

HUMANS' CLOSEST RELATIVE

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In contrast to what was mainly believed in the earlier part of this century, molecular data supports the hypothesis that chimpanzees are humans' closest relative. This relationship is supported by immunological, DNA-DNA hybridization, and DNA sequence data and by chromosomal analyses and protein sequences. It is also consistent with morphological data. Some studies in primate morphology appear to support chimpanzee-gorilla, human-orangutan, or human-gorilla clades, but these similarities could be due to convergences, or they could be a result of accelerated rates of morphological evolution in the human lineage.

It has long been known that humans share a common ancestor with apes but it was only in the last thirty years that techniques were developed to provide strong evidence in support of the hypothesis that within the ape lineage, humans are more closely related to chimpanzees than they are to gorillas, orangutans, or gibbons, and that humans are more closely related to chimpanzees than chimpanzees are to gorillas. The relationship of humans to apes remains, however, a controversial issue among biologists and paleontologists and there are some who believe that humans are more closely related to the African apes (chimpanzees and gorillas) as a group; some who believe that gorillas and chimpanzees are the closest relatives; and there are some who believe in the Red Ape hypothesis that states that humans are more closely related to orangutans. A close examination of molecular evidence-mainly studies in DNA hybridization and chromosomal structure, and studies involving proteins such as albumin and hemoglobin-as well as recent morphological evidence provide the best support for a pattern of primate evolution in which humans and chimpanzees are shown as the closest relatives.

An understanding of the phylogenetic relationship between humans, chimpanzees, gorillas, orangutans, and gibbons would have implications in many fields of science. In medicine, for example, tests for new medications and treatments are often performed on monkeys which require an understanding of how they are related to humans. Furthermore, within the field of evolutionary biology itself, techniques used to test the relationship of humans to apes can often be applied to other species and vice-versa so it is important to test the validity of these techniques by testing various hypotheses.

In 1863 Henry Huxley, in defense of Darwin's ideas of evolution that were expressed just four years before, wrote in his Evidence as to Man's Place in Nature, "It is quite certain that the

ape that most closely approaches man, in the totality of its organization, is either the Chimpanzee or the Gorilla."(Mann, 1996: 169). In the more than 100 years since Huxley and Darwin's time, paleontologists, anthropologists, systematists, and biologists have been puzzling over the exact relationship of humans to apes. In the early and middle part of the twentieth century, theories about the relationship of humans to apes revolved around comparative anatomical issues and the discovery of fossil bones and teeth of extinct species related to the living hominoids. In the 1920's Schultz, a comparative anatomist and primatologist amassed a large amount of data that demonstrated the similarity between humans and one or another of the apes but maintained that the great apes were more closely related to each other than any one of them was to humans. Fossil discoveries, such as those of *Dryopithecus*--which was discovered in 1948 by Louis and Mary Leaky and determined to be twenty million years old--though sparse and incomplete, generally led to the belief that humans split from the hominoid lineage before chimpanzees or gorillas which means that humans would be closest to the African apes collectively (Mann, 1996:171). Since the 1960's molecular comparisons between humans and apes have revolutionized our understanding of primate phylogeny. In 1967, Sarich and Wilson published a paper in Science in which they concluded, "We suggest that apes and man have a more recent common ancestry than is usually supposed."(Gibbon, 1982: 112). They examined and compared the immunoreactivity of serum albumin in humans and apes and found that for this molecule all hominoids (apes and humans) were more similar to each other than any of them was to non-hominoids. These observations led many biologists and anthropologists to take a closer molecular look at humans and apes; for, although there was general consensus that humans were indeed closely related to chimpanzees and gorillas, the exact relationship had not been determined.

