

Molecular anthropology

The study of primate phylogeny and human evolution through the genetic information in the deoxyribonucleic acid (DNA) of genomes and in the proteins that genes encode. The first studies in molecular anthropology used immunological and biochemical methods to obtain information from proteins on the degrees of genetic similarity of humans and other primates. These results not only placed chimpanzees and gorillas closest to humans rather than to orangutans but also indicated that the very close kinship between chimpanzees and gorillas was not any closer than the relation of each to humans. Subsequent studies that extracted genetic information directly from DNA extended this original finding. Indeed, the accumulating comparative DNA sequence data provide mounting evidence that the closest genetic kinship is between chimpanzees and humans rather than chimpanzees and gorillas.

DNA data

The results gathered in DNA studies of primate phylogeny challenge the traditional anthropological view that humans are very different from all other animals. DNA results show that, genetically, humans are only slightly remodeled apes. Humans share with their closest relatives, the chimpanzees and bonobos (pygmy chimpanzees), more than 98.3% identity in typical noncoding DNA and probably about 99.5% identity in the active coding sequences of functional nuclear genes. Humans share about 98.0% identity in nuclear genomic DNA with gorillas, 96.5% identity with orangutans, and 95.0% identity with the most distant ape relatives, the gibbons and siamangs. Apes and humans share with the other branch of catarrhines, the Old World monkeys, about 92% identity in nuclear genomic DNA, and with the platyrrhines, the New World monkeys, about 87% identity. Even with nonanthropoid primates, the tarsiers and strepsirhines (lemurs and loriforms, such as bushbabies), the anthropoids (platyrrhines and catarrhines) share a DNA identity in the range of 76–71%. New information on the social lives and high intelligence of chimpanzees and other apes also challenges the traditional view that humans are very different from other animals. Chimpanzees use tools and have material culture, are highly social, and may even have the mental capacity for abstract thought and symbolic communication, for example, for learning rudimentary forms of language. See also: Deoxyribonucleic acid (DNA)

Traditional primate classifications provide a poor guide to the course of primate phylogeny. These classifications use the vague concept of grades of evolutionary advancement to place the smaller-brained primates in the suborder Prosimii (the primitive grade) and the larger-brained primates in the suborder Anthropoidea (the advanced grade). Moreover, on viewing humans as the most advanced primates, traditional primate classifications have humans as the sole living members of family Hominidae, while the great apes of Africa (chimpanzees, bonobos, gorillas) and Asia (orangutans) are members of subfamily Ponginae of family Pongidae, despite overwhelming evidence that the African great apes share a more recent common ancestry with humans rather than with orangutans. This is the traditional anthropocentric view of the place of *Homo sapiens* in the order Primates. In contrast, a strictly objective view based on molecular evidence, but also congruent morphological evidence from both living and fossil primates, not only places apes with humans within the family Hominidae but also within this family places chimpanzees and bonobos with humans in the genus *Homo*. See also: Apes; Fossil humans; Mammalia

Primate phylogeny

The course of primate phylogeny, as reconstructed from the molecular and fossil evidence, may be sketched as follows. During the Paleocene geological epoch of 65–57 Ma (Mega annum, or million of years before the present), the ancestors of the modern primates divided first into strepsirhines and haplorhines and then, within the haplorhines, into the tarsiiiforms and basal anthropoids. In the early Eocene epoch at about 50 Ma, the strepsirhines divided into lemuriforms and loriforms; and in the middle to later Eocene epoch at about 40 Ma, the basal anthropoids divided into platyrrhines and catarrhines. In the late Oligocene epoch at about 28–25 Ma, while strepsirhines and platyrrhines were dividing into familial clades, the basal catarrhines divided into cercopithecids (Old World monkeys) and hominids (apes and humans).

In the early Miocene epoch at about 23–22 Ma, familial clades divided into subfamilial clades, which by 20–15 Ma divided into tribal clades. Thus, because the last common ancestor of all living apes and humans lived at about 18 Ma, the living hominids are grouped together as subfamily Homininae. This phylogenetic classification not only has each taxon represented by a monophyletic group or clade but also indicates by gradations in taxonomic rank how far back in time is found the last common ancestor of the living members of the clade.

