

GREAT APE GENETIC DIVERSITY AND POPULATION HISTORY

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Humans belong to a larger group of species and subspecies called the great apes. These include four subspecies of chimpanzee, the bonobo, two species of gorillas with two subspecies each and two species of orangutan. Great apes fascinate us because their facial expressions and behavior reminds us about ourselves. Their genomes are also extremely similar to those of humans, sharing between 97% (orangutan) and 99% (chimpanzee) of the DNA sequence. These differences in the DNA sequence are produced by random mutations that accumulate slowly over time.

The chance of mutation per generation is only one in 100 million, but because our genome consists of 3 billion base pairs, each individual still is born with about 60 new mutations per generation. Because mutations accumulate

regularly over time, the number of differences observed between species can be used to measure how long time ago they initially went their separate ways. In our group we use statistical modeling and bioinformatics approaches on whole genome sequences of all the great apes in order to infer their evolutionary history and the Darwinian selection that shaped the other great apes and made us human.

DIVERSITY AMONG GREAT APES

Advances in DNA sequencing technology recently made it possible to determine the complete genome of many individuals of each of the great apes and thus look into the genetic diversity of each species. Figure 1 shows the distri-

bution of each species except humans. Studying 98 full genomes we found that humans and bonobos have very little genetic diversity, whereas the genetic diversity of orangutans and gorillas is three times larger than that of humans. This tells us that over evolutionary time, most great apes species were more numerous than humans and that human dominance is only a very recent phenomenon. The higher levels of diversity implies most of the great apes species have a larger evolutionary potential than humans because they carry more genetic variants that allow them to adapt to any changes to their environments.

POPULATION SIZES THROUGH TIME

The history of a single genome can be inferred from how the genetic diversity is distributed along the genome. Figure 2 shows how the effective numbers of breeding individuals have changed over time in the different great apes species. We have little power to infer what happened over the past 30 thousand years but much better power from 30 thousand years to 1 million years back in time. The Figure shows that humans were less numerous than the other great apes before 100 thousand years ago. At least among the ancestors of modern humans; several species on the human lineages are only known from the fossil record and only those that have left descendants in modern humans, or those we can obtain ancient DNA from, can we analyze in this way. For those extinct human species we do have DNA from, Neanderthals and Denisovans, similar patterns are seen with very small effective population sizes (data not shown).

Within the last 100 thousand years, where modern humans spread out of Africa and colonized the rest of the world, creating the ethnic groups we know today, there has been an explo-

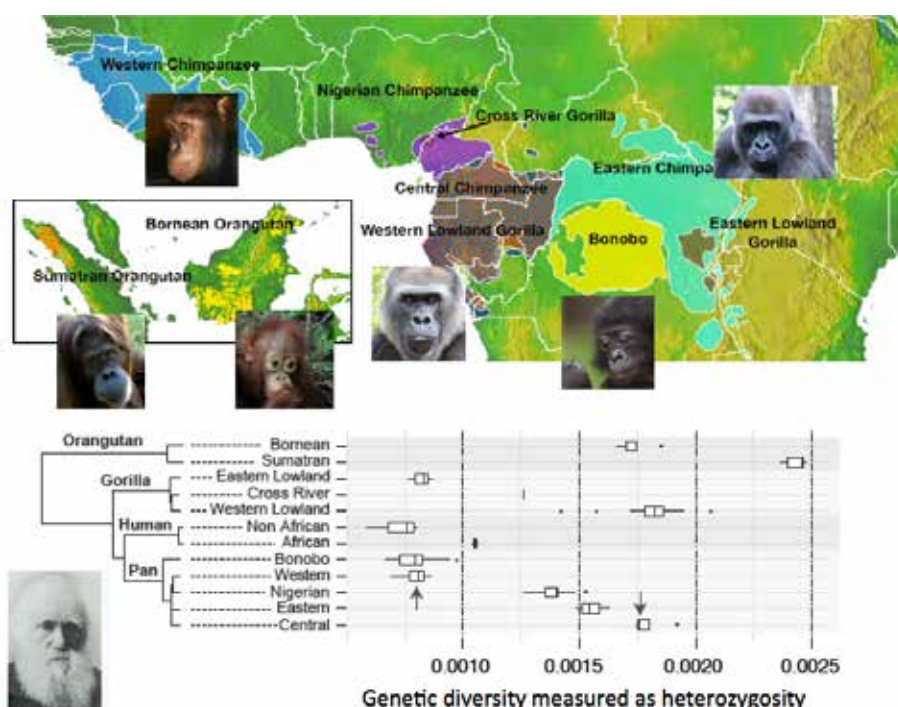


Figure 1. Current distribution of great ape species and genetic diversity. Adapted from Prado-Martinez et al. 2013.