As more and more molecular data was amassed, it became more and more difficult to defend the view that there had been a separation between humans and apes in such a way that apes are more closely related to each other than to humans; molecules were revealing a different picture. Because genes and the DNA that they contain provide the blueprint for the morphologies of species, and because it is this DNA that is passed on from generation to generation, a fine scale comparison of the genetic material itself should provide the clearest picture of the relationship between humans and apes. If one were to predict that humans are more closely related to gorillas, orangutans, or gibbons, therefore, the morphological data that supports these views would have to be congruent with molecular data. If chimpanzees are more closely related to gorillas than either is to humans, then molecular biology would have to reveal that chimpanzees and gorillas are the most similar molecularly. If one predicts that humans are more closely related to chimpanzees, however, then one would expect this to be revealed by a closeness in their genetic makeup; this is what molecular evidence supports.

In the 1960's molecular studies firmly established that the gibbon and then the orangutan were the first to separate from the great ape lineage and therefore could not be humans' closest relatives. In 1967, Sarich and Wilson closely examined the changes that have occurred in the serum albumin in all primate lineages. They used immunological albumin data to construct an evolutionary clock that could furthermore be used to estimate the times of divergence between humans and apes. In order to calibrate their clock, Sarich and Wilson determined the immunological distance (they were able to construct a distance of a single amino acid in several hundred) in albumin of primates whose divergence dates had been previously established by the fossil record. Because they found that albumin was evolving at the same rate in all primates they reasoned that it could indeed serve as a good time marker; the degree of difference between the

albumin of different species is related to the time since the species split. They estimated that the gibbon split from the human-African ape line ten million years ago, that the orangutan split eight million years ago, and that it was only five million years ago that humans and apes shared a common ancestor (Gibbon, 1982: 113). Fossil discoveries had previously shown that humans and apes shared an ancestor twenty million years ago, but the discoveries of Sarich and Wilson did not fit with these dates. Their data revealed that there were fossil ancestors that were yet to be discovered.

An agar-gel precipitin technique employed by Goodman also supports an early divergence of orangutans and gibbons (Goodman, 1963:302). In this procedure an antiserum is produced to an isolated protein of an organism and then reacted with the antiserum of homologous proteins in other species. The extent of the cross-reactions is an indicator of the amount of evolutionary separation between the species. Goodman concludes, "Evidence that the chimpanzee has more recent common ancestry with man and gorilla than with orangutan or gibbon is furnished by the cross reactions of antiserum to chimpanzee serum." (Goodman, 1963:309). The relationship of humans and apes can therefore be found by closely examining the genetic and molecular makeup of humans, chimpanzees, and gorillas.

DNA cross-hybridization has provided a tool for comparing the genetic makeup of humans and African apes and has provided strong evidence to support the theory that chimpanzees are humans' closest relative. In DNA hybridization, the double helix of one species' DNA is separated into its component single complementary strands, along with the DNA of the species under comparison. All of the strands are then mixed together and where the two species have identical sequences along their DNA, the complementary bases join together. The degree of similarity between these strands is reflected in the degree to which the DNA hybrid is thermally

stable. Results published by Sibley and Ahlquist reveal that humans and chimpanzees have the most similar DNA (Sibley, 1984). They converted the melting temperatures of the DNA hybrids into phylogenetic distances (change in T_{50H} values) and found that the distance between humans and chimpanzees is 1.64; the distance between humans and gorillas is 2.27; the distance between humans and orangutans is 3.6; the distance between humans and gibbons is 4.76; and that the distance between chimpanzees and gorillas is 2.28. In other words, humans share 98.4 percent of their DNA with chimpanzees and differ by only 1.6 percent (see figure 1).

Arguments against this kind of analysis have held that the genetic similarities shown between these species could be due to homoplasies which are similar traits possessed by two or more species that have not been derived by both species from their common ancestor. Schwartz (1987), for example, author of The Red Ape, believes that possible rate inconsistencies in the DNA data should not be overlooked and that DNA cannot, therefore, be used to determine the exact relationship between humans, chimpanzees, and gorillas. But Goodman et al. (1994) claim that homoplasies could not be large enough to argue for the separation of human, chimpanzee, and gorilla lineages from their common ancestor into a single trichotomous branching event.

