

Mountain gorillas' genome sequenced in hope of saving declining species from extinction

Mountain gorillas (*Gorilla beringei beringei*) are among the most iconic endangered species in the world and, as such, have become a prominent focus for conservation.

Surviving in only two small and fragile populations in central Africa, there are currently estimated to be about 800 individuals, with just over half living in three national parks on the Virunga mountain range.

The Virunga population of gorillas was made famous by primatologist Dian Fossey's book and subsequent film, *Gorillas in the Mist*. Numbers have doubled from a low point of about 253 gorillas in 1981 thanks to conservation efforts and support from the public, but they remain at risk of extinction.

The drop in population size led to extensive inbreeding which raised concerns that a small gene pool could harm the gorillas' long-term future, particularly their ability to survive infectious diseases and cope with environmental change.

But little work has been done on their genetics, or to establish how they evolved from eastern gorillas (*G. beringei*).

Now scientists have discovered inbreeding has actually benefitted mountain gorillas by removing many harmful genetic variations. They are also genetically adapted to living in small populations.

The authors of the findings, published in the journal *Science*, said it is the first project to sequence whole genomes from mountain gorillas.

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