homo habilis* had a larger braincase and fashioned stone tools (recently it has appeared that some australopithecines may also have known how to make rough stone tools). Also about 3 feet tall, *Homo habilis* was a scavenger and meat eater.

*Homo erectus* lived from 2 million to 300,000 years ago. Human pre-history took place in Africa for several million years. Australopithecines had left the forest of their ape forebears and moved to the savanna, a tropical grassland with tall vegetation, bushes, and scattered trees. About 2 million years ago, *Homo erectus* began to migrate beyond Africa to colonize the Middle East, Asia, Europe and the Far East over several hundred thousand years. The first known signs of human presence outside of Africa are in today's Israel, dating back to a little over a million years ago.

*Homo sapiens* first appeared around three to five hundred thousand years ago, possibly existing alongside *Homo erectus* for a while. The first, archaic *Homo sapiens* showed a braincase size equal to that of modern man, but with a different shape. Archaic *Homo sapiens* has been found in Africa, Europe, and Asia.

From two hundred thousand years ago onward, European *Homo sapiens* (*Homo sapiens neanderthalensis*) has differed from that of Africa or China. This last ancestor of ours appeared outside of Europe, in the Middle East, around sixty thousand years ago, but disappeared completely around 35,000 years ago.

Two schools of thought exist on the demise of *Homo sapiens neanderthalensis*. Either modern humans, migrating from Africa and the Middle East to Europe, replaced them, as the author believes, or else they actually evolved to become modern humans.

In the last 100,000 years, modern humans appear indistinguishable from our present species and are called *Homo sapiens sapiens*. These humans have much more advanced language usage and more advanced tools, more varied and refined than any seen earlier. Forty or fifty thousand years ago, Neanderthals and modern humans coexisted, at least in Europe. They had different head shapes and different tools. With the disappearance of the Neanderthals, we enter the modern age.

## Modern humans—one hundred thousand years ago until now

Three hundred thousand years ago, the human brain was its present size, but its structure was likely not the same. Over the period between three hundred thousand and one hundred thousand years ago, facial features changed from that of the ape-like archaic homo sapiens to their modern form, and our tools evolved and increased in diversity.

During this period, the Neanderthals developed in Europe (they assumed their most representative features about 60,000 years ago). In Africa at the same time, a more modern-appearing archaic *Homo sapiens* appeared, a fact pointing to Africa as the birthplace of modern humans and the center of their early movements.

Because their features are so different from ours, we have a special category of *Homo sapiens* for the Neanderthals—*Homo sapiens neanderthalensis*. Neanderthals seem to have lived in caves, though we do not know that for certain, and they were clearly hunter-nomads who ate venison, cow, ox and horse, among other meats. Neanderthal finds have been made throughout eastern and central Europe and as far away as the Middle East and east of the Caspian Sea. Modern humans have been found in the Middle East as early as a hundred thousand years ago, and the same areas have shown later Neanderthal presence. One theory has it that modern humans unsuccessfully tried to settle the Middle East a hundred thousand years ago and that this was followed by a period of Neanderthal occupation, which ceased at some point, after which modern humans returned. In any case, the last traces of Neanderthals are found in Europe, about 35,000 years ago.

Anatomically modern humans, *Homo sapiens sapiens*, appeared in Europe around 40,000 years ago, when they appear to have replaced Neanderthals, but *Homo sapiens sapiens* appeared earlier in Africa and the Middle East, about 74,000 to 130,000 years ago. This fact suggests that modern humans originated in Africa. So does the fact that archaic *Homo sapiens* who lived in Africa more closely resemble modern humans than archaic *Homo sapiens* found elsewhere.

Three hundred thousand (and maybe more) years ago, various types of archaic *Homo sapiens* lived in various parts of the world. Two hundred thousand years ago, Neanderthal lived in Europe, and one hundred thousand years ago, modern humans lived in South Africa and Israel. Sixty thousand years ago, Neanderthal appeared in the Middle East, when there was no sign of modern humans in the area. Then *Homo sapiens sapiens* began to appear everywhere. Within sixty to seventy thousand years, modern humans were in all parts of the globe. More than sixty thousand years ago, *Homo sapiens sapiens* reached Australia and New Guinea, and possibly China, meaning they had to have used seaworthy vessels. The first traces of modern humans in Europe are thirty-five to forty thousand years ago. The chronological pattern of the finds suggests that they came from the east. This time period marks the last traces of Neanderthal presence. Modern humans later moved into the colder regions of Asia, and from Siberia they journeyed to America, no later than fifteen thousand years ago, but possibly earlier. They may have walked across the Bering Strait when it became dry land during the last Ice Age.

It is difficult to determine whether modern humans supplanted the Neanderthal or whether they merged. We don't know if they were the same or two different species. Generally, where two species compete for resources, only one survives. We cannot rule out fusion, but at the time when both lived in Europe, they had important cultural differences, making the idea less plausible.

A recent concept that has been the subject of wide discussion is "African Eve," a rather misleading name. The implication that the entire human race descended from one woman is incorrect. The concept is based on research done on mitochondria by Allan Wilson, a UC Berkeley biochemist who died in 1991. Mitochondria are tiny organs within each cell, but the mitochondrion is somewhat independent from the rest of the cell, since it carries its own chromosome, which, like all chromosomes, is made of DNA.

Wilson studied changes in the DNA making up mitochondria in a large number of individuals. The key point is that Mitochondria are passed on to children only by the mother. Two children having the same mother will have identical mitochondria, even if they have different fathers. Mutations in the mitochondria are passed on to future generations, but mutation is a rare phenomenon. Looking at the mitochondria of people related on the maternal side, we see no differences, but looking at individuals with no blood relationship, we see many differences.

Wilson compared a number of the components of mitochondria in 182 individuals, including Africans, Europeans, Asians, and natives of Australia and New Guinea. He observed enough differences to draw a diagram or family tree, since individuals with only one difference have a more recent common ancestor than those with two or more different components. This is the same method used in studying the evolution of proteins and is the basis of what is called the molecular clock.

The tree reveals the time and location of the earliest person from whom all 182 people descended, the "ancestress." The first and oldest fork in the tree separates Africans from other Africans. The branches separating all other peoples come later, so the ancestress seems to have lived in Africa.

This conclusion has sparked some controversy because there are other methods of drawing up different trees—but nearly all the other methods and a number of other data all point to the same conclusion. In addition, among the peoples of various continents, the Africans have been shown to be by far the most heterogeneous group, and it is reasonable to assume that the oldest population would display the most diversity.

To calculate the date of birth of the ancestress, Wilson and his team compared the genetic difference between descendents from the first fork leading from the common ancestress to the first Africans and others to that observed between an average human and a chimpanzee. Wilson had already shown that the separation between humans and chimpanzees occurred five million years ago. From this, he calculated that the first separation in the human mitochondrial DNA tree took place 190,000 years ago. Because

of the broad margins of error involved, this date was taken as somewhere between 300,000 and 150,000 years ago.