To provide further support for the human-chimpanzee clade Goodman et al. (1994) examined position by position the sequence characters of aligned nucleotides of DNA from humans, gorillas, chimpanzees, and orangutans to determine the number of synapomorphic positions (derived characters shared by two or more species) that supports each of the alternate branching patterns for humans and primates. They found, in examining both the mitochondrial and nuclear DNA sequences, that there are many more synapomorphic positions that support a human-chimpanzee clade over either the chimpanzee-gorilla clade or the human-gorilla clade (Goodman, 1994:21). Their findings show that in mitochondrial DNA, 72 positions support the

human-chimpanzee clade, 48 positions support the chimpanzee-gorilla clade and 37 positions support the human-gorilla clade. With the nuclear DNA data, Goodman et al. found 58 positions that support the human-chimpanzee clade, 25 positions that support the chimpanzee-gorilla clade, and 14 positions that support the human-gorilla clade.

Analysis of hemoglobin, the protein that binds oxygen in blood, has also provided a good tool for determining the relationship of humans to the African apes and supports the linkage of humans with chimpanzees. The sequences for alpha and beta hemoglobin are known for humans, chimpanzees, and gorillas. Humans and chimpanzees have identical alpha and beta sequences from which gorillas differ by only one residue in each chain. On position 23 on the alpha hemoglobin, for example, gorillas have the amino acid aspartic acid instead of glutamic acid and at position 104 on beta hemoglobin gorillas have lysine instead of arginine. Furthermore, the aspartic acid residue found on the alpha-23 position in gorilla hemoglobin is also found in orangutans, gibbons, and cebids (members of the old world monkeys) which indicates that it is a primitive condition and that glutamic acid is the shared, derived condition in chimpanzees and humans.

Goodman and his colleagues extended this analysis of hemoglobin by constructing a maximum parsimony tree (phylogenetic tree that requires the least amount of evolutionary changes) for humans and apes and showed how their results are consistent with the results obtained from DNA cross-hybridization. Goodman used data on aligned nucleotide sequences of the beta-type globin molecule to construct the most parsimonious trees from the aligned orthologues from humans, chimpanzees, gorillas, orangutans, and gibbons. He found that the most parsimonious tree based on the aligned orthologues was one in which the branching pattern showed that humans and chimpanzees are the most closely related. Figure 2 summarizes

Goodman's results in which a human-chimpanzee clade is supported by eight apomorphic changes, the human-chimpanzee-gorilla clade by 54 and the human-chimpanzee-gorilla-orangutan clade by a 40 apomorphic changes. These clades-that are supported by a diverse range of molecular data-suggest that morphological evidence can sometimes be misleading.

Studies based on the similarity of human, chimpanzee, gorilla, and orangutan chromosomes also support a closer relationship between humans and chimpanzees. When a chromosome is chemically stained, the concentration of DNA at any given position along a chromosome can be highlighted so a stained chromosome will show a series of bands of differing thicknesses and intensities. If the patterns appear identical on the chromosomes of two or more organisms than it is assumed that these chromosomes are homologous and have been retained from one or more common ancestors. Jorge Yunis and Om Prakash conducted a thorough comparative analysis of the chromosomes of humans, orangutans, gorillas, and chimpanzees in 1982. They photographed 20 relatively straight, lateprophase examples of each chromosome and first discovered that the chromosomes of humans, chimpanzees, and gorillas are very closely related to each other and that those of the orangutan are the most different (see chromosome number 6 in Figure 3). This refutes the Red Ape hypothesis that contends that orangutans and humans are the most closely related. Overall, they found that humans and chimpanzees have thirteen identical chromosomes, that humans and gorillas have nine identical chromosomes, and that humans and orangutans have eight identical chromosomes. Yunis and Prakash conclude, "Our detailed comparative analysis of high-resolution chromosomes supports molecular evidence that the great apes and man belong to the Homindae family, which separates into the Ponginae (orangutan) and Homininae (gorilla, chimpanzee, and man). It also provides evidence in favor of

the existence of three ancestors to the great apes and man from which first orangutans, then gorilla, and finally chimpanzee and man diverged.”(Yunis and Prakash, 1982: 1529).