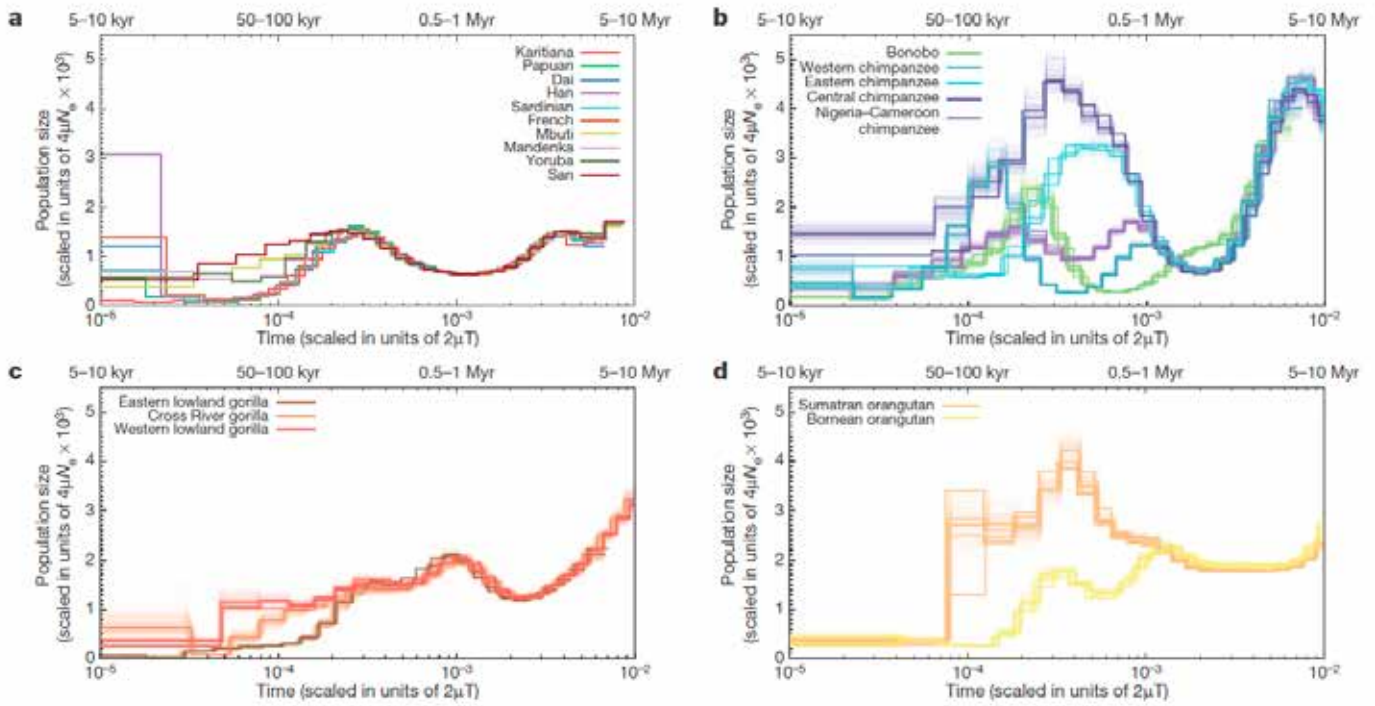


Figure 2. How the effective number of reproducing individuals has varied over the past million years in humans and other great apes species. Figure from Prado-Martinez et al. 2013.

sion in the human population size and at the same time a reduction in the population size of the other great apes. Genetic evidence also reveals that the exit from Africa was associated with a population bottleneck with very few reproducing humans. As a consequence there is far more genetic variation within African populations than outside of Africa, despite the fact that more than six of the seven billion humans alive today live outside of Africa. Today it is clear that the population sizes of most other great ape species have decreased dramatically, in most cases due to habitat destruction and hunting by humans.

