



# The Archaic Diversity Problem Solved

## Mechanistic Explanations for High Neanderthal–Denisovan mtDNA Variation

By Matt Nailor

Creationists have tried to explain the high mutation differences we found in Neanderthal and Denisovan by hypermutation (wood 2012). We will pose a new concept today that will explain their high nucleotide differences (210 Neanderthal, 385 Denisovan) without invoking a change in the mutation rate at all. You see, in 2018 David Thaler et al discovered that when a new group formed, say a new dog breed or new wild species, independent from another group. That there was a large leap in genetic differences between the two. He explained it like this in an interview by Marlowe Hood *“And yet – another unexpected finding from the study – species have very clear genetic boundaries, and there's nothing much in between. If individuals are stars, then species are galaxies,” said Thaler. “They are compact clusters in the vastness of empty sequence space.”*

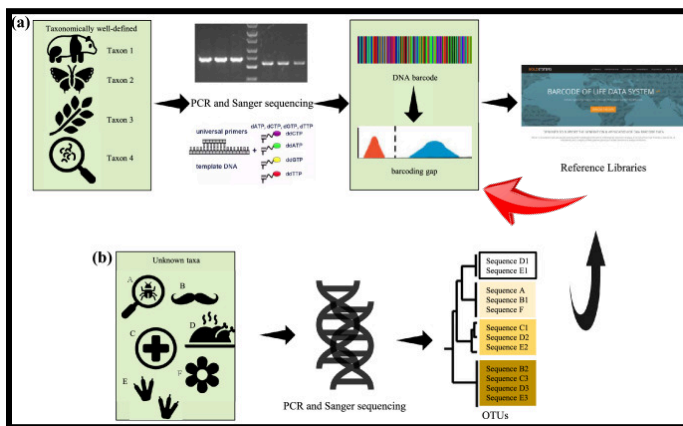


Image 1. The red arrow points to the DNA barcode gap we find between species and subspecies. Image was taken from study titled “Life barcoded by DNA barcodes” by Mali Guo

This “gap” is a mutational leap that occurs in a burst when a new species, subspecies, hybrid, domestication or distinct population emerges. There is no need to invoke hypermutation when we see this in real time. Take for example the modern day canis family. Each new species and subspecies is divided by a large mutational gap, with nothing in between connecting them even though the mutation rate stays the same. Let’s go to the DNA barcoding website BOLD SYSTEMS. We are going to obtain the lowest mutational differences in the database and show how there is a gap between each species.

Before we get into the details, let's use a simple example of how this works. We can all agree that domestic dogs came from wolves. Yet when we test *canis familiaris* to *canis lupus* we find a large genetic boundary “gap” of many mutational differences. No rapid hyper mutation rate, no chain of mutations linking them to each other. This same principle is applied to all life and we can use this observation to explain neanderthal and Denisovan diversity without invoking hypermutation or changing the mutation rate at all actually.

Everyone would agree that chimpanzees and bonobos are related. At some point in the past the bonobo species arose from a speciation event from a chimp. Yet there is a large gap of differences between the two with nothing in between. This massive gap arose like an explosion of mutations that arise out of nowhere. Saltationism (from *saltare*, Latin for *to jump*) is the evolutionary idea that: New species or major biological changes can arise suddenly through large, discontinuous genetic shifts, rather than through many tiny gradual mutations.

Geneticists contemplated such ideas before genetic boundaries were ever discovered, they referred to it as genomic revolutions during speciation. Modern genomics confirms: chromosome changes, genome duplications, and hyper bursts of mutations that can cause rapid speciation and hybridization, sometimes dubbed adaptive radiation which refers to a burst of extremely fast diversification in which one ancestral species quickly splits into many descendant species.

Chimp and bonobo differences within the COI gene fragment are 23 bp different from one another in the COI 650 bp region. This massive difference exists with no link to the chimp, a large gap

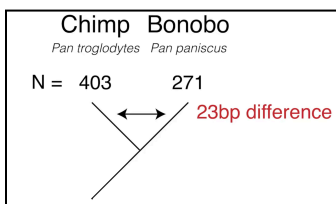


Figure 8. Shows the base pair difference between chimp and bonobo.

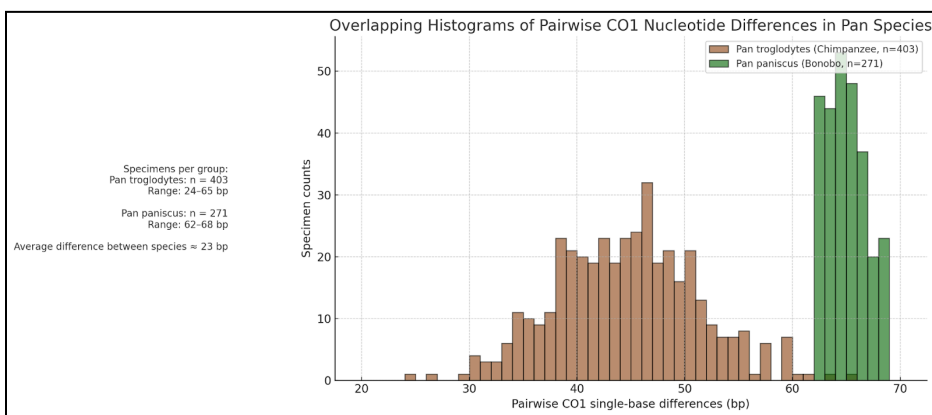


Figure 9. Overlapping histograms were generated in a widescreen format to visualize the distribution of pairwise sequence differences among biologically meaningful pan species groups. Mutation-difference values were plotted for each species, with the number of individuals indicated at left: Pan triglydotes (chimpanzee) 403 species in the database (base pair range 24 – 65).. Pan Paniscus (bonobo), 271 species in the database (base pair range 62 – 68). Average pairwise difference 23 base pairs different. (N = number of species).