Chromosomal analysis is also supported by Brunetto Chiarelli who confirms that the study of banded chromosomes-which show the replication sequences of every major band in the chromosome-reveal that humans are most closely related to chimpanzees (Chiarelli, 1985). In his study, Chiarelli and his colleagues determined the number and types of chromosome mutations that could be detected in the karyotypes of the different apes compared to man and show that “The type and number of changes, up to now detected, demonstrate that the orangutan is the most conservative and the most unrelated to man, among the apes, while the African apes (especially the chimpanzee) share a number of derived changes with the human karyotype”(Chiarelli, 1985:400). As with DNA and hemoglobin, the similarity between the chromosomes of humans and chimpanzees fits in with morphological data that also supports this relationship.

The majority of morphological evidence that has been amassed supports the view that humans are in general more closely related to African apes as a collective group, but morphological evidence is also consistent with humans and chimpanzees being the most closely related. According to Andrews and Cronin, evidence that groups the great apes (chimpanzees, gorillas, and orangutans) as a single group is based on superficial similarities in skull morphology such as the prognathism of the face and in postcranial morphology such as limb proportions and shoulder morphology which were thought to be functionally adapted to brachiation. But these characters have been shown to be either allometric (growth of a feature during ontogeny at a rate different from that of another feature with which it is compared) consequences of increased body

size or primitive characters retained by living apes and therefore have no relevance to the relationship of humans and great apes (Andrews, 1982:239). Furthermore, Colleen Groves, a professor in the Department of Prehistory and Anthropology at the Australian National University used an examination of derived character states to show that humans and chimpanzees are most closely related. He argues that some of the features that have been used to link chimpanzees and gorillas together with the exclusion of humans are not applicable towards a broader comparison between humans and the great apes because of the fact that humans are so automorphous and have gone through so many more changes than chimpanzees or gorillas. Knuckle walking-- often used to link gorillas and chimpanzees-- for example, according to Groves, could be a synapomorphy that was lost in the ancestors to Homo sapiens. He supported this by saying, first, that some of the fossil antecedents (or relatives) of Homo sapiens have osteological features of the carpus that are associated with knuckle walkers. Second, he analyzed shared derived character states between humans and apes in order to show how morphological evidence can be used to show that chimpanzees and humans are the most closely related. He found that chimpanzees and humans share 25 derived morphological character states, that chimpanzees and gorillas share seven, and that gorillas and humans share twelve (see table 4). Because humans and chimpanzees share the most ancestral traits, he reasons that they are the most closely related.

There are many inconsistencies in the data that is used to support or refute hypotheses concerning the relationship of humans and primates. Morphological evidence for the relationship of humans to apes is sometimes not congruent with the molecular data. Jeffrey Schwartz, for example, wrote a book, The Red Ape, that uses comparative morphology to show that humans are more closely related to orangutans. One explanation for the inconsistency between the molecular data that supports a human-chimpanzee clade and the lack of morphological evidence is the fact that it is often

difficult to find synapomorphies between chimpanzees and humans because there has not been enough time for such characters to evolve. Another explanation for this inconsistency is the fact that the morphological dissimilarities between humans and chimpanzees can be explained by the small percent of genetic difference between these species. The rate at which different parts of an animal develop and grow dictates the final shape of an animal, and it only takes a few genetic differences (in genes controlling development) to cause large morphological differences. The similarities between chimpanzees and gorillas could then be due to shared plesiomorphies, and not derived (apomorphic) in a lineage common only to chimpanzees and gorillas. It seems likely, therefore, that the parts of the DNA that are different in chimpanzees and humans code for developmental characters.

