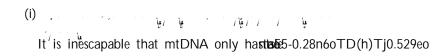
The mo

outcome of this approach has been the development of diagrams using tree-building methods such as I used above, but where the poj0.4440TD(I)Tj0.2560TD(opm)-j0.512ect



.,. B (1999)

teinet心(ha)2.60.8370TD(084TD)Tj(y)Tj0.370TD(.t0.239(i7TD0.2390TD7630TD70TD(.0TD(960.8027AD(ta)T idneyeropponp bana3586(t)T0.8027AjD(b)T(t)TjTD(i7TD0.2390TDou(a350(p)Tj0D(n)Tj13862460TDD(he)Tj0.962460TD(y)^T n rattseona#1960ifffD(i)TzjB9282DTID2et0vi)D(a147jj0081280T4D((ta)3790TD)(647j40732390489,和10(t504)3)jTjja(162941)700(b))T(j50v)72390.和124(0)TTj0092339DDE

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 alleleö a state known as heteroplasmy. Heteroplasmy is the inevitable transition state between the time a new allele arib

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.

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

elsewhere found mutation rates compatible with the rates we and others used in estimating divergence times (Bendall . 1996; Jazin . 1998). In addition, ¢eld data from Polynesia supported the usual rate where new alleles arising from the common central haplotype (¢gure 4) did so at a rate which aged the cluster at about 3000 years, a date compatible with the archaeological dates for ¢rst colonization (Macaulay . 1997). So it seems that

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

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 ¢rst principal component, which accounts for 28% of the variance, to argue for the overwhelming in£uence of the demic dijusion. 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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