Humankind began in Africa: *Homo habilis* and *Homo erectus* first appeared in Africa, and archeological observations suggest that *Homo sapiens sapiens* first appeared in Africa, too—or possibly the Middle East—and spread from there. *Homo habilis* appeared two and half million years ago; *Homo erectus* left Africa one to two million years ago; and *Homo sapiens sapiens* appeared about one hundred thousand years ago or more, since by that time we know that they resided in both Africa and Israel.

Allan Wilson's ancestress was not necessarily a modern human. It is very likely that the appearance of the first *Homo sapiens sapiens*—and the migration from Africa or Israel—took place a long time after the mitochondrial mutation that marked the first division from the ancestress. It is right for the two dates, mitochondrial and archaeological, to be different, and the former must precede the latter historically, possibly by a long interval.

We can search for a male analog to the mitochondrial Eve using the Y chromosome, which is found only in males (since it determines the male gender). We can hope to one day reconstruct a family tree for the Y chromosome and date the carrier of the first surviving mutation—an Adam Y in comparison with the mitochondrial Eve. If we manage to pinpoint the Y-chromosomal Adam's date of birth, it will probably be different from Eve's. That would make it still more difficult to believe in the biblical couple.

## **The theory of evolution and the forces involved in the process**

Differences between people are due to a variety of factors. Some are accidental and some are voluntary changes. Some are biological, meaning genetic, hereditary, or innate. Hereditary mechanisms cause similarities between parents and children and between siblings.

A mutation is simply a change in the order of the gene sequence, a substitution of one component for another in the sequence. When such changes occur in the creation of germinal cells, the mutations can be transmitted to future generations. If a new baby's chromosomes include a mutation, that mutation will be transmitted to all the baby's descendants. Some mutations have little or no effect, while others are of great importance, determining the difference between health and sickness, for example.

Thalassemia is a hereditary form of anemia especially common in the Mediterranean and particularly in Sardinia. Until recently, about 100 children per year would die from this mutation in Sardinia.

But sometimes gene mutations can prove advantageous. For example, for a child to suffer from thalassemia, both parents must have the mutation, though they usually show

no outward signs of it. These people, who have inherited the mutation from one parent but not from the other, are called healthy carriers. Because they have not inherited the mutation from both parents, they do not suffer from thalassemia—but in addition, this mutation provides them with increased resistance to malaria, which was once a very serious illness found in many parts of the Mediterranean, including Sardinia, so increased resistance to malaria functioned as an important survival trait. Healthy carriers are not common, so marriage between two of them is rare. When two healthy carriers do marry, only one in four of their children, on average, will inherit the mutation from both parents (and thus suffer from thalassemia). Two of the other children, on average, would be healthy carriers, while the fourth would be normal (free of the mutation). In the past, children with thalassemia would die in early childhood; but the increased resistance to malaria provided to other children would statistically more than compensate for the loss of the thalassemia victims, providing net survival benefits to carriers of this mutation.

Mutation is rare, because random changes are going to damage the organism, more often than not. In addition, cells have copy checking and correction mechanisms to minimize the frequency of mutations. In a cell, only a few dozen nucleotides are likely to mutate in the course of a generation, out of the total of three billion. So the incidence of error is very small: likely about one per two hundred million nucleotides in each copy.

Identical twins, therefore, have only a few dozen differences between them, but unrelated individuals will have many more differences. Parents and children have fewer differences between them, but the level of differences will be high, because the children's genetic makeup is provided by two genetically different parents. Siblings have, on average, about half the differences between them, as compared to the differences between two random individuals from the general population. Two individuals taken at random will have about one difference per thousand genetic components, or three million differences out of the three billion components.

If we compare individuals from different species, we find greater differences, and the differences increase with the evolutionary distance between the species. The same concepts of accumulation of differences we saw in the protein molecular clock apply to DNA, and these differences provide another molecular clock.

Three factors combine to make individuals different from one another: mutation, natural selection, and chance. Mutations can be harmful, neutral, or beneficial, as far as fitness is concerned. Harmful and beneficial mutations become instances of natural selection (harmful mutations disappearing, and beneficial mutations increasing in prevalence).

Large mutations, such as the loss of a chromosome or production of an extra one, are usually fatal, sometimes even prior to birth, or lead to serious disorders, such as Down syndrome, which is caused by the presence of three copies of chromosome twenty-one, instead of the usual two. Hereditary diseases are caused by harmful mutations. Several thousand such diseases have been recognized, but almost all are rare because their harmful nature tends to lead to elimination by natural selection.

Few mutations are beneficial. Most of those in the past have been accepted by natural selection and have become part of the human species. If a mutation gave resistance to a common disease, those without it died out and only the resistant survived.

Mutation is casual and generates innovations that can either be harmful or beneficial. Selection determines the answer to the question by promoting beneficial mutations and eliminating harmful ones, depending on environmental factors as well as cultural ones. In Europe, the development of agriculture has led to cereals as the primary dietary component over the last 10,000 years. Unlike meat, cereals contain no vitamin D. But they do contain a precursor that becomes vitamin D if exposed to ultraviolet light absorbed through the skin from the sun. Cereal eaters can produce enough vitamin D to survive and grow normally if they are fair skinned. So people can live in northern regions and eat cereals because a fair skin color has been naturally selected. Farther north, others, such as the Eskimos, have gotten enough vitamin D from their diet of fish and meat to make fair skin unnecessary. Sexual selection is less important, but also powerful. Resulting from the choice of mates, this selection is difficult to study.

Natural selection works within a given environment. It is better to be dark-skinned in tropical regions and fair in the north (unless alternative sources of vitamin D are available). This is one reason for different skin colors. Another is resistance to sunlight. Humans have evolved to meet specific environmental conditions in different areas of the planet. These types of biological changes have combined with important cultural developments as well: use of clothing, fire, food preservation, and more. Natural selection has favored those who are capable of making cultural progress, but with regard to these advances, it is culture that has directly influenced survival, while natural selection has had only an indirect effect. But to understand evolution completely, one must take both biological and cultural adaptation into account.

The third component of evolution is chance, technically known as genetic drift. It is especially important in small populations. If we have one mutant in a thousand people, it's not certain that others will be born, so the mutation may disappear. The disappearance is a 37% probability, according to statistical analysis. The probability of having one other mutant born is also 37%; two others is only an 18% probability; and the chance of three is a mere 6%. If the next generation has three mutants, then the probability of the mutation being lost is greatly reduced, and as the frequency of mutants increases, the importance of genetic drift declines.

Genetic drift influences all hereditary features, not just genetic disorders. In the 1950s, the author studied genetic drift in the Parma River Valley of Italy, taking blood samples from residents near Parma, then moving upriver toward the hills and finally entering the mountains, where small communities are located.

Genetic drift is defined as "random fluctuations of frequencies of the various forms of a gene from one generation to another." It can be reliably predicted using two demographic figures: the number of individuals in each population and the migratory exchanges among them. In the Parma Valley research, this information was readily

available from parish records, allowing the author to calculate in advance the expected genetic variations, which were then checked against the blood samples. The results confirmed expectations, sometimes down to the smallest detail.