The molecular evidence that supports a closer relationship between humans and chimpanzees is young and has not yet become mainstream. Imagine that the molecular evidence had come before all of the studies in morphology and paleontology. Might the debate over the phylogenetic relationship between humans and chimpanzees have taken a different turn? Indeed, when the first molecular evidence came out in the 1960's to support a relationship between humans and the African apes, morphologists and paleontologists were forced to re-examine their data. Molecular biologists, anthropologists, paleontologists, and all those interested in the evolution of *Homo sapiens* might never be in agreement over the exact relationship between humans and primates; but one can hope that the different fields of biology and anthropology will unite and work collectively to understand how all of the pieces fit into the primate puzzle.

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Figure 1: Percentage Difference in DNA Among Primates

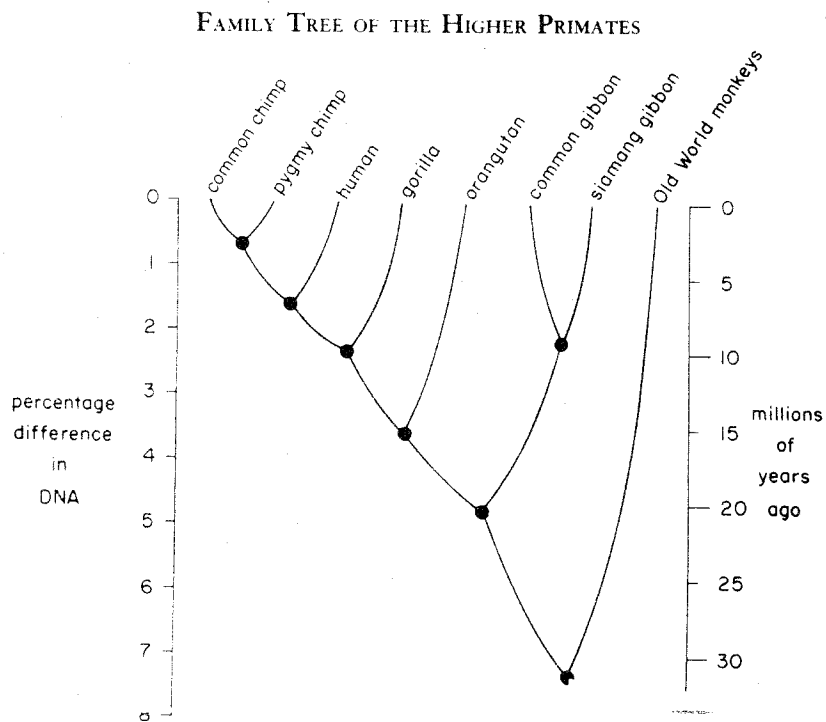


Figure 1. Trace back each pair of modern higher primates to the black dot connecting them. The numbers to the left then give the percentage difference between the DNAs of those modern primates, while the numbers to the right give the estimated number of millions of years ago since they last shared a common ancestor. For example, the common and pygmy chimps differ in about 0.7 percent of their DNA and diverged around three million years ago; we differ in 1.6 percent of our DNA from either chimp and diverged from their common ancestor around seven million years ago; and gorillas differ in about 2.3 percent of their DNA from us or chimps and diverged from the common ancestor leading to us and the two chimps around ten million years ago.

Source: Diamond, Jared. The Third Chimpanzee HarperCollins Publishers Inc., New York: 1992, p. 21

Figure 2: Most Parsimonious Tree Based on Aligned Orthologues

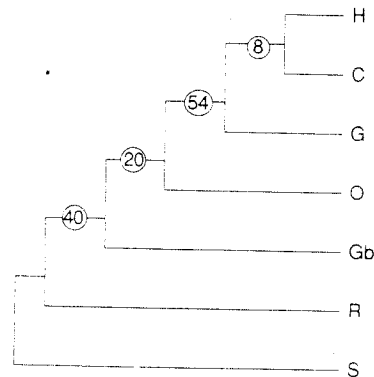


Fig. 4. The maximum parsimony tree found for the seven extended $\psi\eta$ region nucleotide sequence orthologues after examining all 945 of the possible unrooted trees that seven sequences can form. The circled number on each stem to a branching node is the difference in tree lengths between the maximum parsimony tree and the nonparsimonious tree that adds the least length in breaking up the clade represented by that stem. For example, the maximum parsimony tree requires 2036 sequence changes (number of nucleotide substitutions plus number of insertions and deletions), and each nonparsimonious tree that adds the least length (gorilla grouping with either human first or chimpanzee first) requires 2044 sequence changes; thus the circled number on the stem to the human-chimpanzee clade is 8.

