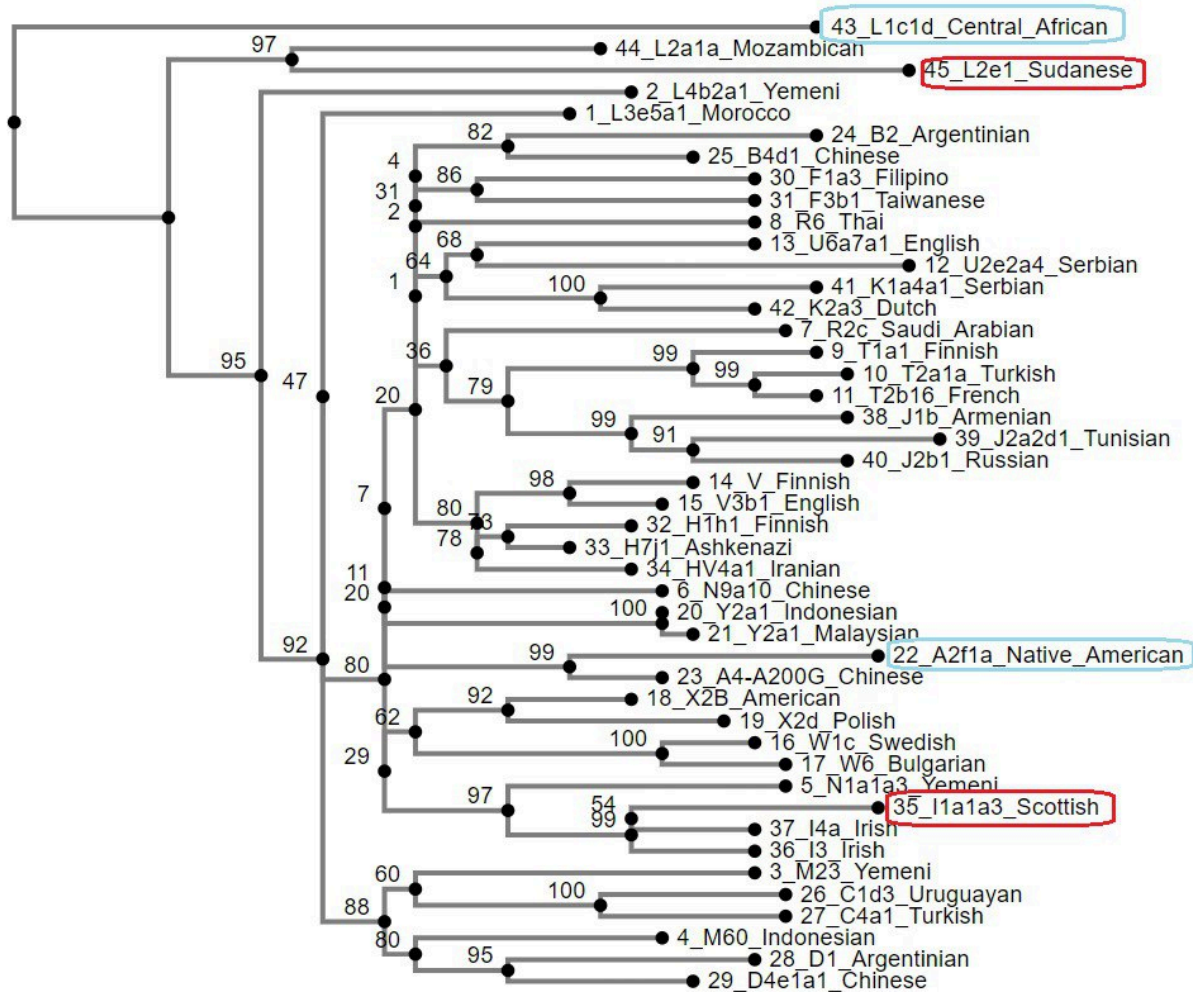Firstly, I aligned mtDNA sequences using MAFFT-FFT-NS-2 alignment with Neighbor-Joining tree with 500 bootstrap replications.
The result tree:

To calculate the age of mtEve I decided to take L1c1d Central Africa and A2f1a Native American sequences and calculated in MEGA distance matrix based on the number of differences:

For age estimation I also needed mtDNA mutation rate and its length - 16569 bp. The mutation rate is still up to debate so I used data from this article
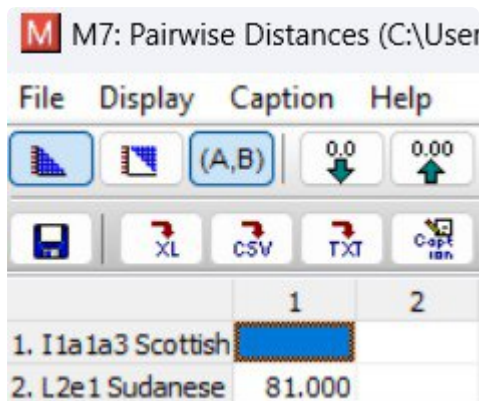I decided to calculate the mean value of known mutation rates based on the table below

and got 2.49 * 10^-8:

Evolution rate × 10–8	95% CI/HPD × 10–8	References
1.67	1.37–1.97	23
1.91	1.72–2.10	This study
1.92	1.16–2.68	8
2.23	1.71–2.75	7
2.4	1.70–3.20	10
2.53	1.80–3.20	24
2.67	2.16–3.16	8
2.74	2.44–3.01	9
4.33	3.90–4.82	This study

$$\text{mtEVE's age} = \frac{91}{2.49 * 10^{-8} * 16569} = 220570$$

For all non-Africans I used L2e1 Sudanese and I1a1a3 Scottish:

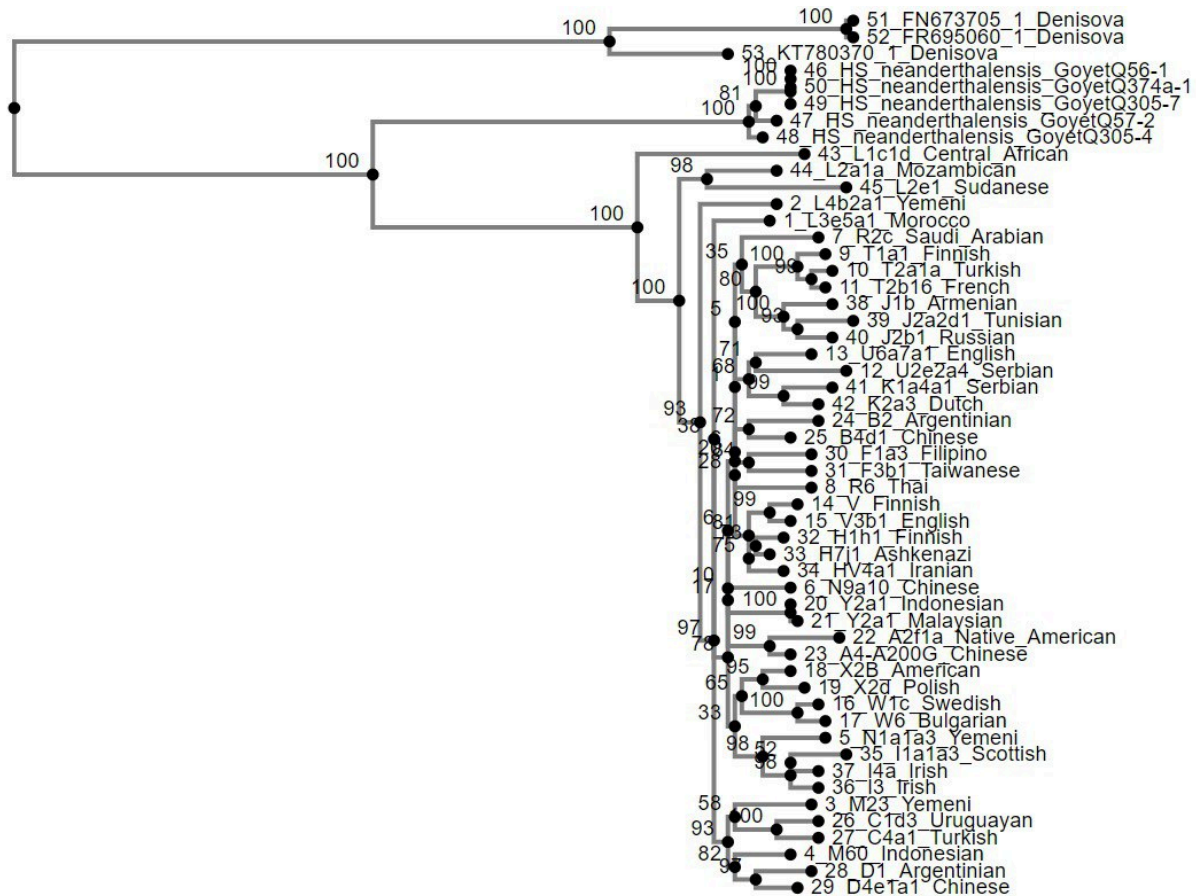$$\frac{81}{2.49 * 10^{-8} * 16569} = 196331$$

So the age of probable mtEve is 220,570 years and the human separation from African population happened 196,331 years ago.

Then I added mtDNA of Neanderthals and Denisova:

We can see that these sequences are clearly separated from the general mass of mtDNA, and Neanderthals are closer to modern humans than Denisova.

To calculate the age of the most recent Neanderthal-modern human ancestor I took L4b2a1 Yemeni and GoyetQ56-1:
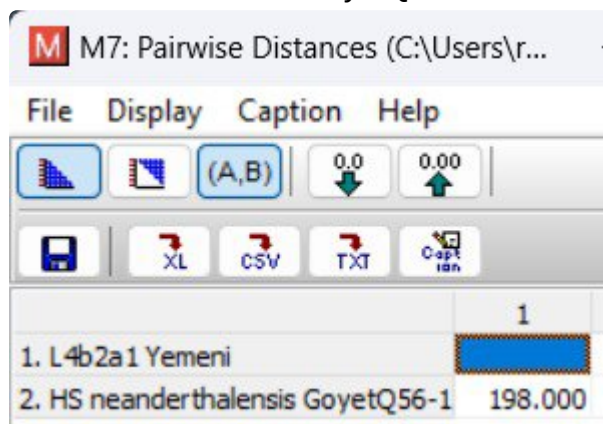
$$\frac{198}{2.49 * 10^{-8} * 16569} = 479921$$

So the Neanderthal-Human ancestor existed probably 479,921 years ago.

Conclusion

Based on many evidence currently estimated time of Homo Sapience presence in Africa is around 200 000 years ago and by constructing phylogenetic tree of mtDNA I've got the same results. The difference comes next as I calculated the separation of non-African population has happened around 196 331 year ago, which is way earlier that proposed by scientists (120 - 100 000). The calculated difference maybe due to the different mutation rates used in analysis. The data of non-African population is also kinda mixed as I expected to see separate groups of East-Asian and N/S-America sequences as the most recent populations of HS (migrated to these areas the latest). For example, I expected to see all Indonesian mtDNA on the same branch, instead it is spreaded across the tree, Native American data placed 'in the middle' of a tree and inside Uruguayan/Indonesian/Argentinian/Chinese group there is Turkish mtDNA.

P.S. The tree with Pan sequences:

The overall structure of a tree was not changed

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