Genetic drift takes longer to have an important effect in larger communities. Eventually, a population with two forms of the same gene should have only one type or the other—unless immigration reintroduces the eliminated type. If immigration is high, the effect of genetic drift diminishes. So migratory exchanges among peoples are also important, and these are not necessarily dictated by chance.

But chance plays two roles in evolution; its influence is felt through the statistical effect of genetic drift, and also through the random way in which mutation occurs. So evolution is not just survival of the fittest, but also survival of the luckiest.

The most important genetic change in human history has been the growth of the brain and development of new cerebral functions, which occurred from about three million years ago onward. Three hundred thousand years ago, our brain reached its present size, more than four times that of the chimpanzee, our closest zoological relative. It is likely that more than one genetic mutation was needed to make the brain grow to this extent. Furthermore, the brain has undergone qualitative as well as quantitative changes, especially in the areas responsible for processing language.

Often, migration is cited as yet another factor in evolution, but migration is not really a single factor, since it can take on different features and functions. Isolation of population groups, if continued long enough, will produce evolutionary differences. Eventually, they will even become different species. In mammals, this takes about one million years. But two populations are rarely cut off from one another completely. Migration diminishes isolation, and with it, the effects of genetic drift.

Mass migration also occurs, to escape famine, natural disaster, war, or overpopulation. When a group moves a vast distance, it often causes complete cessation of contact with the original group, and later genetic drift and adaptation can produce enormous diversification. So in contrast to migration of individuals, mass migration leads to greater diversification among groups.

## **The peoples who have colonized the planet over the last one hundred thousand years**

Near the start of his career, the author posed the question, “Can the history of humankind be reconstructed on the basis of today’s genetic situation?” He spent twenty years obtaining the necessary tools.

He began doing research at Cambridge University before 1950 with the great geneticist Sir Ronald A. Fisher, the father of modern statistics and one of the creators of the mathematical theory of evolution. At first, human genetics worked with blood group

differences (ABO and later, RH) only. Different frequencies of ABO types are found among different peoples: in Europe, the averages are 40% O, 40% A, 15% B and 5% AB. In 1940, immunologist Philip Levine discovered what has come to be known as the Rh substance, a blood component found in about 85% of white Americans, but not in the other 15%. In Europeans in general, 10-15% of the population lacks Rh, though in the Basque region that figure is as high as 30%. It is very rare to find an Rh-negative African, and Asians and American Indians are almost never Rh-negative.

The high incidence of Rh-negative blood among Basques led to a theory that these people descended from a proto-European people who originally had an even higher incidence of Rh-negative, possibly even 100%. Other information that has since come to light suggests that this theory is probably correct.

Another interesting situation concerns the unusual incidence of the O blood type among American Indians. Except for a number of Canadian tribes that have a high incidence of A (but no B), all American Indians are type O. This could be true for one of two reasons: either the small group of original settlers of the American continent (over 15,000 years ago) was very small and contained only type O individuals (an extreme case of genetic drift), or else natural selection has made the other groups disappear, for example, because the O individuals were resistant to a particular disease. Either theory requires further explanation for the presence of the type A individuals in Canada. The lack of A and B groups in North America has been linked to syphilis, which was introduced in Europe soon after the return of Christopher Columbus. Group O individuals appear to be more resistant to syphilis than the other types. These two theories are not mutually exclusive, and the question is still open.

When the author began his work, ABO and Rh were the only genetic groups available for study, and this was not enough information to develop a history of humankind. But he hoped that gaining more data, on additional genes, could provide additional information, eventually leading to the reconstruction of the history of the entire human species (i.e., its evolutionary, or phylogenetic tree). The author developed a method of analysis that would allow him to use data on the genetic differences among populations—provided that enough of such information were to become available.

Around 1960, the available data seemed sufficient to begin this work. Working with the author at Pavia University, Anthony Edwards developed programs for early computers to analyze this data, applying appropriate statistical analyses. Most genes do not vary considerably from one population to the next, but by looking at enough genes, we can find a sufficient number that do, and thereby uncover revealing patterns. Needing to develop a single number that expresses this variation, the two devised the term “genetic distance.” Using Rh-negative as an example, with 20% Rh-negative among all Basques, 15% among the English, and 2% among the Chinese, then a simple genetic distance between Basques and English would be 5% (20%-15%), 18% between Basques and Chinese (20%-2%) and 13% between English and Chinese (15%-2%). Ultimately, they discovered that the exact formula used to obtain this figure is not important, but the use

of as many genes as possible is very important, with the final figure being the average of those found for every gene.

In 1961 and 1962, they analyzed blood data on 15 different population groups, three per continent, for a total of 20 different genetic variations. They assessed the genetic distance between pairs of populations, creating an evolutionary tree that is still approximately correct today, despite the small number of genes used. American Indians turned out to be closely related to the Eskimos, and more distantly to the Koreans. This finding supported prevalent beliefs that the Eskimos and American Indians are both Mongolian in origin and that they arrived in America from eastern Asia via Siberia and Alaska. Because of scanty information, Europeans occupied a sort of intermediary group between Asians and Africans. The extreme poles of human variation were the Africans on one end and the New Guineans and the Australian Aborigines on the other.

By plotting the genetic tree on a world map, the two seemed to obtain an approximate idea of the routes taken by modern humans in their expansion. The forks in the tree should correspond to geographical separations of populations. If the reconstruction is successful, the sequences of the branches should correspond to that of the separations, and the position and length of the branches should correspond to the time in which the splits occurred. But much more work would be needed to confirm and refine these ideas.

The investigators next tried to check these results against a different body of data: physical appearance (hair and skin color, stature, and other measurements accepted by anthropologists, called anthropometrics). Using the same methods of reconstruction, they found a somewhat different tree. Because we know that external body appearance is dictated only in part by heredity, the explanations for the differences seemed to fall into two categories: long-term and short-term environmental effect.

In trying to determine which features are most useful to study, it became apparent that those features that are influenced by environment, and those influenced by natural selection, are both less useful than those influenced by chance. It turns out that DNA contains many duplicates of active genes, some of which are unable to work because of mutations that have rendered them inactive. It has become possible to study these genes only today, and they are extremely rare, but these “silent genes,” or pseudogenes, are therefore immune to natural selection and are therefore of particular value in studying the history of the human species.

The investigators believed that their genetic tree was more useful for these purposes, since physical characteristics are influenced greatly by climate. The author has continued to refine his original tree using additional data that has become available over the years. Today, over 15 times more data is currently available. The results continue to be very similar to the original blood type tree, including a more recent survey based on 110 genes in 42 native populations around the world. The biggest differences continue to be between Africans and non-Africans, reinforcing the prevalent view that the human species originated in Africa and later spread around the world. Non-Africans inhabit two major branches: those who live in Southeast Asia and who most likely reached Australia,

New Guinea, and the Pacific Islands from there; and those who populated Northern Asia and headed eastward through Siberia to America or westward into Europe and Southern India. Some areas of uncertainty remain and will be resolved only after further research.

In trying to determine when the human populations separated, the most reliable dates we have concern the occupation of new continents. So far, four dates look reasonably reliable, though they could change as a result of future research.