Source: Goodman, M. et al. "Primate Evolution at the DNA Level and a Classification of Hominoids" Journal of Molecular Evolution, vol. 30: p. 264, 1990

Figure 3: Chromosome Structures of Humans, Chimpanzees, Gorillas, and Orangutans

Source: Yunis, Jorge and Om Prakash, 1982, "The Origin of man: A Chromosomal Pictorial Legacy." Science, vol. 215, p. 1526

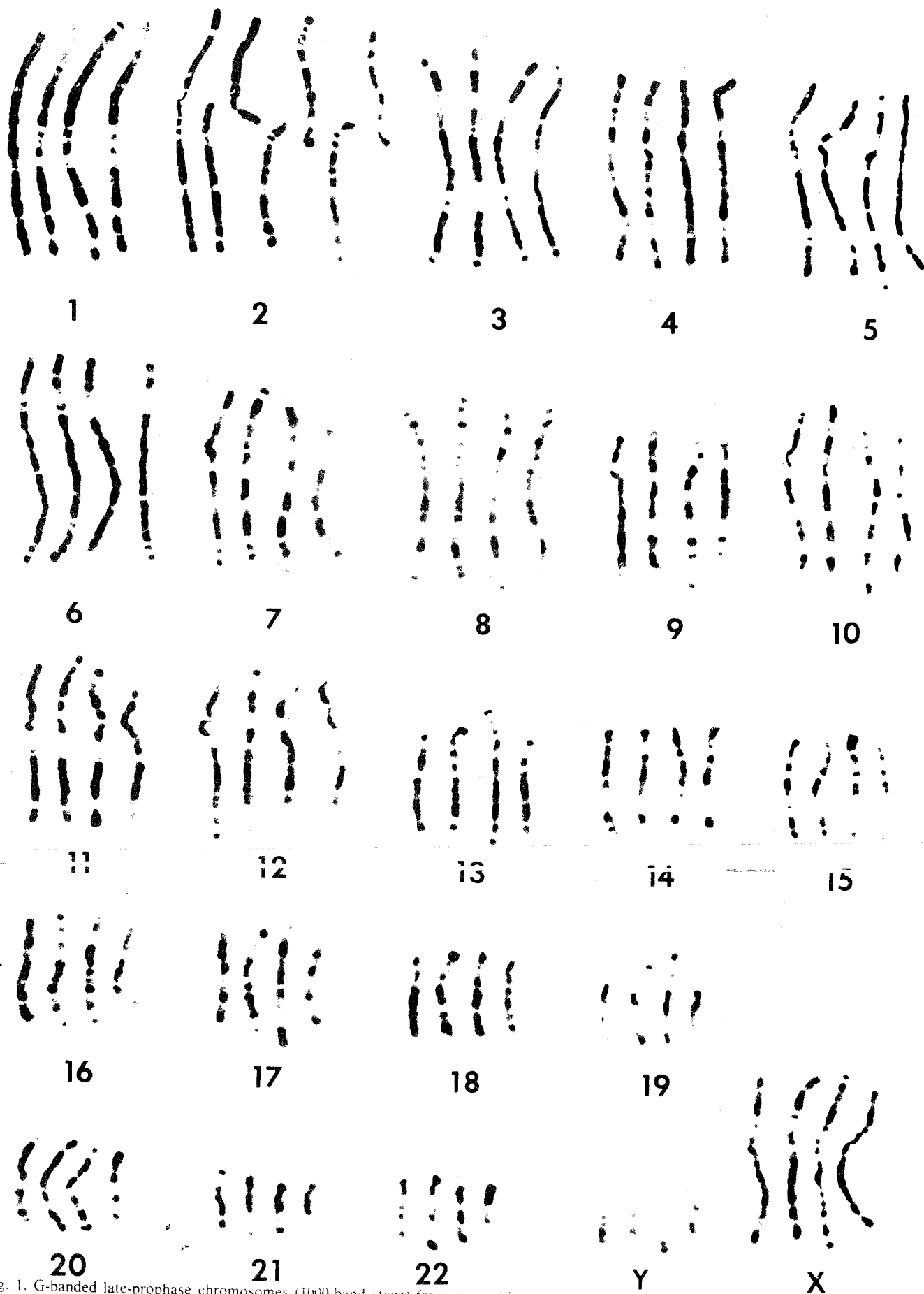


Fig. 1. G-banded late-prophase chromosomes (1000-band stage) from man, chimpanzee, gorilla, and orangutan, arranged from left to right, respectively, to better visualize the extensive homology that exists among them. Heterochromatin is variable and particularly abundant in the paracentromeric region of human chromosomes 1, 9, and 16, the telomeres of chimpanzee and gorilla, the short arm of chromosomes 13 to 15 of gorilla, and the Y chromosome.

Figure 4: Derived character states

TABLE 4a. Derived Character States Common to *Pan* and *Homo*

- 1) I¹ similar in size and shape to I²
- 2) Basal keel of lower canine absent
- 3) Sulcus obliquus of lower molars reduced in expression
- 4) Humerus flattened transversely (convergent with *Pongo*)
- 5) Ankle epiphyses fuse at same time as elbow and hip (instead of after)
- 6) Liver with only 2 lobes (convergent with *Pongo* and *Hylobates*)
- 7) Development delayed: puberty later than 7 years
- 8) Pendulous scrotum
- 9) Uterine fundus flattened sagittally (convergent with *Pongo* and *Hylobates*)
- 10) Baculum very reduced (under 6 mm long, or absent)
- 11) Erect penis very large, over 80 mm long
- 12) Prominent labia minora (convergent with *Pongo*)
- 13) Ejaculate volume more than 1 ml
- 14) Cranial end of heart opposite 2nd rib
