
The mo

outcome of this approach has been the development of diagrams using tree-building methods such as I used above, but where the

hs

(i) It is inescapable that mtDNA only has

trindD(ha)2.60.8370TD(084TD)Tj(y)Tj0.370TD(.t0.239(i7TD0.2390TD7630TD70TD(.0TD(960.8027AD(ta)T

ibayetroponp

ba3586(t)T0.8027AjD(b)T(t)TjTD(i7TD0.2390TDou(a350(p)Tj0D(n)Tj13862460TDD(he)Tj0.962460TD(y)T

ra tteo 2118077D(0)Tj39282D(0)240V)D(a)Tj0028074D(0)a)Tj00.7(i)Tj07239049,TD(T5(a)Tjja(t0241j200(5)D(0)Tj0.11D(0)Tj092390D(B

almost an order of magnitude (Howell . . . 1996). The faster rate was arrived at by extrapolation from a few pedigrees segregating for the mitochondrial disease phenotype LHON. Some individuals within the pedigrees had more than one mitochondrial allele - a state known as heteroplasmy. Heteroplasmy is the inevitable transition state between the time a new allele arrib

control region sequences alone and only one site is required (bp 00073) from the second hypervariable segment of the control region (HV II) to distinguish H from the very rare ancestral U haplotype.

(iii) There has been speculation recently that the mutation rate used for estimating mtDNA divergence is too slow by

11000^14000 BP. Once again, only J is Neolithic. X, a curious and rare group also found in native Americans, remains at 20000 BP (but with a wide confidence interval due to small sample size).

In summary, the phylogeny and mutation rate are largely confirmed. However, correcting for pre-existing diversity does have a significant effect on the cluster dates for Europe which brings most of them into the Late Upper Palaeolithic, but not quite into the Neolithic.

Can we now offer any context for these revised results? Only U5 remains stubbornly Early Upper Palaeolithic with the extant diversity developing over 50000 years in Europe. This is a good match to the first appearance in the European archaeological record of anatomically modern humans, including Cro-Magnon, who brought with them the Aurignacian lithic culture. They shared the continent with taine

lineages. This does not necessarily mean that the Neolithic farming pioneers were composed exclusively of group Jö indeed it would be very surprising if they were. There are also small subclusters of H, T and K that have young dates in Europe and we are currently examining whether these too might be Neolithic in origin. In other words, the overall Neolithic contribution to the mtDNA gene pool might edge over 20%. Cavalli-Sforza and his colleagues used the first principal component, which accounts for 28% of the variance, to argue for the overwhelming influence of the demic diffusion. He now considers this value (28%) to be an estimate of the Neolithic contribution (Cavalli-Sforza & Minch 1997). This is getting too close to our revised value to sustain a controversy on the intrinsic data for very much longer.

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Neolithic, so that the current diversity distribution is a palimpsest of more than one event. We are currently developing statistical methods to disentangle such mixtures.

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