The mo

outcome of this approach has been the development of diagrams using tree-building methods such as I used above, but where the posj0.4440TD(l)Tj0.2560TD(opm)-j0.512ect hs

(i)

It is inescapable that mtDNA only has [illegible]5-0.28n6oTD(h)Tj0.529eo

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

iheyeronpnp

baoa3586(t)T0.8027AjD(b)T(t)TjTD(i7TD0.2390TDou(a350(p)Tj0D(n)Tj13862460TDD(he)Tj0.962460TD(y)T
n

in
ra [illegible]

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 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 ö a state known as heteroplasmy. Heteroplasmy is the inevitable transition state between the time a new allele arib elsewhere found mutation rates compatible with the rates we and others used in estimating divergence times (Bendall . 1996; Jazin . 1998). In addition, field data from Polynesia supported the usual rate where new alleles arising from the common central haplotype (figure 4) did so at a rate which aged the cluster at about 3000 years, a date compatible with the archaeological dates for first colonization (Macaulay . 1997). So it seems that the rate is about right despite the flurry of anxieti [illegible]

11 000^14 000 BP. Once again, only J is Neolithic. X, a curious and rare group also found in native Aa

lineages. This does not necessarily mean that the Neolithic farming pioneers were composed exclusively of group J — 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.

M.