Genetic Nature/Culture

Anthropology and Science beyond the Two-Culture Divide

EDITED BY

Alan H. Goodman, Deborah Heath, and M. Susan Lindee

UNIVERSITY OF CALIFORNIA PRESS
Berkeley Los Angeles London

Chapter 7

98% Chimpanzee and 35% Daffodil

The Human Genome in Evolutionary and Cultural Context

Jonathan Marks

One of the most overexposed factoids in modern science is our genetic similarity to the African apes, the chimpanzees and gorillas. It bears the precision of modern technology; it carries the air of philosophical relevance. It reinforces the cultural knowledge that genetics reveals deep truths about the human condition, that we are but a half step from the beasts in our nature.

But how do we know just how genetically similar we are to them? What is that estimate based on? What real significance does it have for our conceptions of ourselves in the modern world and for the role of genetic knowledge in shaping those conceptions? This is where genetics and anthropology converge, the gray zone of "molecular anthropology," technologically molecular and intellectually anthropological, in principle at least.

I attempt in this essay to do something that is classically anthropology. I take a well-known natural fact and show it to be a construction of the social and cultural order and, in that capacity, in need of deconstruction.

HISTORY

Our biological similarity to the apes was known long before there were geneticists. To eighteenth-century scholars, apes had roughly the same status as Bigfoot does today: they lived in remote areas and were seen only by untrained observers. Consequently, reports about them differed widely in quality and reliability.

These creatures were situated on the boundary between personhood and animalhood and, as a result, were immensely interesting. That boundary is of course the domain of powerful mythological motifs in all cultures, for the distinction between person and animal allows us to situate ourselves in the natural order, to make some sense of our place in it. And the mythology is

just as powerful in the scientific culture, as the scientific literature will easily attest: these creatures are both "us" and "not-us," and *we need to know what they really are* (Corbey and Theunissen 1995; Haraway 1989).

The maturation of biological systematics—how we formally organize and partition nature—came through the work of a Swedish botanist and physician, Carl Linnaeus. Biologists as far back as Aristotle had classified animals; but Linnaeus succeeded in imposing regularity and rigor on the process. An inspiring teacher and prodigious writer, Linnaeus supervised more than 180 doctoral theses during his academic career and took an active role in writing them as well. His students and colleagues sent him plant specimens from all over the world, and Linnaeus fit them all into the system of nature. It was said that God created, but Linnaeus arranged.

His most famous work, *System of Nature,* went through twelve editions as the authoritative guide to the arrangement of plants, animals, and minerals ordained by God and discerned by the author. This work constitutes the bulk of his legacy to the history of biology, and modern biological classification officially dates itself from the tenth edition (1758).

What sense did Linnaeus make of the relationship between people and apes? The father of zoological classification was so confused that he simply divided reported apes into two sets, the more anthropomorphic and less anthropomorphic. He designated the former as a second species of humans (*Homo troglodytes,* which he also called *Homo nocturnus*—nocturnal, cave-dwelling man) and placed the latter in another primate genus *(Simia satyrus).* Paradoxically, not only were the apes simultaneously very much like us and very much not like us, but they were now formally both human and nonhuman at the same time (Bendyshe 1865).

Biologists since the mid–eighteenth century have sought to highlight one or the other side of this paradox. Thus, we follow Linnaeus today in classifying humans as "merely" another species of primate, specifically merely another species of apelike creature. The official version follows paleontologist George Gaylord Simpson's 1945 monograph on classifying mammals, placing us in the superfamily Hominoidea, along with the lesser apes (gibbons) and great apes (chimpanzees, gorillas, and orangutans).

Alternatively, we could choose to emphasize the Otherness of humans by dividing the primate group fundamentally into Quadrumana and Bimana, or two-handed and four-handed, as was popular among Linnaeus's close intellectual descendants. Primates, being generally arboreal creatures, are different from other mammals in the anatomy of their hands and feet, which are grasping structures and lack the claws that other arboreal mammals use. Humans, of course, retain this heritage in their hands, but not in their feet: we are not gracefully four-handed, but pitiably two-handed. This classification would acknowledge the unique aspects of the human feet, which are specialized unlike those of any other primate and have lost the ability to

grasp, except in a very rudimentary manner. It would not deny the common ancestry of humans and apes, but would merely highlight the divergence of humans from their ape ancestry.

We could even distinguish humans from other multicellular life altogether, as the subkingdom Psychozoa (mental life), which the zoologist Julian Huxley proposed in the 1950s. A species that lives completely by its wits—that is to say, one that relies entirely on the technological products of its societies for individual survival—is quite different from other life on earth. Perhaps that is worth acknowledging zoologically (Huxley 1957).

Humans are marked by a large number of physical, ecological, mental, and social distinctions from other life. These are not necessarily improvements, of course—we have no more objective way to evaluate "improvement" in the natural world than we do in the cultural world—but merely differences. Other primate species spend time on two legs, and other vertebrate species are bipedal (birds and kangaroos come readily to mind), but not in the same manner as humans. Other species communicate, but not via the absurdly arbitrary and symbolic media we call language. Other species modify natural objects and use them to aid in feeding (Jane Goodall's observations of chimpanzees stripping twigs and using them to fish for termites are classic), but none relies on its technology to survive as humans do. And in no other species does technology take on an evolutionary trajectory of its own, a result of the social cycle of invention, adoption, spread, and modification. Other species appear to grieve, but none weeps as humans do—and certainly not over imaginary events, like *Les Misérables* or *Love Story*.