So within pan species we find when looking at the 650 bp COI gene fragment that there are 24 differences between the two. Pan mutates much faster than humans in this region, not a single pan species ever tested have even below 24 mutations, yet all hominins have below 20 bp differences with most having 0 mutational differences.

This example found in chimps and bonobos applies to hominin as well. We see most humans with only 0-1 base pair differences between us, while Neanderthals are 7 – 9 bp average away and Denisovan are 17 – 18bp. Since pan species are much more diverse and have mutated much more than humans, their differences reflect that in the “gap”. Meaning, the 23 differences we see between pan – equates to the 7 – 10 bp differences we see between hominins in our tree.

This tells us that when one of these new founder groups spawned from another, there was a new burst of diversity that arose instantly. A “gap” that can be seen even today, as the subspecies branched off. So we have Homo sapiens who the Neanderthal branched off of created an 7 – 9 bp gap, then Denisovan branched off Neanderthal creating another 8 – 10 bp gap from them, equaling a total of 17 – 18 bp gap from homo sapiens. This alignment allows us to make a prediction based on differences we see today in the entire mtDNA.

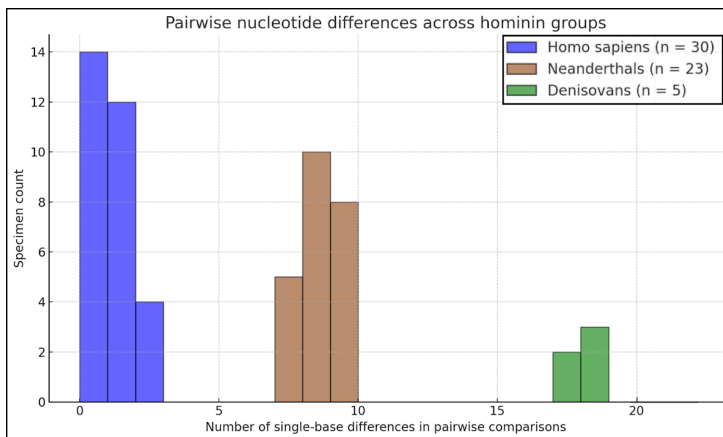


Figure 8. Overlapping histograms of pairwise nucleotide differences across hominin groups. This figure shows how many genetic differences occur within and between Homo sapiens (n = 14), Neanderthals (n = 10), Denisovans (n = 5). The y-axis indicates specimen counts, while the x-axis shows the number of single-base differences in pairwise comparisons. Most Homo sapiens cluster at very low differences (0–1), Neanderthals peak around (7 – 9) mutations, while Denisovans (17 – 18). All COI barcode sequences obtained from

<https://v3.boldsystems.org/index.php/TaxBrowserHome>

Without altering the mutation rate at all, we predict that we can explain the diversity simply through the arrival of these new groups. So now let’s test this prediction. With Neanderthals having 7 – 9 differences away from humans in the 650 bp region, this is 1.08% – 1.38%. Now we need to apply this to the entire mtDNA and see if the total equals the amount of differences we see in Neanderthals.

1.08% of 16,569 bp is 179 nucleotide differences

123% of 16,569 bp is 204 nucleotide differences

1.38% of 16,569 = 229 nucleotide differences

This is precisely in line with what we observe in Neanderthal differences. Let’s follow this trend for testing Denisovan and see if the prediction holds. So from a range of 179 – 229 differences, the arrival of Denisovan from Neanderthal should cause a new gap of differences of the same, a range of 1.08% and 1.38% or 358 – 458 nucleotide differences. This range captures the nucleotide differences. They have 385 perfectly.

The confirmation of this prediction is statistically supported by the levels of diversity seen in both Neanderthals and Denisovans. This is saltationism in action and explains the data perfectly with no alteration of the mutation rate whatsoever.

Since we know that none of these small people groups could have even lived for over 2,000 years based on their small population size (15-20), inbreeding would have killed them (*Krist Vaesen et al 2019*) before that duration. Therefore we want to be able to explain the mutational differences within that window without invoking unobservable scenarios as much as possible and nothing does that better than this observed data we see in DNA barcoding in living species today.

<https://phys.org/news/2018-05-gene-survey-reveals-facets-evolution.html>

**From bar codes to species**

By definition, a DNA bar code is a unique identifier. Between any two humans, it varies at no more than two positions<sup>2</sup>. By comparison, humans differ from chimpanzees at approximately 60 sites, and from gorillas at about 70.