First of all, the oldest modern human remains are about 100,000 years old and were found in both Africa and the Middle East. It is not possible to distinguish clearly which are older, but earlier skulls from Africa show definite trends toward modern human forms, suggesting that *Homo sapiens sapiens* was born in Africa. The presence of modern human sites in the Suez area one hundred thousand years ago suggests that the journey from Africa into Asia (or, less probably, vice-versa) occurred at about that time, so the first diversification between Africans and non-Africans would have taken place then or a little beforehand.

We have dated human remains in Australia and New Guinea at 55-60,000 years ago. The genetic distance between the Oceanian Aborigines (a term for the diverse Australian and Pauan Aborigines) and the Southeast Asians is about half that between Africans and non-Africans, and their date of entry into Oceania (50-60,000 years ago) is about half that of finding modern human remains in Africa and the Middle East.

The occupation of Europe, probably from Western Asia, is dated at 35-40,000 years ago, and the occupation of America, still somewhat unclear, is between 15,000 and 35,000 years ago.

Genetic distance increases with separation time, and we can construct a table showing separation, date of separation, and genetic distance, using the first separation as 100.

<u>Separation of Peoples</u>	<u>Date</u>	<u>Genetic Distance</u>
Africa & rest of world	100,000 years ago	100
SE Asia & Australia	55-60,000 years ago	62
Asia and Europe	35-40,000 years ago	48
NE Asia & America	15-35,000 years ago	30

The dates are approximate, and although data from 110 genes was used to calculate genetic distance, the statistical margin of error is still high (around 20%). Given these facts, the first three dates clearly support the idea that genetic distance increases regularly and proportionately to separation dates. The last comparison is too imprecise to be reliable. But if we work from genetic distance to calculate the date of the occupation of America, using the first three comparisons as a basis, we conclude that the date was 30,000 years ago, which is well within the range suggested by archaeologists.

Our external features are the most different from one another because these reflect adaptation to climate; these are our interface to our environment. It is because they are

external that these racial differences strike us so forcibly, and we automatically assume that differences of similar magnitude exist below the surface, in the rest of our genetic makeup. This is simply not so: the remainder of our genetic makeup hardly differs at all.

Aside from skin pigmentation, no two races are totally different from one another, not even for a single gene. The differences between races are therefore very limited and quantitative, not qualitative. Within continents, the differences are, on average, even smaller. Seen in this light, the confusion, misery, and cruelty caused by racial differences among humans are meaningless.

## **The expansion of agriculture**

The shift from hunting and gathering to an agriculture-based society began ten thousand years ago. This change led to an enormous increase in the number of people the earth could support, and in the 400-500 generations since then, the world's population has increased over a thousandfold.

The author began to analyze the development of agriculture, the cause of the first demographic boom, believing that it would lead to a closer relationship between the two types of phenomena. When a population boom forces a large population to move into a new area, they mix their genes with those of the people who lived in the new area before them, and the genetic makeup of the resulting population is directly calculable, on the basis of the ratio between immigrants and residents.

He started with the Neolithic period, when agriculture began. The name Neolithic means 'New Stone Age,' because the cultivators' stone tools departed from their predecessors' in purpose and therefore in design. The domestication of cereals began in the Middle East, along with the keeping of livestock. This changed the economy, allowed people to have more children, and enabled the building of villages and small cities. In Turkey, at Catal Huyuk, are found layers of a city that began over nine thousand years ago with a population of about five thousand. So agriculture led directly to denser populations and a rise in the birth rate.

Hunter-gatherers probably reproduced like those of today do, an average of five children per couple, one every four years. This gap allows the youngest to be carried and the older ones to walk on their own. More than half die in childhood, so the population stays stable, or almost so. But farmers have no reason to limit their reproduction and there are incentives to have more children—they can feed the extra mouths and the extra people mean extra help in the fields.

Agricultural expansion began about 9,000 years ago, fanning out from an area between Iraq and Turkey. The expansion took 4,000 years to reach the farthest areas of Europe (Britain, Denmark, Spain), about 4,000 km away, averaging about 1 kilometer per year. Throughout this time, Europe was already inhabited by hunter-gatherers from the initial human expansion over the previous 30-40,000 years. These hunter-gatherers are known

as Mesolithics (Middle Stone Age People). The cultivators and hunter-gatherers probably occupied different types of terrain, and since the clearing of the forests proceeded gradually, they probably lived side by side, even in areas where Mesolithics were more numerous. The most densely populated area of Europe during pre-agricultural times was southwest France and northern Spain; the center of this area is where Basque is spoken today, and there is reason to believe that Basque descends from the language spoken by the last Mesolithic hunters in that region.

The author believes that the expansion of agriculture was the expansion of the people who practiced it, rather than the expansion of the ideas and artifacts, the culture, of agriculture. This theory contradicted prevailing views, especially in Britain and the US. The author and his colleagues termed the two phenomena “demic,” meaning the spread of populations (he argues for a particular variety of this hypothesis, where technological innovation determines a population explosion followed by migration), and “cultural,” meaning the transfer of ideas, artifacts and technologies.

Regardless of the phenomena involved, archaeological data indicate slow but regular expansion of Neolithic farmers, quantitatively and qualitatively in agreement with demographic calculations based on population growth and migration. The key factor controlling the rate of expansion was likely the magnitude of the increase in population density permitted by the arrival of agriculture: the population density of Neolithic farmers was ten to fifty times greater than that of the last hunters. Archaeological evidence suggests that Mesolithic hunters in Britain numbered five to ten thousand total.

The development of agriculture was probably due to population density exceeding the limit for survival in the hunting and gathering economy, along with a cooling of the earth’s climate, which caused certain food sources to die out. As a result, agriculture began in three separate areas at about the same time: the Middle East, China (where archaeologists believe that women invented agriculture), and Mexico and the northern Andes. Central and South America have made an enormous contribution to agriculture, including corn, potatoes, tomatoes, cocoa, and cassava (manioc, or tapioca).

From the Middle East, agriculture spread to North Africa, Europe, Iran, Pakistan, and India. From China, it spread to Korea, Japan, Tibet, Southeast Asia, Indonesia, the Philippines, Polynesia, Madagascar, and New Guinea. Agriculture did not reach Australia until white settlers arrived at the end of the eighteenth century.

By observing the African Pygmy hunter-gatherers living beside Bantu farmers, the author became convinced that the spread of agriculture was due to the movements of farmers, but his research had made it clear that archaeology alone would not decide this question. He felt that genetics could provide the needed evidence to support his hypothesis.

The early blood analysis suggested that Rh+ was the prevalent type among Neolithics when they began their trek from the Middle East, and that, at the other end of the scale, indigenous Europeans were largely, or perhaps even exclusively, Rh-. Joining with some Italian colleagues, the author processed by computer all available scientific data on genes

that had been isolated and studied since the Rh study, and then they produced maps for many of the genes. They found many with a pattern similar to that of Rh. Occasionally an absolute maximum or minimum centered on agriculture's original core in the Middle East. But some gene maps looked very different, clarifying the need to look at large numbers, construct a unifying framework, and explore other explanations.