What does genetics have to say about all this?

Nothing.

MOLECULAR GENETICS

Sameness/Otherness is a philosophical paradox resolved by argument, not by data. Genetic data tell us precisely what we already know, that humans are both very similar to, and diagnosably different from, the great apes.

But genetics is able to put a number to that similarity. It is not uncommon to encounter the statement that we are something like 98 percent genetically identical to chimpanzees. You can count the number of base differences among the same region of DNA in humans and chimpanzees and gorillas, and add them up. Or you can do the same thing to the products of the DNA, protein structures. All such comparisons invariably yield the result that humans and chimpanzees (and gorillas) are extraordinarily similar. But that was known to Linnaeus without the aid of molecular genetics.

What is new? Just the number.

If you compare a human and a chimpanzee, it is easy to see that they are remarkably similar in body structure. Every bone of the chimpanzee body corresponds almost perfectly to a bone in the human body—but differs ever so slightly and diagnostically, in ways that are generally related to the human habit of walking upright. And if not related to our bipedal habit, any detectable difference is very likely related to either of two other human physical specializations, our reduced front teeth and our enlarged brain.

The problem is simply that it is difficult to say just how similar a particular chimpanzee body part and its human counterpart are, percentagewise. A percentage, after all, is a scalar, one-dimensional measure, while a body part is a three-dimensional entity. Indeed, four-dimensional, if you consider the developmental aspects of growth—as people mature, they do not merely expand, they also change in form.

If you were to compare human and chimpanzee structure to that of, say, a snail, it would be patently obvious that humans and chimps are over 99 percent identical in practically every way. The human and chimp have bones, they lack a shell, they have limbs, they do not leave a trail of slime as they move; every nerve, every sinew, every organ is almost the same in a chimp and human and very different, if present at all, in the snail.

Exactly how similar they are, of course, is elusive. It would be rather old-fashioned and premodern to say, "Humans and chimpanzees are really, really, really similar," even though it is a true statement.

What genetics offers is the opportunity to place a hard number on two-way comparisons, by virtue of the fact that the genetic instructions (and their primary products) are composed of long chains of subunits, differences that can be tabulated and numerically manipulated. Thus, one can look at a short region around one of the genes for hemoglobin, as my colleagues and I did in 1986, and find a DNA sequence that reads GCTGGAGCCTCGGTGGCCAT in a baboon and GCTGGAGACTCGGTGGCCAT in an orangutan (Marks et al. 1986). One difference in twenty possibilities; the very linearity of DNA sequences makes them easy to compare. And with a much longer DNA sequence, you would expect to get a more precise estimate. In this case, for example, we found a difference between a baboon and an orangutan of about 5 percent in this small region, and a more general level of difference of about 8 percent.

But the comparison can also be misleading in two important ways.

To begin with, such comparisons of DNA sequence ignore qualitative differences, those of kind rather than amount. To take the smallest case, consider a different sequence of twenty DNA bases from the same region: CCTTGGGCCTCCCGCCAGGC in the baboon and CCTTGGGCTCCCGCCAGGCC in the orangutan. If you look at them in parallel rows you find them to be different:

CCTTGGGCCTCCCGCCAGGC
CCTTGGGCTCCCGCCAGGCC

But if you look more carefully, you might observe that the general gestalt of the sequences is roughly the same. If there is one *C* too many in the middle of the top sequence, or one too few in the bottom, the match becomes far more complete. If we look at it again, inserting a small gap for one base too many or too few, we see the similarity that was previously hidden from view:

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CCTTGGGCCTCCCGCCAGGC
CCTTGGGC TCCCGCCAGGCC
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So we may infer an insertion in one lineage or a deletion in the other, in order to make this sequence look maximally similar. But how can we know for sure? This is a very different kind of inference from the DNA base substitutions we were tabulating a few paragraphs ago. This involved ignoring the actual census of differences in favor of a gestalt similarity and then retabulating the differences—a highly subjective procedure, although probably right.

So we have overridden the *observation* of seven differences in twenty with the *inference* of one difference, of a different sort, in twenty. Though again, this is not to say that it is illegitimate. The question is, what does it do to the number, our precise estimate of the degree of genetic difference? First, it inserts an element of subjectivity masked by the number itself; and second, it sums together DNA base substitutions and DNA base deletions, as if they were biochemically identical and quantitatively equivalent. In fact they are neither; this is a classic case of apples and oranges.

And that was an easy one.

Actually, the molecular apparatus has complex ways of generating insertions and deletions in DNA, which we are only beginning to understand. For example, a stretch of DNA from a ribosomal RNA gene is forty bases long in humans and fifty-four bases long in orangutans. The sequences on either side match up perfectly. How do we know what bases correspond between the two species, how do we decide how many substitutions have occurred, when obviously some have been inserted and deleted as well? The authors of the original study inferred five gaps and six base substitutions (Gonzalez et al. 1990), but it could just as easily be two gaps and nine substitutions or five gaps and three substitutions (Marks 2002). While we might, by Occam's razor, choose the alignment with the smallest numbers of mutational events, we still have to decide whether a gap "equals" a substitution, or whether a gap should be considered rarer and, therefore, worth, say, five substitutions.

