Introgression from Gorilla caused the Human-Chimpanzee split

ABSTRACT: The Gorilla Genome Project (Scally, 2012) showed that 30% of the gorilla genome introgressed into the ancestor of humans and chimpanzees, and that the two species diverged through lineage sorting with 15% ending up in *Pan* and another 15% in *Homo*. That introgression is the *Pan-Homo* split, hybridization, which led to speciation as the new hybrid lineages became reproductively isolated from one another.

The NUMT on chromosome 5 fits perfectly with the introgression speciation model, it was formed from mtDNA that had diverged as much as ~4.5 Myr at the time of introgression, perfect fit with the *Gorilla*/*Pan-Homo* split, and the mtDNA fragments that formed it were inserted at the time of the *Homo*/*Pan* split, and ended up in both the *Gorilla*, *Pan* and *Homo* lineages around the same time period, 6 million years ago. (Popadin, 2017)

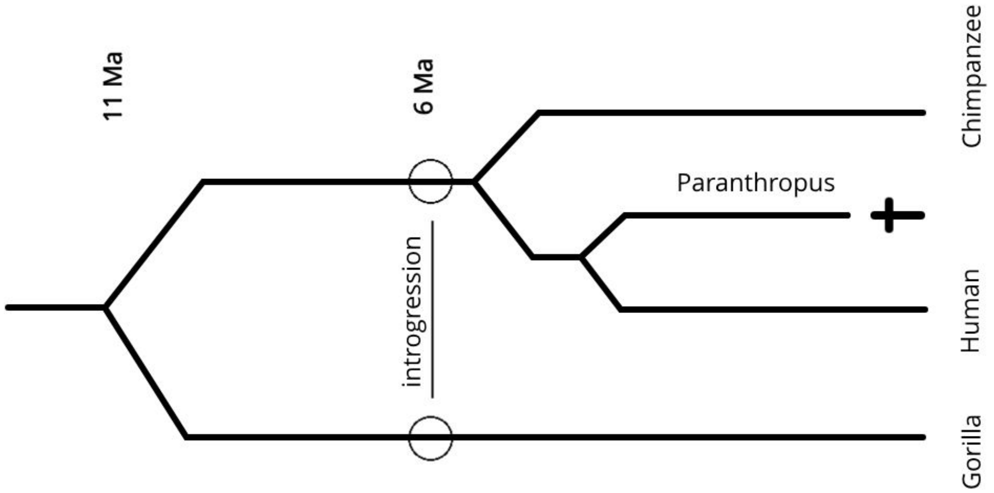

Fig. 1. Phylogenetic tree showing how introgression from *Gorilla* into the common ancestor of *Pan* and *Homo* led to hybridization, with multiple descendant lineages forming through lineage sorting.

Introduction

“During many years I collected notes on the origin or descent of man, without any intention of publishing on the subject, but rather with the determination not to publish, as I thought that I should thus only add to the prejudices against my views.” - Charles Darwin, 1971

Genome sequencing has been evolving along the law of accelerating returns (Kurzweil, 1999), the total amount of sequence data produced doubling approximately every seven months. (Stephens, 2015) With the genetic revolution, phylogenetic relationships are no longer limited to morphological characters, they can instead be read like an open book. This thesis will explore a new chapter, with roots in genetic data from the Gorilla Genome Project (Scally, 2012).

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The Gorilla Genome Project was the first complete genome of *Gorilla*, from a female western lowland gorilla, and it revealed a closer relationship between humans and gorilla than what morphological analyses had shown: in 30% of the genome, gorilla is closer to human or chimpanzee than the latter are to each other. At the time interpreted as incomplete lineage sorting (Scally, 2012), genetic evidence of gene transfer between *Gorilla*, *Pan* and *Homo* around the time of the *Pan-Hom*o split (Popadin, 2017) shows that the lineage sorting is more parsimonious as a result of introgression.

Introgression

Introgression is the transfer of genetic information from one species into the gene pool of another by repeated backcrossing of an interspecific hybrid with one of its parent species.

Introgression may lead to speciation, in which the new hybrid lineages become reproductively isolated from parental populations (Baack, 2007), and since *Pan* and *Homo* have diverged through lineage sorting, with 15% of the introgressed genes ending up in *Pan* and another 15% in *Homo*, it is reasonable to conclude that the introgression caused the *Pan-Homo* split, and therefore that it occurred at the time of the *Pan-Homo* split, around 6 million years ago.

Method

Phylogenetic relationships can be read from genome comparison. That there was gene transfer between *Gorilla*, *Pan* and *Homo* around the time of the *Pan-Homo* split can be read from a NUMT on chromosome 5 (ps5), which diverged between *Gorilla*, *Pan* and *Homo* at the time of the split. (Popadin, 2017) The ps5 NUMT as evidence of gene flow shows that introgression is a more parsimonious explanation for the lineage sorting from *Gorilla* than incomplete lineage sorting (ILS), and since *Pan* and *Homo* diverged through lineage sorting, it can be read that the introgression caused the *Pan-Homo* split. (Fig. 1)

Conclusion

The lineage sorting of 30% of the gorilla genome that is seen in humans and chimpanzees (Scally, 2012) is a result of introgression, an event that caused the speciation of *Pan* and *Homo* (Fig. 1), and the two lineages diverged through lineage sorting with 15% of the introgressed genes ending up in *Pan* and another 15% in *Homo*.

The genetic history tells only part of the story, what remains to be understood is what environmental and ecological factors triggered the hybridization.

References

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