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Fact Check: New "Complete" Chimp Genome Shows 14.9 Percent Difference from Human Genome

BY **CASEY LUSKIN** ON MAY 21, 2025

A groundbreaking paper in *Nature* reports the "Complete sequencing of ape genomes," including the genomes for chimpanzees, bonobos, gorillas, Bornean orangutans, Sumatran orangutans, and siamangs. I noted this in an article here yesterday, reporting that an evolutionary icon — the famous "1 percent difference" between the human and chimp genomes, touted across chose to bury that remarkable finding in technical jargon in their Supplementary Data section. Now for more on the scientific details.

You might be thinking, “Hey, weren’t these genomes sequenced long ago?” The answer is yes but also no. Yes, we had sequenced genomes from these species in the past, but, as the paper explains, “owing to the repetitive nature of ape genomes, complete assemblies have not been achieved. Current references lack sequence resolution of some of the most dynamic genomic regions, including regions corresponding to lineage-specific gene families.”

Or, as an accompanying explainer article puts it:

> In the past, scientists had deciphered segments of non-human apes’ genomes, but they had never managed to assemble a complete sequence for any species. In the current study, however, [Kateryna] Makova and her collaborators used advanced sequencing techniques and algorithms that allowed them to read long segments of DNA and assemble them into a sequence that stretched from one end of each chromosome to the other, without any gaps. “This has never been done before,” says Makova.

In other words, the complete ape genomes were never fully sequenced. And they used the human genome as a reference sequence, which made the ape genomes look more human-like than they actually were.

You Don’t Believe Me?

From the technical paper:

> Most previous genome-wide comparative studies of apes have been limited by the mapping of inferior assemblies to a higher quality human genome. Consequently, human reference biases were introduced.

This is consistent with what the National Center for Biotechnology Information said in 2007 about an early draft of the chimp genome:

> Contigs were assembled using the human genome as a guide, and are therefore “humanized” in their construction. This is an important distinction, as some sequences, such as insertions, deletions, and gene duplications, may not be accurately represented by the current chimpanzee assembly.

Thus, up until now, most versions of the chimp and other ape genomes were effectively “humanized” because they were “assembled using the human genome as a guide.” This effectively makes them appear more similar to the human genome than they truly are. Can these new drafts of ape genomes help fix the problem?

Problem Solved?

Another explainer article in *Nature* seems to suggest that these “complete” drafts of the ape genomes will prove that they are less similar to the human genome than has been claimed:

> Shortly after the first human genome sequence was finalized in 2003, a chimpanzee assembly was released. This was followed by assemblies for other great apes, such as the gorilla, Sumatran orangutan and bonobo, and small apes that are less closely related to humans than are great apes. These genomes offered a valuable opportunity to catalogue the genetic differences that have accumulated during the evolution of apes, including changes that are unique to humans. But, because these initial releases were incomplete drafts, comparisons could be made only between properly resolved portions of the genome. **These studies therefore focused only on relatively small differences, and excluded extremely repetitive sequences and large-scale structural differences, such as inversions and duplications of genomic sequences.** [Emphasis added.]

That last sentence seems to hint that previous comparisons between human and ape genomes “only focused on relatively small differences” and “excluded” the sections that entail “large-scale structural differences.” The explainer article notes that this study has “fully sequenced the genomes of six living ape species, enabling long-awaited comparisons of hard-to-assemble genomic regions.” Thus, one could expect that these newly “complete” ape genomes would reveal much greater differences compared to the human genome.

The New Ape Genomes and the Human Genome

What's odd is that as one reads the technical paper, a direct comparison between the ape and the human genomes is hard to find. This passage seems to be as close as it gets:

> Overall, sequence comparisons among the complete ape genomes revealed greater divergence than previously estimated (Supplementary Notes III–IV). Indeed, 12.5–27.3% of an ape genome failed to align or was inconsistent with a simple one-to-one alignment, thereby introducing gaps.

What exactly does this mean? Well, first they admit that "sequence comparisons among the complete ape genomes revealed greater divergence than previously estimated." But the technical *Nature* paper considers human beings to be an "ape," so implicit in this statement is their belief that comparing "ape genomes" includes comparisons between human and ape (i.e., non-human hominoid) genomes. So for the rest of this article, I'll call humans "humans" and I'll refer to non-human hominoids as "apes," just like most normal people do.

Interestingly, two preprints of the paper (v1 and v2) published last year on *BioRxiv* (which are presumably the versions of the manuscript submitted to *Nature* initially and after one round of revisions) preface this result with these two sentences:

> The oft-quoted statistic of ~99% sequence identity between chimpanzee and human holds for most of the genome when considering single-nucleotide variants (SNVs). However, comparisons of T2T genomes suggest a much more nuanced estimate.

