

UCSD biologists compile genetic history of apes and humans; 'Family Tree' shows that humans had brush with extinction

April 26, 1999

EMBARGOED FOR RELEASE 2 P.M. PST APRIL 26, 1999

Contacts: Pascal Gagneux, lead author, (619) 534-1346; Christopher Wills, second author, (619) 534-5474; David Woodruff, senior author, (619) 534-2375

University Communications, (619) 534-3120

UCSD BIOLOGISTS COMPILE GENETIC HISTORY OF APES AND HUMANS; 'FAMILY TREE' SHOWS THAT HUMANS HAD BRUSH WITH EXTINCTION

A new report by evolutionary biologists at the University of California, San Diego shows that the history of humans is quite different from that of chimpanzees, bonobos and gorillas. The genetics study also supports the controversial idea that humans have had at least one dramatic population reduction during the last million years. The geographic patterns of genetic variation discovered also hold clues to the origin of certain animal-borne diseases, including HIV-1.

The international team of researchers, led by geneticists at UCSD, have completed an unprecedented survey of genetic variation in humans and the African great apes (chimpanzees, bonobos and gorillas) revealing for the first time the full extent of the striking differences in patterns of variation between the species. The new family tree shows that the great ape species are far more variable than the human species. One social group of 55 chimpanzees in West Africa, for example, has much more variation than the entire human species.

The distinct levels of genetic variation reflect differences in the age and history of each species. It is now clear that human genetic history is dramatically different from the histories of our closest relatives.

The study, published in the April 27 issue of the Proceedings of the National Academy of Sciences, shows that our own population has undergone one or several dramatic reductions in numbers sometime during the last million years.

"There was a period in our ancient history during which we came close to extinction," said UCSD Biologist Christopher Wills, second author on the paper.

"Despite their much smaller numbers and restricted ranges, the African apes retain much more genetic variation than humans," said lead author Pascal Gagneux, who conducted the research as a doctoral student in the laboratory of David Woodruff, the paper's senior author. "The family tree also shows that the human branch has been pruned. Our ancestors lost much of their original variability."

The reasons for this loss in variation are unknown, but they likely involved a significant reduction in numbers due to one or a combination of disease, environmental disaster or conflict

The conclusions were based on a comparative study of 1,158 unique mitochondrial control-region DNA sequences found to date in these four species of apes. As mitochondrial DNA is inherited maternally, it permits researchers to reconstruct the history of the females of a species. The results support the "mitochondrial Eve" hypothesis in the history of human species.

The new data also shed light on the origin of HIV-1. Several researchers have concluded that HIV-1 originated in central African chimpanzees after three were discovered with chimpanzee Immunodeficiency Virus (SIVcpz).

Gagneux notes that the understanding of the evolution of chimpanzee viruses, and the reason why some can infect humans and cause serious disease, will depend on a solid understanding of the natural history of chimpanzee populations and their genetic diversity.

The new study is the first with large numbers of all four ape species of known geographic origin. The genetic material from wild apes was obtained non-invasively from DNA amplified from shed hair and fecal samples.

The results confirm that chimpanzees and bonobos are our closest living relatives. The data suggest that they, and gorillas, are now threatened with extinction and their survival depends on human help. The new family tree identifies genetically different clusters of apes, each with its own irreplaceable genetic attributes and evolutionary history. These genetic findings have important implications for both the conservation of the remaining wild apes and the reproductive management of those in captivity.

"Conservation of the remaining great apes is critical," said Woodruff, "as they still have so much to teach us about ourselves."

Pascal Gagneux, the leader of the scientific team and an authority on chimpanzee evolution, currently is a post-doctoral fellow in Ajit Varki's laboratory at the UCSD Cancer Center. Second author Christopher Wills, a leading evolutionary biologist and author of the 1998 book *Children of Prometheus* (Perseus Books) on human evolution, developed a powerful computer program to analyze the pattern of variation at the half-million genetic sites studied. Senior author David Woodruff, an evolutionary biologist and conservation geneticist, developed non-invasive methods of genotyping wild chimpanzees. He published the first studies of their natural genetic variability.

Other co-authors, from Germany, Switzerland and the United States, contributed DNA samples from across Africa.

The study was supported by the Swiss and US National Science Foundations and the National Institutes of Health.

Note: Copies of the paper may be obtained by calling the National Academy of Sciences Office of News and Public Information at (202) 334-2138.

(April 26, 1999)