Using principal components analysis in 1978, the author and his colleagues found that the high point of most significant genetic components centered right on the Middle East and diminished with distance from that spot, clearly suggesting a genetic expansion originating in the Middle East and continuing on to influence the whole of Europe in a fairly regular way. Considering the Middle East a part of Europe for this purpose, the genetic variation throughout Europe was large at the time when agricultural expansion began, because the population was sparse (possibly only 100,000 people or so total); people were divided into small, relatively isolated groups; and as a result, genetic drift had determined high variations, much the way it does today in isolated mountain villages. The last Ice Age, having peaked about 18,000 years ago, played a part, too, by splitting the peoples of central Europe into a western section, including the Cro-Magnon, and an eastern section. It was probably at this point that the populations of eastern and western Europe began to diverge, resulting in the Rh differences, among others.

This gradient must have been generated by the slow but regular diffusion of Neolithic farmers into the different genetic background of the Mesolithic hunter-gatherers. While the two people clearly coexisted in the outermost areas of expansion, in Spain and Denmark, for example, there is no sign of conflict between the groups. We don't start to find defensive structures until millennia later. This peaceful coexistence must have encouraged the exchange of goods and services and intermarriage. The evidence of this intermarriage remains in the genetic traces of the hunter-gatherers found in the gradient of the first principal component. This gradient tallies almost perfectly with the archaeological dates for the sequence of agriculture's appearance in Europe.

The author and his colleagues ran a computer simulation at Stanford to reconstruct the Neolithic migration from the Middle East through Europe. This simulation showed hunter-gatherers disappearing everywhere a few hundred or thousands of years after the arrival of the cultivators. Simulations of other migrations demonstrated that principal component analysis often can separate expansions originating in different places because each expansion generates a different genetic landscape, indicating the origin and most important areas of expansion. These maps can suggest the existence of previously unknown migrations, though they cannot help to date them without additional, reliably datable archaeological facts.

In Europe, the first five principal components are statistically significant. The second principal component shows a north-south trend, possibly relating to genetic adaptation to climate. Later work has shown a correlation between these genetic differences and the linguistic differences between speakers of Indo-European and Uralic languages. The third component reveals a secondary expansion related to the development of animal grazing in southern Russia. The fourth component resembles the Greek expansion, which

peaked around 1000 to 500 BC, but surely began earlier. The fifth component shows the resistance to the expansion of the cultivators by the Upper Paleolithic and Mesolithic peoples of western Europe, who remained somewhat genetically distinct from their neighbors. This phenomenon is most evident in the area where modern Basque was once spoken. Though these sorts of maps do not indicate whether they describe an explosion or an implosion, what we know today suggests that this is a residual population that has resisted genetic, linguistic, and cultural infiltration from neighbors.

Expanding this type of analysis beyond Europe demonstrates significant traces of numerous phases of expansion, convincing the author that the history of modern humans has been punctuated by repeated migrations involving a technological advantage that can be passed on to children and a high enough population growth to provoke sustained emigration levels. The word “expansion” is distinguished from “migration” by implying a centrifugal migration stimulated by local demographic growth. The introduction of agriculture is the most powerful example because over the last 10,000 years, it has enabled a thousandfold or more increase in population, from millions to billions. The expansion over the period from 100,000 years ago (or maybe 50-60,000 years ago) to 10,000 years ago involved population growth of only about one hundredfold. The following stages have been identified, though the dates are uncertain:

The first modern humans lived about 100,000 years ago, numbering between 20,000 and 100,000, and inhabiting the areas where the modern human race first developed: eastern Africa or the Middle East, or both.

Their expansion ended about 10-15,000 years ago, reaching virtually all parts of the globe we inhabit today and numbering about 5 million.

The limited food supply provided by the hunter-gatherer lifestyle stimulated the start of livestock and crop-raising activities in more than one area about 9,000-10,000 years ago. This change generated an unprecedented increase in population density.

Certain animals especially facilitated expansion: the horse enabled nomadic herders from southern Russia to expand into Europe, central Asia, and India; Camels helped the Arabs expand into northern Africa, and in the southern Andes, the llama was a key to the success of the Inca empire.

Transport was facilitated by animals, but also by technological innovations such as the wheel, the sail, the outrigger canoe, and the compass and celestial navigation.

Military innovations enabled expansion through conquest, including metal defense and attack weapons as well as the use of the horse.

Innovation seems to play a predominant role in each stage of expansion, though we cannot tell for certain which innovative factor determined the first phase, where modern humans spread across the globe. Here are some possibilities:

The development of advanced language permitted better communication between individuals and groups and therefore facilitated expansion to totally new areas. If, as seems likely, human language has made huge leaps forward in the last fifty to 100,000 years, some sort of biological evolution must have permitted it. Therefore, the innovations were not only cultural and technological, but also biological.

Improvements in transportation were probably essential for travel to distant regions.

Expansion to areas with profoundly different climates led to significant biological and cultural adaptation.

Today we can reconstruct the probable causes of expansions that have left identifiable genetic traces. For others, we rely on archaeological data. Where archaeological research has been limited or non-existent, or where archaeological traces are not available, we can hypothesize from genetic maps a number of probable expansions, suggested in part by linguistic evidence.

The routes of expansion from the Middle Eastern agricultural center go not only west toward Europe, but also east, toward Iran, Pakistan, and India. We know of a farming civilization in Pakistan that included two cities that could have numbered as many as 50,000 inhabitants each at their peak. About 3,500 years ago, these cities were abandoned (probably because of a change in the course of the Indus River), and Asiatic nomadic herders arrived, bringing Indo-European languages to Iran, Pakistan, and India.

Several different expansions occurred in Africa, and in China there are profound genetic differences between the northern and southern Chinese, probably reflecting the development of two separate agricultural cultures.

There was apparently an expansion from around the Sea of Japan, centered on Japan and Korea. It's possible that the Japanese expansion may be linked to one of the Paleolithic migrations from eastern Asia to America.

## **The diversification of languages**

Languages evolve to differ, becoming first dialects and later different languages, though the dividing line between dialect and separate language is vague. In certain regions, more than one distinct language is spoken. For example, in the Iberian Peninsula, Spanish, Portuguese, Basque, and Catalan are all spoken. Language changes (and diversification into separate languages) can be swift. Until around 1,500 years ago, Latin was spoken in western Europe, but today, Italy, France, and Spain have all developed separate languages from that same ancestor. Iceland was colonized by Norwegians around 900 AD, but today, Icelanders can understand Scandinavians only with great difficulty, and Scandinavians can really not understand Icelandic. The minimum time it takes for a language to become different enough to become incomprehensible is a thousand years.

All languages are similarly complex in structure; all have literature and poetry, even if through largely oral traditions. About 5,000 languages are currently in use, not counting dialects. Languages can differ in semantics, grammar, syntax, and phonetics. “Mater” in Latin survives as “mother” in English, “madre” in Italian and Spanish, “mere” in French, “mutter” in German, “Mor” in Swedish, “mat” in Russian, and “metera” in Greek. In all of these cases, the first letter has survived, but the second consonant is not always present, and the vowel changes frequently. In the ancestral language common to the Indo-European languages, the reconstructed word is “ma.”