T2T means examining "telomere to telomere" — i.e., examining the entire chromosomes throughout the genome. These sentences were evidently removed during revisions for the published version in *Nature* — an interesting editorial decision. So what is the paper saying about the difference between humans and chimpanzees?

As we'll see, the statement above — that "sequence comparisons among the complete ape genomes revealed greater divergence than previously estimated" — is true. But it doesn't reveal the extent of the differences between human and ape genomes that this study uncovered. So let me cut to the chase:

Look back at those numbers, "12.5–27.3%." The same numbers show up again buried deep in the Supplemental Data where they compare various ape to human genomes. They're findable if you know where to look, but should I say "buried" — or "hidden"? From what I can tell, the Supplemental Data reports that the ape genome that is most similar to the human genome is the chimpanzee genome. And it shows a 12.5 percent "gap-divergence" — i.e., difference — from the human genome! And when you look at the "gap divergence" where the human genome is the target and the chimp is the query, the difference is 13.3 percent. Let me be clear: According to this study, the human and chimp genomes aren't 98.8 percent the same (or 1.2 percent different) — as, for instance, the Smithsonian Institution's National Museum of Natural History claims (see my "Visitor's Guide" for more). In fact, they are no more than 87.5 percent similar — i.e., the human and chimp genomes are at least 12.5 percent different if not 13.3 percent different! In fact, the 13.3 percent difference is more relevant since this reflects how similar the whole human assembly is to the chimp genome.

What Exactly is the "Gap Divergence"

Before we go further, I want to explore exactly what the authors mean by "gap divergence" or "gap difference." The paper defines the "gap divergence" as follows:

> Gap divergence is defined as the fraction of positions in the target haplotype that are not aligned to the other haplotype, which could be due to biological processes (e.g., gene loss/gain and insertions/deletions), missing data, or technical problems (e.g., alignment failure due to SVs, repetitive elements, etc.).

So how do they determine the gap divergence? From what I can tell, it's based upon dividing the target genome within the genome alignment into 1 million base pair (1 Mbp) segments and seeing how many of the bases within each 1 Mbp segment have no aligning base within the query genome that has been aligned to it. If the entire 1 Mbp segment has no alignment by the target genome, it has gap divergence of 100 percent. If 10,000 bp have no alignment, it has gap divergence of 1 percent; if 1,000 bp have no alignment, it has gap divergence of 0.1 percent, etc. According to the study's results, the mean gap divergence in each 1 Mbp segment of the human genome (as target) aligned to the chimp genome (as query) is 12.5 percent. Thus, 12.5 percent of bases in the human genome have no aligning base in the chimpanzee genome within the whole genome-alignment.

The figure below — created for illustrative purposes and not from the study — helps show the differences between "SNVs" and "Gaps" between the two genomes:

30 nucleotides of target genome with 3 SNVs and 9 gaps relative to query genome
SNV divergence = 10%
Gap divergence = 30%
Total divergence = 40%

As you can see, the Gaps represent nucleotides or segments of nucleotides that simply don't exist in one genome or the other, while the SNVs represent nucleotides that do exist but are different. The two types of differences can be added up to calculate the total difference between the genomes.

An Upper Estimate

And why is there a range of 12.5 percent to 27.3 percent in the main text?

That's because the upper estimate of the non-alignability between the gorilla genome and human genome is a whopping 27.3 percent. In fact, if we look at the Supplementary Figure III.12, we find the following percentages of "gap-divergence" between various ape genomes when compared to the human genome (non-sex chromosomes):

- Sumatran orangutan (*Pongo abelii*) vs human: 15.4 percent and 16.5 percent "gap-divergence" (i.e., minimum difference)
- Gorilla (*Gorilla gorilla*) vs human: 17.9 percent and 27.3 percent "gap-divergence" (i.e., minimum difference)
- Bonobo (*Pan paniscus*) vs human: 12.5 percent and 14.4 percent "gap-divergence" (i.e., minimum difference)
- Chimpanzee (*Pan troglodytes*) vs human: 12.5 percent and 13.3 percent "gap-divergence" (i.e., minimum difference)

Do you see how easy it is to summarize that data? These are huge findings for both science and the wider culture, yet the technical *Nature* paper, and the two *Nature* explainer articles, failed to clearly bring out these points. They buried them in technical jargon and a lack of clarity deep in the Supplemental Data, and the sentence about "The oft-quoted statistic of ~99% sequence identity" was removed in the revisions of the paper. *Nature*, I feel confident in assuring you, is not a haphazardly edited journal. These were deliberate choices by someone during the editing process. The lack of clarity is simply incredible.