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The phylogenetic classification of living hominids is as follows [each age (in Ma units) shown for a taxon is the age of the last common ancestor of all living members of that taxon]:

Family Hominidae
Subfamily Homininae (18 Ma)
Tribe Hylobatini
Subtribe Hylobatina (8 Ma)
Symphalangus syndactylus: siamang
 Hylobates lar: white-handed gibbon
Tribe Hominini (14 Ma)
Subtribe Pongina
 Pongo pygmaeus: Borneo orangutan
Subtribe Hominina (7 Ma)
Gorilla gorilla: gorilla
Homo (6 Ma)
H. (Pan) (3 Ma)
H. (P.) troglodytes: chimpanzee
H. (P.) paniscus: bonobo (pygmy chimpanzee)
 H. (Homo) sapiens: humankind

After Homininae divided into tribes Hylobatini and Hominini during the late Miocene epoch at about 8 Ma, subtribal hylobatans of the hylobatin clade divided into *Hylobates* (gibbons) and *Symphalangus* (siamangs). The hominin clade in the middle Miocene epoch at about 14 Ma divided into subtribes Pongina, from which *Pongo* (orangutans) evolved, and Hominina. The latter, in the late Miocene epoch at about 7 Ma, divided into *Gorilla* and *Homo*, and at about 6 Ma *Homo* divided into the subgenera *Homo (Homo)*, out of which humankind evolved, and *Homo (Pan)*, which in the Pliocene epoch at about 3 Ma separated into *H. (Pan) troglodytes* (chimpanzees) and *H. (Pan) paniscus* (bonobos, or pygmy chimpanzees). Other subtribal clades such as those of New World monkeys as well as those of Old World monkeys also divided into genera during the late Miocene epoch at about 10–7 Ma. Then genera divided into subgenera or species groups in the late Miocene to early Pliocene epoch at about 6–4 Ma. Thus, classifying humans, chimpanzees, and bonobos as members of the same genus is equivalent to how other primate clades at the same age are classified.

Ongoing evolution

After the divergence of *Homo (Homo)* from *Homo (Pan)*, humankind's emergence was marked by mutations (such as DNA sequence changes) that spread to fixation in the ancestors of all modern humans. These mutations are the human-specific factors which distinguish the human species genetically from all other species. To obtain a comprehensive catalog of these mutations, genomes of a chimpanzee and a bonobo (closest relatives to humans) and a gorilla (next closest relative) need to be sequenced and compared to the sequence of a human genome. Scientists who call for a Human Genome Evolution Project as a companion to the Human Genome Project envision that the overall goal would be to identify and analyze the functions of human-specific genetic factors involved in the evolution of unique features of human anatomy (for example, bipedal locomotion, greatly enlarged brain) and behavior (such as speech, higher-order cognitive functions).

Ongoing evolution involves mutations that have not spread to fixation, either because they occurred too recently or because natural selection has maintained a polymorphic state. These mutations occur at frequencies that occasionally differ from one human group to another. They account for the genetic diversity found in the human species. Extensive comparative data now exist on the genetic diversity due to mitochondrial haplotypes (each, a set of genetic determinants located on a mitochondrial genome). These mitochondrial genetic variants arise from mutations in the DNA carried by mitochondria, the maternally inherited (from ova) cellular organelles that drive oxidative metabolism. These organelles have their own genomes that encode key proteins and RNA molecules found in mitochondria. Although a mitochondrial genome is quite small (16,000 nucleotide base pairs in length) compared to the nuclear genome (3 billion base pairs in length), each somatic cell contains many mitochondria; thus mitochondrial DNA can be readily prepared and haplotypes of such DNA in different individuals can be determined. The species-wide distribution of mitochondrial haplotypes in present-day human populations compared to the distribution in chimpanzees reveals that humans show less DNA diversity than chimpanzees. In fact, the diversity that humans show is no larger than that shown by a chimpanzee subspecies. While populations in different subspecies of chimpanzees share only 28% of the total species diversity, human populations in different ethnic groups (European Norwegians and South African hottentots) and even within the

same group share 85–90% of the total species diversity. The human genetic diversity due to mutations in nuclear DNA (the DNA carried by the chromosomes of cells) also shows this same pattern in which most of the variation within the human species as a whole is contained within single populations. These findings argue that all living humans are biologically not only members of the same species but also the same subspecies and even the same race, the human race. A further inference from the data on mitochondrial genetic diversity is that the birth of the human race took place in Africa about 200,000 years ago.

Recently, small pieces of mitochondrial DNA were recovered from bones of an undated Neandertal specimen. On comparing mitochondrial haplotypes from present–day humans to the Neandertal haplotype and to chimpanzee haplotypes, and assuming a molecular clock with a reference date of 6 Ma for the age of the last common ancestor of humans and chimpanzees, the estimated date for divergence of the Neandertal haplotype from the lineage to the last common ancestor of the present–day human haplotypes is about 800,000 years ago, as compared to about 200,000 years ago for the age of the last common ancestor of present–day human haplotypes. These age estimates as compared to those for the last common ancestor of haplotypes from different chimpanzee subspecies suggest that Neandertals belonged to the same species as humans do, but a different subspecies. The results so far gathered on nuclear genetic diversity in present–day human populations leave open the possibility that as the founder members of the human subspecies, *Homo sapiens sapiens*, multiplied and spread from one continent to another, the gene pool of these migrants could have been enriched by admixture of some genes from the preexisting archaic human populations. See also: Mitochondria

Morris Goodman

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