We can calculate the speed with which languages change. If we compare a language with its 1,000-year-old forebear, we find an average of 86% cognates. So if we compare two languages that separated 1,000 years ago, we can expect each to retain an 86% affinity with the original language. If there have been no exchanges between the resulting languages, and they have evolved independently of one another, the two derivative languages will have cognates totaling 86% of 86% (74%). Icelandic is a known exception to this rule, perhaps because its isolation has prevented it from changing as much as other Scandinavian languages.

Glottochronology works in the same fashion as the molecular clock, and may therefore allow us to reconstruct the story, and even the timing of the separation of languages. Although the results are approximated because of various potential sources of error, Glottochronology works on the assumption that there is a fixed probability of semantic alteration over a given unit of time, leading to expression of meaning by way of a new word. But the calculated separation times are not very accurate.

A more reliable predictor of a language’s origin is its grammatical structure, because grammar and syntax are more stable than phonetics or semantics. For example, English has borrowed a large number of Latin words, but it retains the structure of Anglo-Saxon.

Joseph Greenberg of Stanford University is the principal contemporary taxonomist, and his method consists of comparing several hundred words in hundreds of languages.

Glottochronology estimates the percentage of cognate words (words derived from common roots, or cognates) among two languages. One important study compared a list of 100 words and a number of estimations of percentage of cognates among pairs of languages. The words are those which are expected to have changed least over time, such as the numbers one, two, and three, along with parts of the body, universal aspects of nature, personal pronouns, and certain grammatical rules, etc. The results showed that the percentage of cognate words in two languages decreases with considerable regularity, the longer the time of separation between the two languages. For example, by comparing the Latin of two thousand years ago with Latinate languages of today, and then by repeating the procedure with pairs of languages that have a shorter or longer known separation time, one can build a curve relating percentage of cognates to time of separation. This curve can then be used to calculate the separation time of any two languages, based on the percentage of cognates between them.

Using these methods, the author and his colleagues added a linguistic hierarchy to the study of human migrations. They grouped the world's 5,000 languages into 17 families of varying size: four in Africa, one in Australia, one in New Guinea, three in America, two in Europe, and the other six in Asia, with a certain amount of overlap near continental borders. The geographical distribution of these language families can be linked to the history of the expansions of humanity, and it tallies well with current knowledge of migrations and genetic diversification.

Indo-European stretches across Europe and southern Asia, breaking off around Turkey, where the Altaic family is used. Altaic is distributed from most of Siberia and Mongolia all the way to the Pacific Ocean, possibly including Korean and Japanese. Uralic straddles the Ural Mountains and is used in Asia and Europe up around the Arctic Ocean. There are two Caucasian families in the mountains of the Caucasus close to the southern border of Europe and Asia. In Asia, the Sino-Tibetan family covers all of China and Tibet. The Dravidian family also covers a limited region, mainly in southern India, but it may have once been spoken in Pakistan, Iran, and all of India. The Afro-Asiatic family is used in northern Africa, including the Middle East, Arabia, and Ethiopia. In sub-Saharan Africa the languages stem from the Niger-Kordofanian family. Between the Afro-Asiatic family and the Niger-Kordofanian family are found the Nilo-Saharan languages. At the far south of Africa is the Khoisan family. In America are the three Amerind families: Eskimo-Aleut, Na-Dene, and Amerind. Australian Aborigines still speak a multitude of different languages belonging to the Australian family, but the natives of New Guinea speak languages derived from the Indo-Pacific family. Polynesians speak languages from a family called Austronesian. At least five languages, including Basque and several languages in Asia, do not fall into any of these categories.

Many of these families are now accepted by almost all linguists, and similarities between groups of families are now being recognized. But many linguists are convinced that we cannot establish relationships from more than 6,000 years ago. Glottochronologists think that after that time, the percentage of words in common has dropped to below 10%; using a list of one or two hundred words, this small level of similarity makes the work statistically unreliable. Nevertheless, using other methods and focusing on words with a high preservation rate, a group of Russians and one American linguist believe they can establish the next level up, combining a number of families into a Eurasiatic superfamily. These researchers group Indo-European and Uralic with Altaic, but they differ over other details.

Most linguists do not deal with issues such as these, and so this work remains relatively controversial among academics. This situation reminds the author of an event from the 19th century: in Paris in 1866, the French Society of Linguistics formally banned the study of linguistic evolution.

Other superfamilies have been postulated, and linguists seem to be working their way toward the creation of a single evolutionary tree of language—but this is future work. Nevertheless, the classification done to date raises the question of whether or not there was ever a time when humankind had only one language. Research has demonstrated

that there is at least one word that seems to be common to all languages, the root word *tik*. The meanings of the words from this root all center on the concept of synonymy between finger and one. The Indo-European verb *to indicate* includes this root. A number of other words exhibit great similarity among nearly all language families, including those from which we get the English *who*, *two*, *arm*, *vagina*, and *water*.

At the beginning of the twentieth century, an Italian, Alfredo Trombetti, suggested that all languages shared the same origins, but he was mocked by his fellow scholars. An English translation of his work is being planned today. We're a long time from any sort of agreement on this question, but even if we did agree, two other questions remain: If there was a single human language, when did it exist? The answer to this question is before modern humans' first diaspora, which means at least 60,000 years ago. And the other question is: When did humans first start speaking?

Evidence from the craniums of *Homo habilis* suggests that even at that early stage, there was a biological basis for some language skills. Behind the eye are the areas of the brain we now know are important for language, and these areas (Broca and Wernicke) are found in the left hemisphere, making the left side of the brain slightly larger. We see this asymmetry in the earliest *Homo habilis* skulls from more than two million years ago, but not in the apes closest to humans.

We know that chimpanzees and gorillas can learn hundreds of words and use them in sentences using computers or sign language. But they lack the ability to produce human sounds. The human brain ceased to grow three hundred thousand years ago, but it must have taken a long time after that for humans to reach their present level of articulation. The belief is that the Neanderthals, who lived between thirty-five thousand and three hundred thousand years ago, lacked a fully developed larynx and pharynx. But because these organs are not skeletal, this is conjecture based on what remains we have.

Another reason to think this facility developed recently is that all languages are very similar in their degree of complexity. The intelligence needed for complex language is also needed for the tools and other innovations that have allowed humanity to expand throughout the world and to increase population density as well. As human tools have changed and evolved, indicating the presence of local cultures distinct from their neighbors, so we would expect refined languages to have changed as well.

Linguistics and biology would appear to follow parallel paths in tracing evolution, but language evolution involves a different sort of spread of words and expressions, independent of language evolution, for example loan words from one language entering another. This represents a current that biology need not concern itself with because interbreeding between individuals of different species cannot produce offspring. Linguistics does include changes in language analogous to mutation. But these linguistic innovations are not subject to natural selection; instead, they are subject to cultural selection.

