

## Chimp populations show great genetic diversity, with implications for conservation

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The researchers found chimpanzees from different populations were substantially more different genetically than humans living on different continents.

Chimpanzee populations living in close proximity are substantially more different genetically than humans living on different continents, according to a study published in *PLoS Genetics*. Research conducted by scientists from the universities of Oxford and Cambridge, the Centre Pasteur du Cameroun, and the Biomedical Primate Research Centre suggests that genomics can provide a valuable tool for chimpanzee conservation, with the potential to identify the population of origin of an individual chimpanzee or the provenance of a sample of bush meat.

Common <u>chimpanzees</u> in <u>equatorial Africa</u> have long been recognized as falling into three distinct populations, or sub-species: western, central and eastern chimpanzees. A fourth group, the Cameroonian chimpanzee,



has been proposed to live in southern Nigeria and western Cameroon, but there has been considerable controversy as to whether it constitutes a distinct group.

Scientists examined DNA from 54 chimpanzees, measuring the DNA at 818 positions across the genome that varied between individuals. Analysis of patterns in the data showed Cameroonian chimpanzees to be distinct from the other, well-established groups. Dr Rory Bowden, who led the study, said: "These findings have important consequences for conservation. All great ape populations face unparalleled challenges from habitat loss, hunting and emerging infections, and conservation strategies need to be based on sound understanding of the underlying population structure. The fact that all four recognized populations of chimpanzees are genetically distinct emphasizes the value of conserving them independently."

The authors also contrasted the levels of genetic differentiation between the chimpanzees from the different groups with those based on similar data for humans from different populations. Even though all the chimpanzee populations lived in relatively close proximity, with the habitats of two groups separated only by a river, chimpanzees from different populations were substantially more different genetically than humans living on different continents.

Professor Peter Donnelly, Director of the Wellcome Trust Centre for Human Genetics at the University of Oxford, and a senior author on the study, said: "Relatively small numbers of humans left Africa 50,000-100,000 years ago. All non-African populations descended from them, and are reasonably similar genetically. That chimpanzees from habitats in the same country, separated only by a river, are more distinct than humans from different continents is really interesting. It speaks to the great genetic similarities between human populations, and to much more stability, and less interbreeding, over hundreds of thousands of



years, in the chimpanzee groups."

The conservation implications of the study could extend to other species. New techniques such as next-generation sequencing, which have become available since the study was initiated, will allow a catalogue of genetic variation to be obtained cheaply and easily for other species, simply by sequencing a small number of individuals. Such a catalogue could then be used to perform a study like this one, to identify genetically distinct groups, and subsequently to develop simple and cheap tests of population of origin.

Dr Nick Mundy, from the University of Cambridge, said: "Because they are humans' nearest relatives, the structure and origins of chimpanzee populations have long been of wide interest. Future studies will be able to use genome data to uncover the adaptations that are unique to the Cameroonian chimpanzees."

**More information:** Bowden R, MacFie TS, Myers S, Hellenthal G, Nerrienet E, et al. (2012) Genomic Tools for Evolution and Conservation in the Chimpanzee: Pan troglodytes ellioti Is a Genetically Distinct Population. PLoS Genet 8(3): e1002504. doi:10.1371/journal.pgen.1002504

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