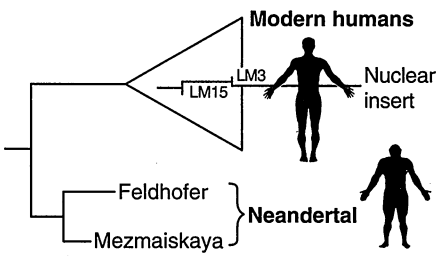
from these short branch lengths that LM3 diverged before the most recent common ancestor, because mtDNA has a higher substitution rate than nuclear DNA.

Such suggestions of homoplasy (random or systematic convergent evolution) are confirmed by phylogenetic analyses (*8*) using the same model as Adcock *et al.*, but with additional modern Aboriginal and African sequences (see the figure). These trees show that LM3 and KS8 are well within modern human variation; the nuclear insert is probably attracted to LM3 due to homoplasy. This phylogenetic position is also obtained when Adcock *et al.*'s original limited set of sequences is used if a model of heterogeneity of rate between sites is incorporated (*9*).



The roots of human origins. This simplified phylogenetic tree was obtained by using the same sequences and substitution model as Adcock *et al.* (*1*) with additional modern human sequences from Australia (*10*) and Africa (*11*).

Lastly, even if the problems with both the data and the analysis were ignored, the phylogenetic tree of Adcock *et al.* would not support the "multiregional model" for modern human origins, because all the modern human sequences are closely related to each other, whereas the Neandertal sequences form an outgroup. Consequently, to see the data of Adcock *et al.* as a significant problem for the Out of Africa model seems an exaggerated claim.

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7. Table 1 of Adcock *et al.* contains an error at site 199 suggesting that LM3 and the human nuclear insert differ by 14 substitutions.
8. Maximum likelihood trees were constructed using PAUP* 4.0b4 (Sinauer, Sunderland, MA). A heuristic search was performed by using the HKY85 model of substitution and a transition-transversion ratio of 18. The complete phylogeny is available at http://evolve.zoo.ox.ac.uk/data/Mungo/. A complete version of the phylogenetic tree represented in the figure is available to *Science* Online subscribers at http://www.sciencemag.org/cgi/content/full/292/5522/1655/DC1
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Response

COOPER AND HIS CO-AUTHORS SUGGEST THAT DNA is unlikely to have been preserved in the ancient Australians we studied. We do not know which environments will preserve DNA for 60 or 60,000 years, just as we do not know why there are fossil remains from some regions but not others. All our bone samples (*1*) were coated with thick carbonate crusts when they were excavated. The LM3 burial lay largely within a carbonate-rich horizon in the Mungo dune, "one of the best locations for the preservation of bone" (*2*). A relatively rapid encrustation of the bones might have produced conditions favoring preservation of the bones and any DNA they contained.

Our procedures were at least as stringent as the "standard" ancient DNA authentication tests cited by Cooper *et al.* None of the samples had been handled by either Aboriginal or non-Aboriginal people before extractions began. We took internal samples under sterile conditions. Our paper details the care taken to replicate and confirm results. Because cloning can cause polymerase chain reaction (PCR) artifacts, we sequenced amplification products directly. For each of our 10 ancient bone samples, a unique DNA sequence was consistently obtained from the independent isolations and PCR amplifications. In the initial Neandertal report (*3*), independent sequence results were not achieved. Only contaminant sequences were obtained in the second laboratory until primers, based on the Neandertal sequence from the first laboratory, were used to amplify a small portion (about 10%) of the mtDNA segment studied. This is not an independent replication. If our results were compromised by the occurrence of deamination, as Cooper *et al.* suggest, we would have expected sequence differences among the independent DNA isolations and PCR amplifications from each bone sample. We did not find any such heterogeneity.

We agree that the exact branching position of the lineage leading to LM3 and the nuclear insert sequence cannot be reliably estimated from any of the extensive phylogenetic analyses we conducted. Nonetheless, we are confident of the grouping of LM3 with the insert sequence. This is overwhelmingly indicated in all our analyses, particularly the likelihood mapping. The grouping of the LM3 and nuclear insert sequences is unlikely to be due to a long branch attraction effect because the branch leading to LM3 is very short and much shorter than branches leading to the many other sequences we analyzed. The relatively long branch leading to the insert sequence makes it highly unlikely that this sequence, and hence the LM3 sequence, diverged after the most recent common ancestor of the sequences in living humans (*4*).

We did not claim to have disproved the entire recent "Out of Africa" model. We suggested that mitochondrial sequence data from ancient human samples have to be considered in any model of human origins and that it is not sufficient to base a theory solely on data from extant populations. The significance of our study is that we have isolated ancient mtDNA sequences, including one that is 60,000 years old, from undisputed Australian modern humans. The fact that this LM3 sequence belongs to a lineage related to the nuclear insert and is now extinct suggests there may have been many mitochondrial lineages in Pleistocene populations of anatomically modern humans.

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CORRECTIONS AND CLARIFICATIONS

NEWS FOCUS: "New data in chemistry show 'zero' diversity" by Jeffrey Mervis (18 May, p. 1291). The chair of the division of chemistry at Harvard University was misidentified. His name is James Anderson.

REPORTS: "Presynaptic kainate receptor mediation of frequency facilitation at hippocampal mossy fiber synapses" by D. Schmitz, J. Mello, R. A. Nicoll (9 Mar., p. 1972). The electrophysiological traces in the report contained sharp transients and steps that were not present in the original data. The conclusions of the paper are not affected. The corrected figures can be viewed in full text version of the paper in *Science* Online.