Certain evolutionary processes are unique to language—for example, lexical diffusion, where a linguistic form is applied by analogy to words where it would not ordinarily apply. An example would be the regular conjugation of a verb which was originally an irregular verb, or the changes in pronunciation over the years of words such as “white,” “bite,” and “mite.” These words were originally pronounced phonetically, but due to what has come to be known in linguistic circles as “the great vowel shift,” the syllable represented by the letter *i* is pronounced as a diphthong, and the final *e* has become silent.

Within the definition of lexical diffusion would be the rules by which sounds go through regular changes, first identified in the 19th century as “phonetic laws.” An example of these would be the change from *p*, *t*, and *k* in the ancient languages of Greek, Latin, and Sanskrit to modern English *f*, *th*, and *h* (“pater” becomes “father,” for example). These “laws” have been demonstrated many times, and it is clear that sounds change with a very surprising regularity, suggesting the possibility of some underlying biological cause.

In 1988, the author and some colleagues published a paper intending to begin to answer the question of whether there is a parallel between genetic and linguistic evolution. Analyzing the data used to build their evolutionary tree of human populations, the authors found a very close correspondence between the 5,000 languages in use today and the nations and native tribes of today. The authors reduced the 1,500 populations for which they had data to 42 by regrouping them along geographic and ethnic lines. They then compared the resulting genetic tree to the linguistic family and superfamily tree. They found that the linguistic families unite branches of the genetic tree that are close together and have divided only recently, and the largest linguistic superfamilies correspond with major branches of the genetic tree.

In *The Origin of Species* in 1859, Charles Darwin spoke of the similarity between the evolution of mankind and the evolution of our languages. This similarity should not be surprising, for the same migration and isolation which foster genetic distinction also fosters linguistic diversity as well.

## **Our cultural and genetic heritage**

The author was amazed at the pygmies, that they were so different from him in every possible way, and yet their humanity, their essential nature, was undeniably identical to his: their kindness, humor, dignity, intelligence and courage were as evident as that of any people he had ever known. Because they are so clearly the same as us, the way in which the incredible difference between our way of life and theirs came about was a great puzzle. The difference between the economies is not enough; the explanation stems from a radically different cultural legacy dating back thousands of years.

Twenty-five years before the publication of this book, the author began research on cultural heredity, defining culture as “The total pattern of human behavior and its products embodied in thought, speech, action, and artifacts, and dependent on man’s capacity for learning and transmitting knowledge to succeeding generations through the

use of tools, language and systems of abstract thought.” While some animals clearly have culture (they gain knowledge and pass it on to succeeding generations), humans clearly have the most culture. The basis of culture is the ability to accumulate knowledge and to receive it from previous generations and to hand it off to the next.

It is important to note that evolution does not mean progress. Evolution, whether biological or cultural, tends to move toward increasing complexity—but there are exceptions. Language, for example, tends to simplify as it changes over time. Nevertheless, it is our cultural legacy that makes us recognizably American, Italian, or Pygmy, and it is therefore the essence of culture. What interested the author was figuring out in what ways culture is constant and how it changes over time.

Culture will surely prove more complex than biology. Leaving aside the workings of the brain, it is indisputable that we constantly alter our personal knowledge system on the basis of what we learn not only from our experiences but also from the experiences of others. Consciously or subconsciously, we use this knowledge system to guide our behavior. Who the others are that transmit this information depends on age. In our first years, it is the parents and immediate family members who are most influential. As we grow, our circle broadens and we learn from a wider range of people. Eventually we grow independent enough that anyone can become our mentor or disciple. This series of transactions is cultural transmission, and it is the vehicle that permits cultural inheritance. Transmission can take place both across and within generations. Writing enables direct transmission across many generations.

While genetic transmission can take place only from one generation to the next, cultural transmission is not limited in this fashion and can therefore be very rapid at times. Cultural transmission from parents to children behaves much like biological transmission: it is very stable over long periods of time and is highly conserved. This feature is strengthened by the fact that humans have greater sensitivity to certain influences during the early years of life. There are critical periods in psychological development during which cultural influences leave indelible traces. This process is known as imprinting. If the influence is missing at this critical time, the individual may never develop correctly in the way determined during that phase.

Transmission from one generation to the next is known as vertical transmission. Horizontal cultural transmission assumes many forms: one person to another (a joke, recipe, piece of gossip), teachers to students, politicians to constituents, religious leaders to their congregation, other influential members of society to the society at large. Some cultural mentors may draw huge numbers of disciples (consider the Pope, or political leaders). When one individual determines the behavior of many people, culture can alter quickly. The concept of social pressure reverses this pattern: many people act on one individual to make him accept certain prescriptions or new ideas. More often, social pressure works to prevent change, becoming an important agent of cultural conservation.

In horizontal transmission, a change can occur by virtue of an innovation that catches on if it is considered useful or acceptable. In this context, innovation could be seen as a

cultural mutation. It is similar to a biological mutation, except that it is not random; it usually has some motivation and, in fact, usually stems from an attempt to solve a problem. If the solution is successful, the innovation will likely catch on.

Rapid change is certainly cultural, because genetic change is extremely slow. When considering behavioral changes, it is extremely difficult to analyze a genetic component because personality and behavior are strongly influenced by aspects of an individual's past, which are rarely even identifiable, or by inner motivations (such as envy, hypocrisy, anger, or mendacity), which are even more opaque.

The most studied behavioral characteristic is IQ, which does not measure intelligence but the ability to carry out certain numerical, geometrical, linguistic, and abstract shape operations. While some have persuaded themselves that this test measures only innate abilities, intelligence is the product of personal experience, which is complex and differs from person to person. The IQ scale is calibrated to remove the effects of age and gender, and it is designed such that when a person takes a similar but not identical test a short time after his initial test, the results tend to be much the same. These facts lead many to believe that IQ tests reveal something significant and useful. In fact, it is not clear what, exactly, is measured by the test—but it is clear that it does not measure only innate qualities, and that it is not culture-free.

In 1969, Arthur Jensen, professor of education at UC Berkeley, published an article stating that the 15-point difference in average IQ between American whites and blacks was mainly genetic and therefore irremediable. Stanford physicist and Nobel laureate William Shockley was a vocal supporter of Jensen's argument. But the basis for these views was erroneous. The study on which these conclusions were based ignored the difficult family environments and disadvantaged economic and educational backgrounds of most of the blacks in the study. Only blacks and whites from similar intellectual, economic, and social backgrounds should have been compared. Later studies that did so showed no difference in IQ between black and white students.

Another theory was put forth by a Harvard psychologist, Robert Herrnstein, who posited that the difference was not racial or ethnic but rather it was due to differences in social class. However, Herrnstein argued that this was hereditary, based on the idea that a high IQ is a prerequisite for achieving wealth and social position. A French study of IQ and school grades among working-class children adopted by rich families were the same as those of children born and raised in wealthy surroundings.