The Technical Details

Deep in the Supplementary Data we find Figure III.12 which explains the gap divergence between different species:

***Author’s note** (July 8, 2025): I post here the full chart from Figure III.12 of the Supplemental Data from Yoo et al. (2025) because some people are claiming that I originally omitted data from the chart because it somehow refuted my argument. No, that’s false. The only reason I posted only the human-ape genome comparisons (the top eight curves) was for simplification purposes because that was the only portion of the chart that was relevant to my argument; the intraspecific genetic differences (the bottom five curves) are irrelevant. My argument is not that human-ape genetic differences necessarily refute evolution; it’s that evolutionists who for decades have claimed humans are only 1 percent genetically different from apes were wrong. The top eight curves demonstrate my point very clearly. There was and is no data in the chart that negatively affected my argument, and I always linked to the Supplemental Data where people could see the complete dataset if they wish. There is nothing to hide here. In fact, I already extensively addressed objections regarding intraspecific genetic* *differences here before recent critics started commenting.*

The caption in the Supplemental Data reads: “Plots show 1 Mbp segments binned by gap divergence for each pairwise alignment,” where a pairwise alignment is an attempt to align two sequences to determine their degree of similarity or difference. Thus, we’re looking at a direct measure of the *minimum degree of difference* between the two genomes.

Adding in the Single Nucleotide Variation (SNV)

But there’s another type of variation between genomes also identified in the paper — single nucleotide differences (called “single nucleotide variations” or sometimes “short nucleotide variations” or SNVs). Again, buried in the Supplemental Data we find Figure III.11 which shows the percentage of SNVs between human and various ape genomes reported in this study. Here’s what they found:

- Sumatran Orangutan (*Pongo abelii*) vs Human: ~3.6 percent different
- Gorilla (*Gorilla gorilla*) vs Human: 1.9 percent – 2.0 percent different
- Bonobo (*Pan paniscus*) vs Human: 1.5 percent – 1.6 percent different
- Chimpanzee (*Pan troglodytes*) vs Human: 1.5 percent – 1.6 percent different

If we add the gap divergence to the SNV differences, we end up with these total degrees of difference between human and ape genomes:

- Sumatran Orangutan (*Pongo abelii*) vs Human: ~19 percent – 20.1 percent different
- Gorilla (*Gorilla gorilla*) vs Human: ~19.8 percent – 29.3 percent different
- Bonobo (*Pan paniscus*) vs Human: ~14.0 percent – 16.0 percent different

- Chimpanzee (*Pan troglodytes*) (target) vs. Human: ~14.0 percent different
- Human (target) vs. Chimpanzee (*Pan troglodytes*): ~14.9 percent different

So now what we're seeing is that there is about a 14.9 percent total difference between the human genome and the chimp genome. That represents a much greater degree of difference than the often-claimed statistic that we are only 1 percent genetically different from chimpanzees!

Is This the Final Word?

Undoubtedly more analysis is needed to determine the extent to which nucleotides exhibit "one-to-one exact matches" between the human and chimp genomes, even in the regions that could be more easily aligned. So I suspect that the degree of difference between human and chimp genomes may go up in the future.

For now, we can safely say that this latest study shows that the human and chimp genomes are at least 14.9 percent different. This means that the human and chimp genomes are at least *a full order of magnitude* more dissimilar than the public is typically told.

Of course we're talking here about the 44 non-sex chromosomes in the human genome. It's also worth noting that compared to chimps, the human Y chromosome has a whopping 56.6 percent gap divergence (and 3.9 percent SNV divergence), and the human X chromosome has 4.4 percent gap divergence (and 1.1 percent SNV divergence). But that too is all buried in the Supplemental Data.

These are all groundbreaking findings — and it's a shame that *Nature* would not report the data clearly and would make all of this so hard to find — using jargon that most non-experts won't understand. Why did they do this? It's important to realize that publishing scientific papers can be a bit like sausage-making: it's often messy, and the final form that you read usually represents compromise language that all of the authors, reviewers, and editors were willing to publish — and may not represent precisely how every author of a paper feels. So perhaps some authors of this study would have preferred to state the implications more plainly. But we can still ask, *Why didn't* Nature *state the results clearly and let the chips fall where they may?*

I suspect that this radical finding has implications — not just for science, but also for human exceptionalism, for the reliability of heavily marketed talking points, and more — that people will be discussing for a long time. And perhaps for some in the worlds of science and science reporting, especially those who touted the now discredited figure about a mere 1 percent difference from chimps, those conversations may not be welcome.

July 8, 2025: This post has been updated.

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Casey Luskin is a geologist and an attorney with graduate degrees in science and law, giving him expertise in both the scientific and legal dimensions of the debate over evolution. He earned his PhD in Geology from the University of Johannesburg, and BS and MS degrees in Earth Sciences from the University of California, San Diego, where he studied evolution extensively at both the graduate and undergraduate levels. His law degree is from the University of San Diego, where he focused his studies on First Amendment law, education law, and environmental law.

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