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Human       CCTCCGCCCCGCCG    CTCCGC GCCGCCGGGCA          CGGCC        CCGC
Orangutan   CC          GTCGCCTCCGCCACGCCGCGCCACCGGGCCGGGCCGGCCCGGCCCGCCCCGC

Human            CCTCCGCCGCGCCCGCT        CCGCGCCGCCGGGCACGGCCCCGC
Orangutan   CCGTCGCCTCCGCCACGCCGCGCCACCGGGCCGGCCGGCCGGGCCGGCCCGCCCCGC
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Human       CCTCCGCCCCGCCG    CTCCGCGCCGCCGGG CAC  GGCC                CCGC
Orangutan          CCGTCGCCTCCGCCACGCCGCGCCACCGGGCCGGGCCGGCCCGGCCCCGCCCCGCCCCGC
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The problem is that we cannot tell which DNA sequence alignment is right, and the one we choose will contain implicit information about what evolutionary events have occurred, which will in turn affect the amount of similarity we tally (Mindell 1991). How similar is this stretch of DNA between human and orangutan? There may be eight differences or eleven differences, depending on how we decide the bases correspond to each other across the species—and that is, of course, assuming that a one-base gap is also equivalent to a five-base gap and to a base substitution. This is the fundamental problem of homology in biology: What is the precisely corresponding entity in the other species?

In a more general sense, however, the problem of taking quantitative estimates of difference between entities that differ in quality is prevalent throughout the genetic comparison of human and ape. The comparison of DNA sequences presupposes that there are homologous sequences in both species, which of course there must be if such a comparison is actually being undertaken. But other measurements have shown that a chimpanzee cell has 10 percent more DNA than a human cell (Pellicciari et al. 1982). (This does not mean anything functionally, since most DNA is functionless.) How does one work that information into the comparison or into the 98 percent similarity?

In the example above, the problem began with the assumption that forty DNA bases of human sequences were homologous to fifty-four DNA bases of orangutan sequence. A simple estimate of similarity and difference necessarily must be confounded by variation in size of the entities being compared.

If we compare the genes for α-globin on chromosome 16 between human and chimpanzee (half of hemoglobin, the molecule that transports oxygen and carbon dioxide in our blood), we find a near identity of the base sequences. But we also find that, with rare exceptions, humans have two copies of the α-hemoglobin gene, aligned in tandem; chimpanzees, however, have three (Zimmer et al. 1980). Or, if we look at the genes that code for the Rh blood group, again the nucleotides of the genes match up almost perfectly between the two species, but humans have two such genes and chimpanzees have six (Westhoff and Wylie 1998). How can we make simple numerical sense of that?

An odd recognition of the fact that mutational modes are complex has recently occurred. Tabulating both nucleotide substitutions and insertions/deletions, researchers have found the chimpanzee and human genomes *not* to be over 98 percent identical, but closer to 95 percent identical (Britten 2002). The problem, however, is not that the two genomes are "only" 95 percent identical, but that any tabulation of the precise amount of identity is forced to shoehorn the results of several different mutational pro-

cesses into its grand tally. Neither number has the force of accuracy, because the precise number obtained depends on what one recognizes as a meaningful difference (only nucleotide substitutions, or the genomic fruit salad of changes?), how one counts it (is a three-hundred-base insertion three hundred differences or only one?), and whether there is any scientific value at all in trying to derive an official amount of genetic difference between the two species' genomes in the first place when the official amount necessarily combines differences of quantity and quality.

The second misleading area of DNA sequence comparisons entails a consideration of the other end of the scale. The structure of DNA, the famous double helix, is built up of four simple subunits. Each of our reproductive cells has a length of DNA encompassing approximately 3.2 billion of these subunits, but there are still only four of them: adenine, guanine, cytosine, and thymine, or A, G, C, and T. This creates a statistical oddity. Since genetic information is composed of DNA sequences, and there are only four elements to each DNA sequence, it follows that two DNA sequences can differ, on the average, by no more than 25 percent. Certainly a very small stretch of DNA might be zero percent similar to another very small stretch (AAAAT matches GGCCG nowhere, after all), but *on the average, two random stretches of DNA will be statistically obliged to match at one out of four places.*

In other words, two stretches of DNA generated completely at random, completely independently of one another, would not be zero percent similar, but rather, would be 25 percent similar.

But what would constitute a comparison of two DNA segments that emerged completely independently of one another? When we compare DNA sequences, of course, we are comparing corresponding DNA sequences, such as the gene that codes for the electron-transport protein cytochrome c. Such correspondence, or homology, in biology is a reflection of common descent. A human and a chimpanzee have similar genes for cytochrome c because they are descended from a common ancestor that had a gene for cytochrome c similar to both.

In fact, so do humans and fruit flies. Their DNA sequences did not emerge independently of one another but are products of the divergent histories of lineages that became separated some hundreds of millions of years ago.

