

Microbial omics HW2

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1 Methods

mtDNA samples were aligned with Mafft algorithm. Tree was constructed using IQTree tools and exported in iTOL as newick for cosmetic manipulation. Distant matrix of all vs all mtDNA species was calculated with MEGA 11 software.

2 Age of mitochondrial Eve

In order to reconstruct the age we would want to estimate number of differences between the human haplogroup that will be at the first split of the human phylogenetic tree (probable descendant of the ancestral variant) and basically any of the other haplogroups. The descendant of the ancestral variant on our tree (Figure 1) appeared to be the the L1 haplogroup, that is, according to literature, is the most "ancient" among all modern haplogroups and it is told that it diverged from L1-6 lineage around 140000 years ago.

To infer the age of MtEve, mean difference (n. of nucleotides) of L1 haplogroup with all the others was used and appeared to be equal of 85 nucleotide changes. As for the mtDNA mutation rate, value of $1.91 \cdot 10^{-8} \text{ mutations/position/year}$ was chosen according to one of the recent papers (LINK).

Using all this data, we can estimate age of the MtEve as

$$85/16569/(1.91 \cdot 10^{-8}) = 268589.6$$

years, which is in some consistence with the modern knowledge about its age of 200,000 to 300,000 years ago.

3 Age of divergence of Denisovans and Neanderthals

Using the same approach, we could estimate age of divergence of Denisovans and Neanderthals relative to modern Humans.

3.1 Divergence of Neanderthals

Mean difference were calculated for all *H. s. neanderthalensis* vs all *H. s. sapiens* mtDNA sample differences, which is equal to 209 nucleotide changes. Using the same formula, we could estimate the age of divergence as

$$209/16569/(1.91 * 10^{-8}) = 660414.5$$

years ago, which is aligning with some well known data about mtDNA divergence.

3.2 Divergence of Denisovans

On our tree denisovans are the sister taxa for neanderthals/modern humans clade, which is quite interesting, because when using autosomal data, the picture is different, and neanderthals/denisovans are the sister clade for modern humans.

Continuing in the exact same way, we can calculate mean difference between denisovans and modern humans, that is 380 nucleotide changes. Assuming the same mutation rate, the age of divergence of denisovans from human/neanderthal lineage is

$$380/16569/(1.91 * 10^{-8}) = 1200754$$

years ago, which is bigger than is it is believed to be according to the mtDNA data. We can only assume that chosen mutation rate can not be used for all the history of humanity.

4 Speculations on geographic distribution of *Homo*

If we imagine that we have only the mtDNA data (and related phylogenetic tree) and sites of discovery/sites of the haplogroups distribution, the following statements are true:

1. As there is common ancestor of chimps and humans, humanity originated in Africa (let us not proof that further)
2. Both neanderthals and denisovans are found only in Eurasia, not in Africa
3. All the modern humans are in one monophyletic group
4. Ancestral haplogroups of modern human are African (MtEve most probably originated in Africa)

Given that predispositions and looking at the tree and the dates, we can speculate, that the root of all *Homo* on the tree 1 is some ancient specimen that lived in Africa around 1 million year ago. Today we know that it might be African *H. erectus*, and time of divergence between denisovans and neanderthals/humans is the time of some migration of *H. erectus* into Asia, resulting in finding denisovan people in Altai, with dating of remains around 250-30 K years old. This migration most probably happened along southern shore of Eurasia, in southern Asia and even Australia, as the highest percentage of denisovan DNA is found in southern asians and australians.

So the remaining population of African *Homo* somewhere about 660 K years ago probably divided once again, with one part migrating into Europe, where the neanderthals were found (France, Spain, . . .). At this time, common ancestral populations were most probably the African *Homo heidelbergensis*. However, today one of the popular opinions is that neanderthals are descendants of the more ancient *H. antecessor*, which was found in Spain and dated up to 1.2 millions of years ago, which excludes possibility of common ancestor living in Africa around 600-700 years ago.

Remaining *Homo* population in Africa started their third migration in Eurasia around 270 K years ago. Some of humans remained in Africa, and some migrated in Eurasia, probably with some contacts with indigenous Eurasians *Homo* - neanderthals and denisovans. That would explain why there are distinct clusters of African and non-African *H.sapiens*. Migrations of modern humans resulted in the formation of all the mitochondrial haplogroups are very complex and can't be speculated just with one tree and couple of deductive steps. The reason is the rapid growth of the number of humans, especially after Last Glacial Period, and higher mobility of modern Humans in comparison with any more ancient species.