SPECIATION TIMES

Using evolutionary analysis of whole genomes it is possible to measure when the different species of great apes diverged from one another. Because the individuals from the ancient population that split into new species were related through ancestors that lived further back in time, this speciation time is more recent than the time at which genomes initially started to diverge. Figure 3 shows our current best estimate of the different speciation times and the number of reproducing individuals at different times. A more detailed analysis of the speciation processes reveal that the

speciation of human and chimpanzee did not happen at once but may have extended over a million years where the new species diverged while still exchanging some genes.

This type of speciation is reminiscent of humans and Neanderthals. These diverged 500 thousand years ago, but when they met again around 60 thousand years ago exchanged genes such

that everybody not of African origin carries a couple of percent Neanderthal DNA. Chimpanzees and bonobos, on the other hand, appear to have split apart abruptly around 1-2 million years ago. This may coincide with the formation of the present run of the Congo river, which separates bonobos from chimpanzees and may have been the barrier that lead to their speciation.

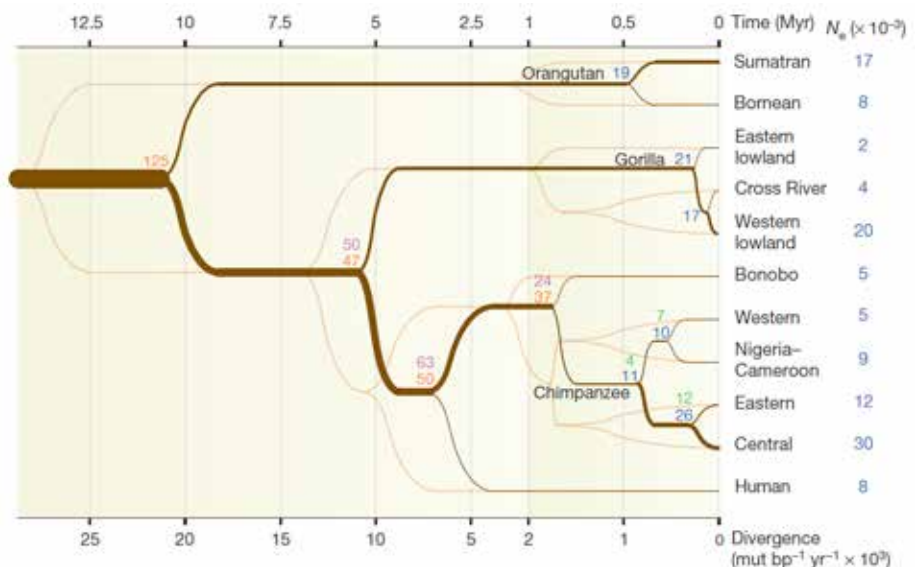


Figure 3. Divergence times and time to speciation for the different great apes species. Figure from Prado-Martinez et al. 2013.

OUTLOOK

Having established with some certainty the speciation and population history of the great apes we are now addressing the challenge of identifying the underlying evolutionary forces leading to adaptation and speciation in the great apes. The great apes constitute an excellent model for understanding these evolutionary questions in general. This is because the great apes are so closely related that their genomes behave in similar ways, yet they are sufficiently diverged that they are independent outcomes of the evolutionary process.

This means that we can look for patterns of genetic diversity shared among the different species. We recently became aware that specific regions of the X chromosomes in many great apes species experience strong Darwinian evolution. By contrasting the different great apes in these regions we could form the new hypothesis that speciation in great apes is much dependent on an ongoing fight between the Y and the X chromosome in male meiosis for the transmission to the next generation. This hypothesis is presently being tested.

We also find evidence that Darwinian selection has had a larger impact

on great apes evolution than what is generally believed and we have evidence to support that such adaptive evolution is limited by the availability of new mutations. This means that smaller populations will adapt more slowly than larger populations. Today, the human population is big enough that we expect every possible mutation to appear every generation, and our species current evolution is thus not likely to be limited by the waiting time for new mutations to enter our gene pool – a situation that was not the case in our earlier evolutionary history.

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