In fact, so do humans and daffodils. Their DNA sequences are not independent of one another, either. The only such DNA sequences would be those that result from independent origins of DNA-based life; and then we still expect them to be 25 percent identical, by virtue of the way in which DNA is constructed.

Thus, if one compares the DNA of a human and a daffodil, the 25 percent mark is actually the zero mark, and since humans and daffodils do share a common ancestry, one would expect them to be generally more similar than 25 percent—say about 35 percent.

In the context of a 35 percent similarity to a daffodil, the 98 percent similarity of the DNA of human to chimp does not seem so remarkable. After all, humans are obviously far more similar to chimpanzees than to daffodils.

But more than that, to say humans are about one-third daffodil is more ludicrous than profound. There are hardly any similarities one can identify between a daffodil and a human being. DNA comparisons thus overestimate similarity at the low end of the scale (because 25 percent is actually the zero mark of a DNA comparison) and underestimate comparisons at the high end. At least snails, in the previous anatomical comparison, move around and eat; they cannot photosynthesize; they are much more similar to us than daffodils are. So from the standpoint of a daffodil, humans and chimpanzees are not *even* 98 percent identical: they are probably 100 percent identical. The only difference between them is that the chimpanzee would probably be the one *eating* the daffodil.

The problem is that, in being told about these data without a context in which to interpret them, we are left to our own cultural devices to impart meaning to them. Here, we generally are expected to infer that genetic comparisons reflect deep biological structure, and that 98 percent correspondence is an overwhelming similarity. Thus, "the DNA of a human is 98 percent identical to the DNA of a chimpanzee" becomes casually interpreted as: "Deep down inside, humans are overwhelmingly chimpanzees. Like 98 percent chimpanzee."

We do not really know precisely how similar the DNA of chimps and humans is, except that they are very similar, as are their bodies. Genetics appropriates that discovery as a triumph because it can place a number on it, but the number is actually rather unreliable. And whatever the number is, it should not be any more impressive than the anatomical similarity; all we need to do is put that old-fashioned comparison into a zoological context.

The paradox is not that we are so genetically similar to the chimpanzee; the paradox is that we presently find the genetic similarity to be so much more striking than the anatomical similarity.

THE NATURE OF THE COMPARISON

Where does such a number, ostensibly representing our basic similarity to another species, come from? Three sorts of data have produced these tabulations. The first is a comparison of protein structure from 1975 by Berkeley geneticists Mary-Claire King and Allan Wilson (1975). Proteins are long strands of elementary subunits that can be compared, and that are reflections of gene structure. Examining the differences between forty-four known proteins possessed by humans and chimpanzees, King and Wilson found they were 99.3 percent identical.

We know that only about 1 percent of the total DNA of a cell is actually

expressed as proteins, and that protein-coding regions are the most slowly changing parts of the DNA. The reason is that mutations or changes to functional DNA are more likely to do systemic damage to the organism than are mutations to nonfunctional DNA. Consequently such mutations are most unlikely to be perpetuated in the species, as their bearers fail to thrive and reproduce as efficiently as the other creatures who lack the damaging mutations. Mutations to nonfunctional DNA occur at the same rate; but because they are not expressed, they do their bearers no harm. One would expect that DNA fraction to differ more widely across species. Consequently, the King and Wilson estimate of 99.3 percent is an overestimate of the similarity of human and chimpanzee DNA, being derived from a skewed sample of the DNA reflecting only protein-coding regions.

The second class of data was made available in the mid-1980s with the development of direct DNA sequencing technology. DNA is a long, linear molecule, again composed of simple subunits that can be compared. Bits and pieces of it have been compared between human and chimpanzee, amounting to less than 100,000 DNA bases in length. But there are 3.2 billion bases in a human genome, so obviously we have here a minuscule proportion and, again, one biased toward regions that contain functional units, genes—which tend to be where people look for DNA to sequence.

The most comprehensive comparison we have is actually infinitesimal in scope, about forty thousand bases of the region of the β-hemoglobin genes on chromosome 11. And we find human and chimpanzee, base for base, to be about 1.9 percent different (Bailey et al. 1992). The difference between the .7 percent estimate and the 1.9 percent estimate is a consequence of the fact that this DNA comparison includes much more nongenic DNA than genic DNA (which is the only class that would be translated into protein differences). Indeed, the DNA sequences of genes included in that region are virtually identical between the two species.

But again, that is a high estimate, because it focuses on a region known to contain genes and is therefore more conservative than we should expect the overall DNA to be. Genes are rare in the genome. Not only that, but we know the evolution of human hemoglobin has been sensitive to specific environmental problems—such as malaria—and therefore may have its own evolutionary idiosyncrasies.

Another piece of DNA that has been well studied is the mitochondrial DNA, or mtDNA. Whereas 3.2 billion nucleotides form the twenty-three chromosomes of a human nuclear genome (the DNA of a human gamete, half that of an ordinary cell), there is a tiny fraction of DNA located outside the nucleus. The mitochondrion, a subcellular organelle universally labeled in biology textbooks as "the powerhouse of the cell," generates metabolic energy for the physiological processes of life. It also has 16,500 nucleotides of DNA, which code for some of the molecules used by the mitochondrion.