- 15) Caudal end of heart opposite 7th rib (convergent with *Pongo*)
- 16) Thoracalis suprema artery present
- 17) Hairs on dorsum reduced to at most 100 cm²
- 18) Only 3 lobes on right lung (convergent with *Pongo*, which has only 1)
- 19) Throat sac reduced with few or no recesses
- 20) Parotid gland free from M. sternocleidomastoideus
- 21) Premaxillary suture always obliterated in adults
- 22) Molar protoconid grooves reduced (convergent with *Pongo*)
- 23) Axis of ear bones over 90°
- 24) Spine of axis (cervical 2) less than 150% body height
- 25) No thecal luteinization in second half of cycle (convergent with *Pongo*)

TABLE 4b. Derived Character States Common to *Pan* and *Gorilla*

- 1) High angle of torsion of humerus
- 2) Deep head of M. flexor pollicis brevis absent
- 3) Parotid gland small
- 4) Six sacral vertebrae
- 5) White pygal tuft, at least in young
- 6) Trigonid basin of lower molars enlarged
- 7) Vallate papillae tend to be very prominent

TABLE 4c. Derived Character States Common to *Gorilla* and *Homo*

- 1) Brachial index less than 80
- 2) Power arm of foot more than 35% length of lever arm
- 3) Fluorescent body (or bodies) in sperm
- 4) Chest hairs very sparse, 5 cm² or less
- 5) Rectum flexed
- 6) Ear breadth less than 70% of length
- 7) Kidney more than 0.3% of body weight (convergent with *Pongo*)
- 8) Valvulae conniventes well developed in adult
- 9) Gestation length more than 260 days
- 10) Testes less than 0.1% of body weight (convergent with *Pongo*)
- 11) Ovaries more than 40 mm long
- 12) Interstitial tissue abundant in pregnant state

Source: Groves, Colin 1986, "Systematics of the Great Apes." Comparative Primate Biology, vol 1 p. 191