As a brief conclusion, these speculations are in alignment with popular modern views on the history of humanity, which is represented, for example, on this tree.

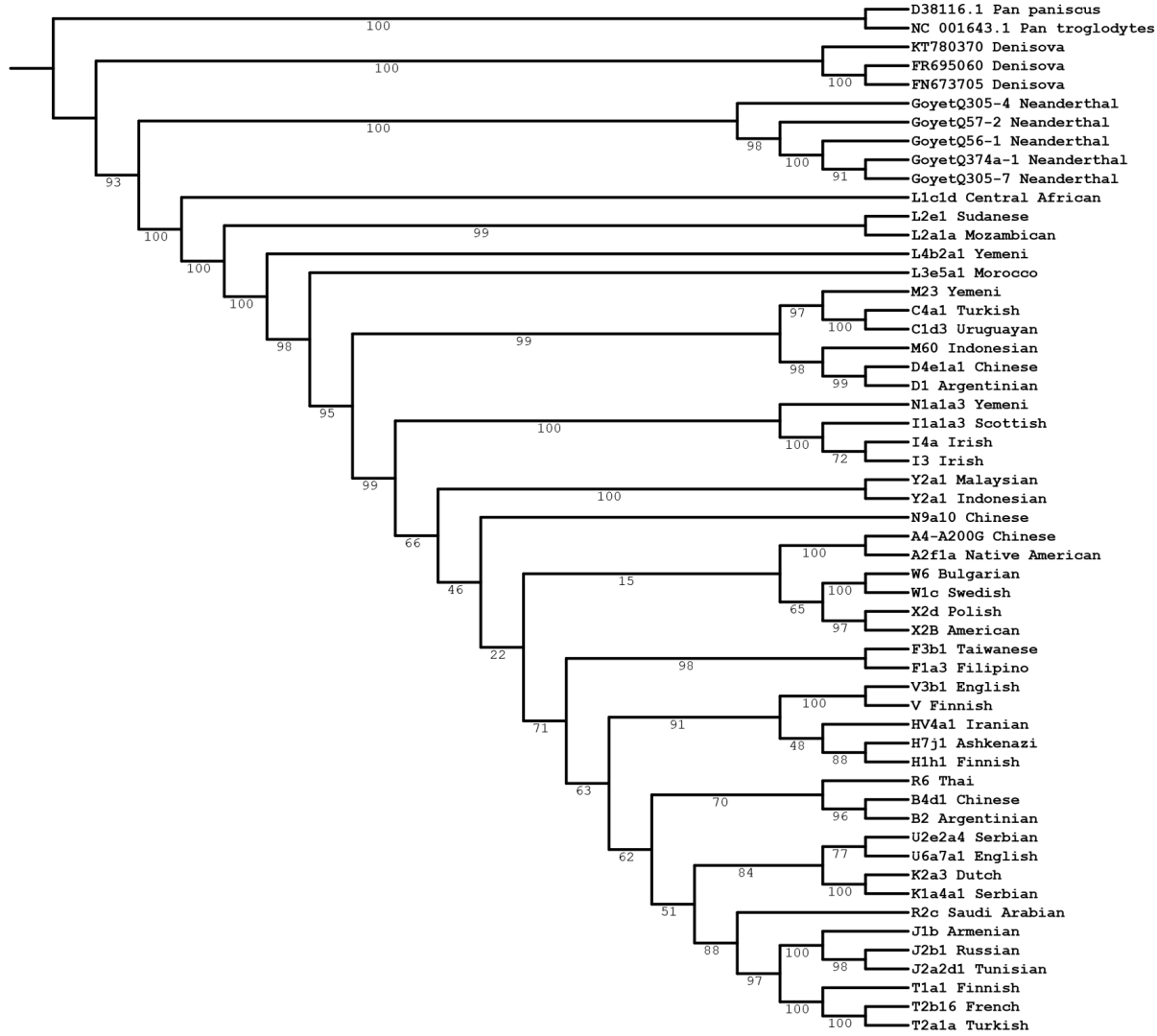


Figure 1: Phylogenetic tree of modern humans, neanderthals, denisovans and chimps