The mitochondrial DNA, however, is not 1 percent different among humans, chimpanzees, and gorillas. It is 9 percent different (Arnason et al. 1996). Why? Because mtDNA mutates at a much higher rate than nuclear DNA. The mutations have little or no effect on the life of the organism, and so the differences simply accumulate through time. Two organisms, therefore, will be far more similar in their nuclear DNA than in their mtDNA. For example, the "mitochondrial Eve" work was based on tabulating the differences detectable among human beings (.2 percent difference), whose nuclear DNAs are so similar as to preclude that kind of study.

The point is an important one: Different bits of DNA evolve at their own rates, and therefore—as a result of the 6–7 million years of evolutionary time separating humans, chimps, and gorillas—some bits are 10 percent different, some are not comparable because they are different in kind rather than amount, and most are less than 3 percent different.

DNA hybridization was a technique popular in the 1980s. It promised a mass genome comparison, rather than a high-resolution snapshot of a single region (Sibley and Ahlquist 1984). The technique began, however, by discarding the half of the genome that was most redundant and, presumably, least full of genes. What remained was bonded to the DNA of a different species, and the temperature at which the strands of this "hybrid DNA" came apart was estimated. Since hybrid DNA is held together by fewer bonds than native DNA, the difference in thermal stability might be a crude indicator of how many DNA mutations differentiate the genes of the two species. Assuming (conveniently) that 1 degree of difference in thermal stability between human-chimp DNA hybrids and human-human DNA equals 1 percent genetic difference, they concluded that humans and chimpanzees are 1.8 percent genetically different. Yet a different study calculated the conversion ratio at 1 degree equals 1.7 percent difference (Caccone et al. 1988), and thus humans and chimps would be over 3 percent different rather than 1.8 percent. And this experiment examines only half the total DNA in the first place. So it actually boils down to a demonstration that half the DNA of humans is either 98.2 percent or 97 percent identical to that of chimpanzees.[1]

More important, DNA hybridization was based on an archaic view of the genome.[2] It underestimated the extent to which serial redundancy pervades the genetic blueprints—even "unique-sequence" genes come in clusters or families of genes structurally similar to one another, the results of ancient "rubber-stamping" duplication events. Thus, when the DNA of one species is hybridized to that of another, a gene can pair with either its perfect partner (ortholog) or a different gene from the same family in the other species (paralog). In the example here, from the genes for hemoglobin, human α-1 globin has an orthologous counterpart in the gorilla and at least six paralogous counterparts. The experiment favors pairing orthologous DNA, but a

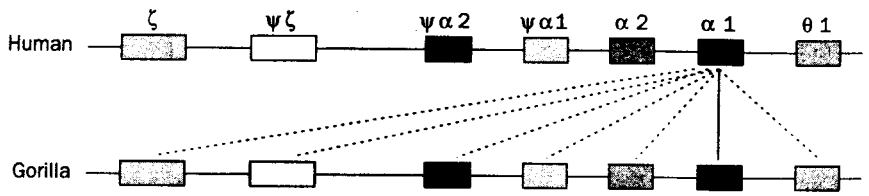

Figure 7.1 Molecular homology. Because of the prevalence of serial duplications of genetic material, a piece of human DNA (here, the α-1 globin gene) has one orthologous counterpart (solid line) and several paralogous counterparts (broken lines) in the gorilla genome.

small proportion of the hybrid DNA mixture invariably will be composed of poorly paired paralogous DNA hybrids. For close relatives, the proportion of this unwanted DNA may be greater than the small difference between the orthologous DNA segments the technique was designed to detect! (See figure 7.1.)

This estimate of genetic similarity along a single dimension consequently misses a significant component of difference—arguably the most important discovery in evolutionary biology in the last few decades—genome complexity. It is not that the human genome is more complicated than the chimpanzee's, but merely that the evolutionary processes operating to differentiate them from one another are far more diverse and extensive than mere nucleotide substitution, which leads to base-pair mismatch, would suggest.

CHROMOSOME STRUCTURE

Yet another kind of comparison involves examining the structure of the chromosomes. Since the primary function of chromosomes is to get the immensely long DNA strands through cell division smoothly by condensing them into a manageable number of structures, it does not really matter whether there are ten, twenty, or fifty of them. Any number in that range will do well. Consequently we find that nearly all mammals fall in the ten-to-fifty range, and in general, that closely related species have similar numbers of chromosomes.

Each of the twenty-three pairs of human chromosomes has a nearly identical counterpart in the apes. Perhaps a half dozen have undergone minor structural changes; but if you can recognize the standard pattern of bands on human chromosomes (known as G-bands), you can recognize chimpanzee chromosomes. It is not known precisely what the bands are, but they can be generated easily in many ways, the most common being to expose the chromosomes to a mild enzyme treatment, which breaks down some of the protein complexes in the chromosome packaging. This permits a stain to bind

preferentially to certain areas, creating arrays of alternating stained and unstained regions—bands. And those arrays are nearly identical in humans, chimps, and gorillas (Marks 1983).

