

Genetic archaeology finds parts of our genome more closely related to orangutans than chimps

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In a study published online today in *Genome Research*, in coordination with the publication of the orangutan genome sequence, scientists have presented the surprising finding that although orangutans and humans are more distantly related, some regions of our genomes are more alike than those of our closest living relative, the chimpanzee.

The [fossil record](#) helped to establish evolutionary relationships and estimate divergence times of the primate branch leading to humans, but not until the advent of [genome](#) sequencing technology has it been possible to learn more detail about speciation times, genetic and phenotypic divergence times, and the [genetic variation](#) present in [common ancestor](#) species.

With the addition of the orangutan to the collection of sequenced primate genomes, an international group of scientists led by Mikkel Schierup and Thomas Mailund of Aarhus University in Denmark set out to shed light on these questions in primate evolution. "There remains signals of the distant past in DNA," said Mailund, "and our approach is to use such signals to study the genetics of our ancestors."

When a population "splits", the genetic variation they each inherit from the common ancestor will change over time as the populations diverge, possibly giving rise to two different species. Because humans, chimps, and [orangutans](#) all have a common ancestor, it is possible that humans

and orangutans may still share genetic variants that were later lost in more closely related primates.

Mailund and colleagues employed a mathematical framework to find regions of the orangutan genome where humans and orangutans are more closely related than humans and [chimpanzees](#) as a result of a phenomenon called incomplete lineage sorting (ILS). ILS can reveal information about the time of speciation events, as well as the genetic diversity of the ancestral species.

The study found ILS with orangutan and chimp in approximately 1% of the human genome. *"n about 0.5% of our genome, we are closer related to orangutans than we are to chimpanzees," Mailund said, "and in about 0.5%, chimpanzees are closer related to orangutans than us."*

Schierup explained that because humans and orangutans split millions of years prior to the human/chimp split, the presence of ILS suggests that the ancestral species of human and chimps maintained high [genetic diversity](#), in contrast to the genetic bottleneck humans are believed to have experienced following divergence from chimps.

As primates along the human lineage diverged, the genetic variation of the common ancestors disappeared long ago and was replaced by new variation. Schierup noted that studies such as this are critical for understanding genetic variation in common ancestors that would be missed by examining population genetics of present day species.

More information: The manuscript will be published online ahead of print on January 26, 2011. Its full citation is as follows: Hobolth A, Dutheil JY, Hawks J, Schierup MH, Mailund T. Incomplete lineage sorting patterns among human, chimpanzee and orangutan suggest recent orangutan speciation and widespread selection. *Genome Res* [doi:10.1101/gr.114751.110](https://doi.org/10.1101/gr.114751.110)

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