Still, this work does not prove that IQ has no hereditary basis. But we can use other methods for determining the relative importance of hereditary and environmental factors. Looking at instances where identical twins were raised in different social environments can provide some information, since identical twins have identical genetic makeup. We can also look at similarities between parents and children, especially by comparing children to mother and father separately. The number of cases where identical twins were raised in different environments is very limited, but it is also instructive, especially since it enables a comparison between the IQ of the child, of each biological parent, and

also of each adoptive parent. The most satisfactory overall analyses of IQ data estimate that genetics, the developmental environment in the sense of culture, and strictly individual factors (such as birth order) have a roughly equal bearing (1/3 each) on an individual's IQ.

Ironically, in the late 1970s it was found that the Japanese have an IQ on average 11 points higher than the Americans, close to the 15 point difference between American whites and blacks. Oddly enough, no one has suggested that the difference between Japanese and American IQs is genetic. On the contrary, this difference fostered vigorous debate about how to improve the US schools to close the gap.

Cultural transmission has not received any in-depth analysis. The author expresses some surprise at this, along with a belief that this type of analysis should be the central discipline of cultural anthropology. The author, along with Marc Feldman, published a book, *Cultural Transmission and Education*, in 1981, which made extensive use of math in attempting to provide rigorous proof of their ideas. Anthropologists paid scant attention, though economists (who are used to math) took notice. The author has since begun a number of projects building on this work. He has determined that very strong similarities usually exist between parents and children in the matters of religion and politics. Religion, including frequency of prayer and the choice of faith, are usually transmitted from the mother to the child, probably because these are inculcated very early in life, when the mother is most influential. Political beliefs, to which both parents contribute, is almost as strongly held as religion, again because it is probably an early influence as a result of frequent family discussions and as a result of the manner in which the family itself operates. In France, three types of family structures have been identified: 1) patriarchal authoritarian, conditioning children to accept absolute monarchy and dictatorship, 2) patriarchal benevolent, favoring acceptance of moderate socialism, and 3) strictly nuclear, where the reciprocal rights of children and parents tend to cease with the adulthood of the children. This last favors migration of young people to areas where there are opportunities for work and also favors the development of the industrial economy and general economic liberalism.

## **Race and racism**

In the decades after World War I, racism increased in Europe (as is well known) and in the US. In the US, eugenicists used incompetent science to justify political measures to limit immigration and foster general racial intolerance.

The concept of race itself is a complex and indeterminate matter, as illustrated by the attempt to answer the simple question, "How many races exist on earth?" We have no answer. Each classification seems equally arbitrary.

Darwin noted the cause of the difficulty: in passing from one population to another, features usually vary continuously and gradually; close analysis of genetic frequency maps shows that discontinuity is rare. Areas where genetic variation is fast and relates to

more than one feature coincide with geographic boundaries, including mountain ranges and wide waterways, or, sometimes, linguistic boundaries. These factors make it difficult or impossible to classify race or to answer specific questions such as, “Is there such a thing as an Italian race, or a Jewish one?”

The idea of race in the human species serves no purpose. The structure of human populations is extremely complex and changes from area to area; clear distinctions are impossible.

Racists often worry about racial purity, but there are no pure races. Every group of people, no matter how small, is genetically variable. Genetic purity simply does not exist in human populations. Genetic purity could be created, to some extent, by a breeding program using very close relations—by marrying brothers and sisters, fathers and daughters, and so on. Furthermore, we would need to run such a program for twenty to thirty generations, and even then we would not have achieved a perfectly pure group, in which all genetic variation had been eliminated. We can do this, in an imperfect way, with animals and plants, but we know that one of the usual consequences is very high sterility, which makes it difficult to keep such breeds alive.

The reality is exactly the opposite: to guarantee normal fertility and health, marriage between close relations must be avoided, or at least kept within limits. In general, marriages between people of very different origins create a more robust line of descendants. There is absolutely no known biological disadvantage to interracial marriage.

Racism is the conviction that one race is biologically superior to the others. That is what underlies racists’ concern for the purity of the race: they do not want this superiority to diminish. But we know that no race is pure, so to think about conserving purity is absurd.

The idea of biological superiority of the successful nations of the day has no sound argument in its favor. It stems from the confusion of culture or civilization with genetic makeup, and nation with population.

## **Our genetic future, genetic engineering, and the Human Genome Project**

Since his appearance one hundred thousand years ago, *Homo sapiens sapiens* has changed and diversified into the groups found on the earth today. Modern humans still have a long way to go to learn to live peacefully together. We have undeniably made social progress, but we need to make more progress quickly, before we destroy ourselves or our world or both. It would be difficult to change our genetics, much easier to change our culture.

The forces of evolution have been altered radically by the developments of the last ten thousand years. The number of people living on the planet has increased over a

thousandfold since agriculture began. As a result, the effects of genetic shift are now much more modest, and we could almost say nonexistent. From this point of view, it is very unlikely that the existing groups will continue to diversify. Some forms of natural selection have also disappeared, due to reductions in the infant mortality rates. What has hardly changed at all is the birthrate. As a result, world population is increasing at a staggering pace and in some countries will actually double over the next twenty years.

Various religions have chosen to view abortion as a crime. Governments' failure to change reproductive habits is understandable, because they are extremely difficult to control. The position of religious authorities that refuse to help humanity in this necessary crusade is unjustifiable, a burying of one's head in the sand, a refusal to see the monstrous extermination awaiting humanity in little more than a generation—through famine, epidemic, and war, the three great forces redressing demographic equilibrium since the beginning of life on earth.

As far as genetics is concerned, the average human will evolve very little. The most significant fact will be the shifting ratio between races. Individual migratory exchanges will also inevitably become more frequent, as will interracial marriage, which is in no way bad news.

Genetic engineering is the construction of new organisms in which a section of DNA has been artificially modified, or has been replaced by a section taken from a different organism or perhaps made by synthesis. The process of genetic engineering is not "tampering with nature," as it might at first appear. Nature itself provides examples of mechanisms that operate in a similar way. Modification of our genetic makeup through genetic engineering is not yet possible, and won't be for some time to come. Everything tried so far, and to the tiniest degree achieved, has involved nongermlinal cells, also known as somatic cells. These changes cannot be transmitted to later generations. Humanity does not yet have the technical knowledge or the moral wisdom to undertake genetic improvement itself. Modifying somatic cells seems on the other hand, permissible, and desirable to avoid major disorders.

With current progress in artificial insemination, however, it is becoming possible to check whether there are signs of known faulty genes in the cells of a developing embryo. Inserting genes into it is another matter and potentially dangerous for the progeny. The author believes it should not be done.

The medical applications of genetics are directed at the treatment and prevention of hereditary diseases and are nothing to fear. The idea that what is genetic cannot be corrected is often erroneous, and progress is foreseeable in this direction.

Some other social issues are less costly to resolve than health problems and are today even more pressing. It is evident that our intellectual, moral, and social upbringing is deficient and must be improved. History shows that civilizations flourish where variety of expression and very disparate contributions are exploited; they decline when intolerance and the inability to interact with those who are different prevail.

The biological history of humankind is that of its evolution, and cultural history is an integral part that has both influenced it and been influenced by it. The two must become inseparable if we wish to avoid our heartrending ocean of suffering. The animal part of our nature, often lacking in restraint, is responsible for many of these excesses, but our cultural history should teach us how to avoid them.