The exception is human chromosome 2 (the second largest chromosome, for they are numbered according to size). One can look at the chromosomes of a chimpanzee forever and never see the large pair known as chromosome 2 and found in the human. What one sees, however, is two small pairs of chromosomes in the chimpanzee, which, when joined end to end, produce a dead ringer for human chromosome 2 (IJdo et al. 1991).

Apparently a fusion occurred in the human lineage, creating chromosome 2 and reducing the count from twenty-four pairs to twenty-three pairs. Is that what makes us human? Yes and no. Yes in a narrow, diagnostic sense: given the chromosomes from a cell of any living species, if you find chromosome 2 among them, they are from a human. No in a functional sense: the fusion is not what gives us language or bipedalism or a big brain or art or sugarless bubble gum. It is simply one of those neutral changes lacking outward expression, which is neither good nor bad but merely diagnostic.

The chromosomes of humans and chimpanzees also differ in a subtle but reliable way under a slightly more complex treatment known as C-banding. C-banding seems to mark specifically a few chromosomal zones containing highly redundant "junk" DNA sequences (satellite DNA). In the human the characteristic zones are at the middle, or centromere, of each chromosome; are slightly below the centromere on chromosomes 1, 9, and 16; and make up most of the Y chromosome.

We are the only species with such a pattern. If one looks at the chimpanzee's cells using the identical procedure, one encounters the centromeric bands readily enough, but the marked regions of chromosomes 1, 9, 16, and Y do not contain satellite DNA. Not only that, but something entirely unfamiliar will be evident—bands at the tips of nearly every chromosome and even in the middle of a chromosome arm (figure 7.2). The terminal bands are present in the gorilla's cells as well; the bands have been seen in every chimpanzee and gorilla studied, and in no human or orangutan (Marks 1993).

What is the cause of the bands on the tips? Something trivial: the emergence of yet another functionless class of DNA, which somehow managed to "colonize" the ends of the chromosomes. This class of DNA packs itself more densely into the chromosome than the rest of the DNA does, and it absorbs more stain. If you had a tube of cells and did not know whether they were derived from a human or a chimpanzee, a C-band analysis would tell you immediately.

The story is recursive. We find ourselves to be always genetically very similar to chimpanzees and yet diagnosably different. This is not terribly different from the conclusions we can draw from comparing anything else

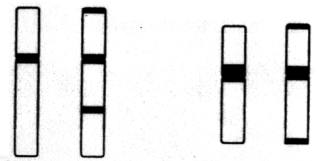

Figure 7.2 Some diagnostic differences between human chromosomes. Chromosome 7 of a human and its chimpanzee counterpart (left pair) can be readily distinguished by the terminal C-band and interstitial C-band in the chimpanzee chromosome. Chromosome 16 (right pair) has a prominent C-band below the centromere in humans, and terminal bands in chimpanzees.

between chimpanzees and humans—hair, organs, skin, muscles, bones. So the paradox of our exceeding genetic similarity seems less paradoxical. We learn that we are similar to, but invariably slightly different from, our closest relatives. It could not really be any other way, given the fact of evolution.

THE CENTRAL FALLACY OF MOLECULAR ANTHROPOLOGY

The argument I criticize here is the one that begins with our unimpeachable genetic similarity to the chimpanzee and concludes that we are therefore "nothing but" chimpanzees genetically. In fact, the data have been around for a surprisingly long time. The fact that it took decades to grasp the simple and direct implication alone might suggest that the argument is specious. By the 1920s, the similar blood reactions of human and ape sera were well-known. And shortly after the celebrated trial of John T. Scopes (convicted of teaching evolution in Tennessee in 1925), H. L. Mencken's literary magazine ran the article "The Blood of the Primates" (Hussey 1926). It was quite clear about the results: "The sanguinity of the horse and donkey, which are capable of hybridization, is less close than the kinship of Homo sapiens and the anthropoids."

The article, of course, failed to draw the conclusion that we are apes, in spite of the data. That inference would have to wait for the rise of molecular reductionism in the 1960s and expresses what we can call the Central Fallacy of Molecular Anthropology.

Ultimately this fallacy is not a genetic one but a cultural one—our reduction of life to genetics. Geneticists are among its most frequent perpetrators, and of course it is in their interest to perpetuate it. In the 1960s, when it became possible to make direct comparisons between the proteins of different species, the biochemist Emile Zuckerkandl was impressed by the fact that only one difference in the 287 amino acids in (half of) hemoglobin could be found between a human and a gorilla. So impressed, in fact, that he could proclaim that, "from the point of view of hemoglobin structure, it appears that [a] gorilla is just an abnormal human, or man an abnormal gorilla, and the two species form actually one continuous population" (Zuckerkandl 1963).

The claim was nonsense to the distinguished paleobiologist George Gaylord Simpson (1964): if you cannot tell a gorilla from a human, he suggested, you should not be a biologist. If you cannot tell them apart by their hemoglobin, *just look at something else.*

Suggesting that the relationships of our *blood* are the relations of *us*, that we are our blood, is simply a metaphoric statement, actually metonymy, the substitution of a part for the thing itself. Perhaps it is resonant with us because our brain evolved to make metaphoric connections, and because blood is such a symbolically powerful substance. Blood is, after all, a metaphor for heredity.

