

Mountain gorillas stuck in genetic bottleneck

Full genome reveals surprising level of inbreeding and could aid conservation efforts.

Boer Deng

09 April 2015



Gorilla Doctors/UC Davis

Mountains gorillas live in two isolated populations in Central Africa.

Kaboko, a mountain gorilla, had a rough start in life: in 2007, the three-year-old orphan was caught in a poacher's snare in the Democratic Republic of the Congo. Rescuers, who were forced to amputate his hand to treat his injuries, gave him a name that means "one missing an arm" in a local language.

Kaboko died in 2012, but his DNA lives on. Researchers have used genetic information from him and six other animals to construct the first complete genomic sequence for the mountain gorilla (*Gorilla beringei beringei*), which they report in *Science* along with the genome of the closely related eastern lowland gorilla (*Gorilla beringei graueri*)¹. The data may help conservationists to improve the plight of the critically endangered mountain gorilla, which is found only in Central Africa.

The genomes reveal that the genetic diversity of both subspecies has been declining for 100,000 years. That is surprising, says Ajit Varki, a molecular biologist at the University of California, San Diego. "You have animals that have no predators and easy sources of food — in a way they have everything going for them — and yet they have been heavily pressured," he says. Some of that pressure is probably attributable to natural changes in the extent of Central Africa's forests, and some to the emergence of humans, but Varki says the relative balance of these factors in the distant past is hard to determine.

The more recent impact of humans is clear. Heavy hunting caused the gorilla population to drop to fewer than 300 animals by the 1970s². The number has since risen to more than 800, thanks to conservation efforts promoted by primate researchers such as Dian Fossey.

Still, the latest study reveals that genetic diversity of eastern gorillas remains low. The paired chromosomes of an individual mountain gorilla typically have the same DNA sequence for 34.5% of their length. The figure in eastern lowland gorillas is even higher, at 38.4%. Both subspecies have much lower genetic diversity than the western gorilla (*Gorilla gorilla*, 13.8% shared sequence) and even the children of human parents who are first cousins (11%)³.

Worth the wait

The gorilla is not the first non-human primate to have its complete genome sequenced — that was the chimpanzee (*Pan troglodytes*), in 2005⁴. But mountain gorillas were among the most difficult primates to study. Unlike other great apes, no mountain gorillas live in captivity. In the wild, the animals are found in only two places: the Virunga Volcano Massif and the Bwindi Impenetrable Forest, two habitats some 30 kilometres apart that straddle the Democratic Republic of the Congo, Rwanda and Uganda.

Researchers spent six years waiting for permission to study mountain-gorilla blood samples collected by the charity Gorilla Doctors, which treats injured wild gorillas. The delay was caused by the strict paperwork required by the Convention on International Trade in Endangered Species of Wild Fauna and Flora, [a treaty that governs the flow of such materials](#).

But that long wait did have some benefits. “Technology and our knowledge of genomics were getting better during all that time,” says Peter Sudmant, a geneticist at the University of Washington in Seattle and a co-author of the study. As a result, the mountain-gorilla genome is of higher quality than previously published genomes of other gorilla subspecies.

A complete mountain-gorilla genome will help conservationists to determine the degree to which genetic bottlenecks have increased the animals' susceptibility to disease and reduced their ability to cope with environmental change.

“On top of there being so few, these gorillas breed very slowly, and the population grows just about 1% a year,” says Damien Caillaud, a research scientist at the Dian Fossey Gorilla Fund International, a conservation group in Atlanta, Georgia. “That means if we’re not careful, the numbers could very easily go the other way.”

Nature | doi:10.1038/nature.2015.17277

References

1. Xue, Y. *et al. Science* **348**, 242–245 (2015).
2. Weber, A. W. *Biol. Conserv.* **26**, 341–366 (1983).
3. Woods, C. G. *et al. Am. J. Hum. Genet.* **78**, 889–896 (2006).
4. Mikkelsen, T. S. *et al. Nature* **437**, 69–87 (2005).