Our Chimp Cousins Get That Much Closer

Mitochondrial DNA data suggest chimps are closer to us than to gorillas—but a 20-year struggle isn't finished

ARE CHIMPS MORE CLOSELY RELATED TO gorillas or to human beings? That seemingly innocent question provoked a war among evolutionary specialists that has lasted more than 20 years. Now one side has new ammunition—in the form of mitochondrial DNA studies showing that chimps have more in common with us than with gorillas. This data, coming from independent U.S. and Japanese teams, is consistent with a growing body of results based on nuclear DNA sequences, prompting one chimp-human partisan, Charles Sibley of San Francisco State University, to claim, "We've won the war."

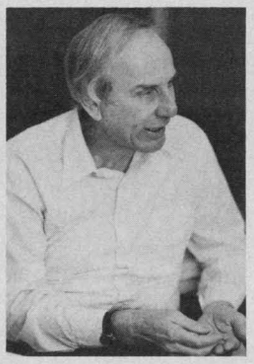
But don't assume a surrender treaty is about to be signed. The embattled minority who think chimps are closer to gorillas has by no means conceded defeat. "I think the attempt to close this question is extremely premature," says Jonathan Marks, professor of anthropology at Yale, who questions the quality of almost all the DNA data now available—and points to a few studies that suggest a chimp-gorilla connection.

The first shot in the war was fired in the early 60s, when Morris Goodman of Wayne State University undermined the conventional classification system that put humans in one family—Hominidae—and chimps and gorillas in a second family: Pongidae. Goodman's work, based on cross reactions between immunologic blood proteins, suggested humans are very closely related genetically to the two species of African apes and that all three belong in one family.

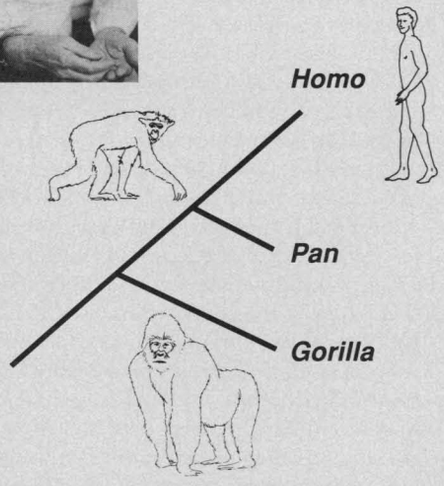
Most evolutionists thought Goodman's data were shaky, and they stuck to the old system. But molecular biologists persevered. In 1984, Sibley and Jon Ahlquist, both then at Yale, published DNA hybridization data showing that not only were we close to the apes, but that chimps actually had more in common genetically with humans than with gorillas.

DNA hybridization is based on seeing how much of one set of DNA fragments will "hybridize," or bind to another, providing an indication of how many sequences they share. But it is tricky to do, tricky to interpret, and less precise than having the actual sequences. Partly as a result, the Sibley and Ahlquist results were subjected to a withering bombardment from Marks and Vincent Sarich of the University of California at Berkeley. Marks and Sarich questioned their methods of data analysis and even charged that Sibley and Ahlquist had falsified data.

It wasn't long afterwards, however, that actual DNA sequences from nuclear genes began coming in that offered strong support for close ties between chimps and humans. Perhaps the best work came from Goodman and his colleagues, who looked at some very long sequences—more than 10,000 bases at last count. In 1987 they reported that there is only a 1.6% difference between humans and chimpanzees in non-coding regions of the globin gene cluster. By contrast, there is a 2.1% difference between chimps and gorillas in the same sequences. Other studies tended in the same direction.



Three-way split. *Maryellen Ruvolo's mitochondrial DNA sequences suggest our family tree looks like this—supporting Morris Goodman, who overturned the conventional classification.*



The recent work by a team from Harvard University, the University of Michigan, and Texas A&M University extends those results to extra-nuclear DNA for the first time in a clear-cut fashion. The mitochondrion is the cytoplasmic organelle that processes energy for the cell, and its DNA includes genes for ribosomes, transfer RNAs, and energy-processing enzymes. The U.S. team, led by Harvard molecular evolutionist Maryellen Ruvolo, sequenced a 700-base-pair stretch of a gene for one of those enzymes: cytochrome oxidase subunit II. In work reported at the Fourth International Congress of Systematic and Evolutionary Biology, held in Maryland in July, they find a 9.6% difference between chimps and humans in the enzyme-gene sequence; chimps and gorillas differ by 13.1%.

A separate group led by Satoshi Horai at the National Institute of Genetics in Japan also reported mitochondrial DNA results in July showing "confidently," they say, "that the chimpanzee is the closest species to human." Their findings, reported at the International Congress of Primatology meeting in Japan, were based on an analysis of 4900-base fragments of mitochondrial DNA, including regions that encode 11 transfer RNAs and four proteins.

This expanding body of data has convinced many in the field that the case is, if not closed, rapidly closing. "The data are getting stronger and stronger, and anybody with an open mind would almost certainly come down in favor of human and chimp being closer than chimp and gorilla," says Jeffrey Powell, a Yale evolutionary geneticist whose own DNA hybridization study found a close association between chimps and humans.

But two of the original partisans—Marks of Yale and Sarich of Berkeley—say their opponents haven't proved their case. "I dare say I'm probably in a minority, but there's no way—no way—the case is closed," says Sarich. Both he and Marks argue that almost all the nuclear DNA data is suspect in some way. The only persuasive evidence, they say, is Goodman's globin-gene studies, and those are contradicted by another persuasive study published last year by Harvard Medical School physiologist Howard Green.

Green found that the chimp and the gorilla share four repeated portions of about 30 bases each in the gene for involucrin, a skin protein. Humans do not share those sequences. What is more, humans and chimps do not share any repeats in the involucrin gene that are not also shared by other species.

But Green's results arein a minority, leading some nonpartisans to think chimps will ultimately prove to be closer to humans. Roy Britten, a respected molecular biologist at the California Institute of Technology, says: "I think that the chimp is going to be closest to humans." But, Britten adds, "We just haven't demonstrated it yet." And what would it take to settle the question? "I suppose very large amounts of sequence data would settle it," says Britten. ■ ANN GIBBONS