But it is not literally true that we are our blood; and science is supposed to be about literal truths, not literary ones.

There is one sense in which we can acknowledge that we are apes: phylogenetically. We fall within a group constituted by the great apes—those large-bodied, tailless, flexible-shouldered, slow-maturing primates: the chimpanzee, gorilla, and orangutan. And indeed, we are more closely related to the chimpanzee and gorilla than they are to the orangutan. This implies that the category of great ape is artificial, for it comprises species that are not each others' closest relatives, or rather, that it excludes a member of the group of relatives—namely, us.

We are excluded by virtue of the fact that we have diverged relatively rapidly from the classic ape form and mode of life and have evolved to fill a different niche, that of an ape which is bipedal and culture reliant. So although we fall within the great-ape category genetically and are recently descended from them biohistorically, we are nevertheless different from them by virtue of having evolved a very large number of readily observable specializations or novelties. We have left them in our wake, so to speak. The apes seem to resemble each other more than they resemble us because they did not develop the things we did.

But does this mean we are apes, as the genetic enthusiast Richard Dawkins (1993) has argued? Consider a different group of animals: say, a sparrow, a crocodile, and a turtle. Two are crawling, green-scaled reptiles, and one is a

bird. As it happens (like humans and gorillas, relative to orangutans), the sparrow and crocodile are more closely related to each other than either is to the turtle. The two reptiles are more similar to one another, but they are similar simply because the birds, which originated from a group of reptiles, developed a set of specializations and flew away, leaving the green, scaly creatures behind. Since the kind of reptile from which the birds originated was related to the crocodile, it happens that the sparrow and crocodile, a few hundred million years later, are more closely related than either is to the turtle.

But does that mean that the sparrow is a reptile? No, it means it is closely related to reptiles; the reptiles subsume its group. If the word *bird* is to have any meaning, it must mean something different from the word *reptile.* Birds are birds; reptiles are a different kind of group, unified in this classification by *not* having evolved the specializations of birds.

We can go even farther back in biological history. Several hundred million years ago, a group of fish developed specializations of their limbs that enabled some of their descendants to venture out of the sea and onto land. A living representative of that group of teleost fish is the famous "living fossil," the coelacanth. Since all living land vertebrates (or tetrapods) are descended from that particular group of fish, it follows that if you compare a coelacanth, a human, and a tuna, the closest relatives are the coelacanth and the human, not the two fish.

Let us return to the apes, then. The argument is that humans are apes because we belong to the group that produced chimpanzees and orangutans; and because we are more closely related to some apes than those apes are to other apes, we fall within that category. But we also belong, in a larger sense, to the group that produced coelacanths and tuna—namely, fish—and we are more closely related to some fish (coelacanths) than those fish are to other fish (tunas). We fall (by virtue of being tetrapods) within that category as well.

In other words, *we are apes, but only in precisely the same way that we are fish* (figure 7.3).

Doesn't seem quite so profound now, does it?

This is not so much a revelation about our basic natures as a revelation about how we name zoological groups. As constituted by a group of related species that a subset has evolved away from, the species that remain unchanged will constitute a paraphyletic category. They may look similar, but they are defined on the basis of lacking the specializations of the other group—tetrapods in the case of paraphyletic fish, birds in the case of paraphyletic reptiles, and humans in the case of paraphyletic great apes.

What appeared at first to be a revelation about our animal nature is instead a revelation about how we box up nature to make sense of it. Making sense of the world through classification is a fundamentally human act, and each human group does it in a different way and thus imposes a distinctive structure and meaning on the world.

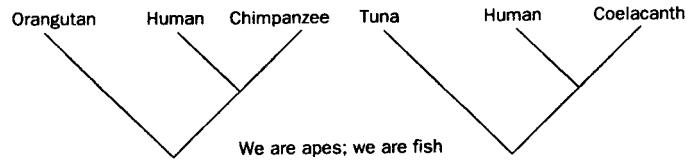

Figure 7.3 The paraphyletic nature of the category "apes" is equivalent to the paraphyletic category "fish" and the position of humans within it. Thus, the phylogenetic argument that "we are apes" because we fall into that category is precisely as valid as the argument that "we are fish."

Modern science classifies animals by two criteria, descent and divergence. This practice sometimes creates confusion, such as the occasional paraphyletic category, in which divergence takes precedence over proximity of descent. A school known as cladism prefers to classify by descent only, and thus would recognize only closest relatives—and would bury the categories great apes, reptiles, and fish. Ultimately this is a philosophical decision, is unresolvable by recourse to data, and displays the variation of ideas about classifying among scientists (Hull 1970). Scientists are a human society, and like other human societies, they make sense of their world by organizing it into groups.

But in the case of apes and humans, this has more to do with the work of Émile Durkheim and Marcel Mauss than with the work of Charles Darwin and Thomas Huxley.

CONCLUSIONS

The similarity revealed by genetics between humans and apes is interesting but not profound. The meaning imparted to that similarity is derived from (1) the nature of DNA and the scalar, decontextualized comparisons it affords, and (2) our unfamiliarity with the nature of genetic comparisons.

What seems like a paradox, the genetic similarity and the anatomical difference, is itself largely a consequence of three hundred years of anatomical study and an order of magnitude less of genetic study. In historical perspective, however, the paradox vanishes. When Edward Tyson published his *Ourang-outang, sive Homo sylvestris, or the Anatomy of a Pygmie* in 1699, he explicitly was struck by its extraordinary *similarity* to the human form. It was precisely that physical correspondence that led scholars of the eighteenth century, notably Lord Monboddo and Jean-Jacques Rousseau, to consider the chimpanzee as merely a different human variety, indeed within our own species. *When anatomical studies of the apes were a novelty, apes were considered to be astonishingly similar to humans.*

Centuries later, we have become familiar with the apes physically. They are exceedingly similar to, yet diagnosably different from, the human. Their similarities to us are boring; their differences are interesting.

Genetically, apes are less familiar, but the same pattern is evident. We are similar to them, yet diagnosably different from them. The combination of the novelty of genetics and its cultural power has permitted the observation that we are similar to the apes to acquire a new vitality, but it most often leads to recapitulating eighteenth-century philosophy. To the writers of a contemporary, popular biology book, half of our species are "demonic males," a factoid "written in the molecular chemistry of DNA" (Wrangham and Peterson 1996: 198), although without any Southern blots or sequence data to substantiate the point.

To another writer, we are a "third chimpanzee" (Diamond 1991), a conclusion easily derived by overstating the similarities between humans and chimpanzees. Indeed, when physical and behavioral comparisons were novel, Lord Monboddo came to a similar conclusion:

> That the Orang Outang is an animal of the human form, inside as well as outside: That he has the human intelligence, as much as can be expected in an animal living without civility or arts: That he has a disposition of mind, mild, docile, and humane: That he has the sentiments and affections peculiar to our species, such as the sense of modesty, of honour, and of justice; and likewise an attachment of love and friendship to one individual, so strong in some instances, that the one friend will not survive the other: That they live in society, and have some arts of life; for they build huts, and use an artificial weapon for attack and defence, viz., a stick; which no animal, merely brute, is known to do. They shew also counsel and design, by carrying off creatures of our species, for certain purposes, and keeping them for years together, without doing them any harm; which no brute creature was ever known to do. They appear likewise to have some kind of civility among them, and to practice certain rites, such as that of burying the dead. (Monboddo 1774: 275)

To a third, our newfound genetic similarity means "we are apes" (Dawkins 1993)—and in spite of the slightly ambiguous referent, this British biologist presumably means "we" *Homo sapiens*.

And to some animal rights activists, the same genetic similarity means apes should be accorded human rights (Cavalieri and Singer 1993), in spite of the facts that (1) they are not human, (2) we cannot even guarantee human rights to humans, and (3) we do not base the allocation of rights on genetic similarity (Marks 1994b).

Examining the empirically well-attested genetic similarity of humans and apes can show somewhat paradoxically that the genetic similarity is a constructed fact. Its meanings are contestable and not "read" from nature. Ultimately this may serve as an example of the reciprocal illumination shed by genetics and anthropology, which may someday result in the development of a truly molecular *anthropology*.

NOTES

The material in this paper is derived from my book *What It Means to Be 98% Chimpanzee* (Berkeley: University of California Press, 2001). My deepest appreciation goes to Alan Goodman and Deborah Heath for the invitation to participate in the symposium, their incisive comments on this paper, and their brilliant editing, as well to the other participants for their helpful input. This paper is dedicated to the memory of Ashley Montagu (1904–1999) and Sherwood Washburn (1912–2000).

1. The issue of "resolution of the trichotomy" (i.e., determination of the closest relatives among humans, chimpanzees, and gorillas) is off the present subject. While some data certainly do associate humans and chimps exclusively of gorillas (notably mtDNA [Gagneaux et al. 1999]), these data are frequently the most problematic, often being based on unarticulated assumptions or containing internal contradictions (Marks 1994a, 1995). Most molecular data actually fail to associate any pair (see Ruano et al. 1992; Johnson and Coppen 1999), and much of the newest data links chimps and gorillas, as per the traditional arrangement (Dangel et al. 1995; Deinard et al. 1998; Djian and Green 1989; Fracasso and Patarnello 1998; Livak et al. 1995; Marks 1993; Meyer et al. 1995; Retief et al. 1993). The genetic linkage of humans specifically to chimpanzees is thus not so much a constructed fact as a false one.

2. Marks et al. 1988; Sarich et al. 1989; Sibley et al. 1990; Marks 1991. Of more esoteric interest is the claim of Caccone and Powell (1989) to have replicated the findings of Sibley and Ahlquist (1984, 1987). They claimed to have obtained the same numbers as those reported by Sibley and Ahlquist and to have obtained the same tree, thus ostensibly validating both the previous study and the technique itself. In fact they matched numbers that the previous authors admitted had been falsified, which is itself quite a feat; and they matched them with a different measure (δT_m versus $\delta T_{50}H$)—as if three inches could match three centimeters. Sibley and colleagues (1990) published their true values comparable to those reported by Caccone and Powell (1989), and these neither match nor resolve the phylogeny. The technique is now in disrepute and rarely used (see Marks 1991 for a lengthy discussion).

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