absence [−] of the five sites along one chromosome), namely (+−−−−), (−+−++) and (−++−+), are common in Eurasia, while a fourth, (−−−−+), is common in Africa and absent elsewhere. A punctuationalist evolutionary explanation is advanced: that a 'small' founder population of *H. s sapiens* migrated from Africa to Eurasia, losing the characteristic African haplotype (−−−−+) en route to Eurasia by genetic drift. Present-day 'new' haplotypes, that is, other than the four common haplotypes assumed to "predate the racial divergence", may in most instances "be derived from the four common ones by single crossovers".

Forty years ago Fisher[7] first applied the crossover hypothesis in human genetics to the rhesus (Rh) blood group system, suggesting less common Rh types "are *maintained* [our italics] by such occasional cross-overs" of the more common types in the British population. Wainscoat *et al.* propose a similar origin for haplotypes (+−−++) and (−++++) in Melanesia and Polynesia, presumably from (+−−−−) and (−+−++) for the former and (−+−++) and (−++−+) for the latter. Since the Eurasian recombinants' frequencies are 2.0% and 1.1%, while the putative parental frequencies are 65.6%, 19.8% and 6.7%, the explanation has distinguished precedent. But in Africa, which Wainscoat *et al.* do not discuss, using analogous logic, (−+−−+) should be a recombinant form of the common haplotypes (−+−++) and (−++−+). Curiously, this recombinant's frequency in Africa is 19.7%; the frequencies of the presumptive parental types in Africa are 9.8% and 1.6%. In fact, the recombinant's frequency in Africa is the same as the frequency of the second most common haplotype, (−+−++), in Eurasia.

We are certain that Wainscoat *et al.* would agree that their data are limited and interpretations preliminary. Nevertheless, we believe that unwarranted credence accrues to the sequence of events they outline, however hedged, when it is presented simply as the loss of one haplotype in a founder population's move from Africa to Eurasia. It ignores the need to interpret the 20% frequency of an apparent recombinant form in Africa, and the ostensible reduction of all three common haplotypes in Africa: to 4.9% (+−−−−), 9.8% (−+−++) and 1.6% (−++−+) from the current Eurasian frequencies 65.6%, 19.8% and 6.7%, respectively. Jones and Rouhani[2] in their imaginative "Out of Africa" scenario see no need to explain how, for example, the common haplotypes (+−−−−), (−+−++) and (−++−+) went from 75% in their proposed "ancestral African populations" to their current combined frequency in Africa of 16.4%.

Our view is not that the data are incompatible with the proposition that *H. s. sapiens* evolved in Africa and moved to Eurasia, but that they do not provide any evidence for that, and are, in fact, equally compatible with the position that *H. s. sapiens* originated in Eurasia and migrated to Africa, or perhaps other alternatives. It could be argued that in Africa not only (−+−−+) but also the common haplotype (−−−−+) are recombinants: Wainscoat *et al.* suggest that (−−−−+) in Papua New Guinea may have arisen through recombination, even though it could not be by a single crossover between any of the three common Eurasian haplotypes. If so, one might ask whether the African population, characterized (80%) by thus possibly recombinant forms, is more likely to be ancestral or derived. We believe the genetic data provided by Wainscoat *et al.* are at the very least a toss-up in terms of African or Eurasian *H. s. sapiens* origins, and that the genetic distance analysis presented in their Fig. 1 dendrogram, an analytical approach notorious for its pitfalls[8], speaks basically to what is not at issue, namely that the Eurasian and African frequencies are very different.

It should not be forgotten, as Antonarakis *et al.*[9] note, that while the mechanism for producing nonrandom association of DNA sequences located in the region of the β-globin gene cluster is unknown, possible explanations include selection pressure for specific DNA sequences within the region. Selection and migration[10] may be a better model for the observed data than reconstructions based on an assumption of drift and migration alone, with direction of migration emerging from, rather than imposed on, such a study.

EUGENE GILES
STANLEY H. AMBROSE
Department of Anthropology,
University of Illinois,
Urbana, Illinois 61801,
USA

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WAINSCOAT *ET AL.* REPLY—We agree that data on β-globin gene haplotypes[1] should be analysed in relation to their evolutionary implications for human populations. Giles and Ambrose do not question our conclusion that there is a major division of human populations into African and Eurasian groups, but they raise the important issues as to which haplotypes and indeed which populations are ancestral. We believe that a small number of common haplotypes predated the racial divergence and that many of the rare haplotypes have since arisen by crossovers between them. Giles and Ambrose emphasize the fact that the second most common haplotype in Africa (−+−−+) could result from recombination between two haplotypes (−+−++) and (−++−+) which, although common in Eurasia, are relatively uncommon in Africa. It is, however, also possible that this African haplotype (−+−−+) is derived from the most common African haplotype (−−−−+) by a single point mutation rather than by recombination. Fortunately, these questions may be answered by sequence analysis of the haplotypes as demonstrated by the elegant study of the 'R' and 'T' haplotypes in a segment of the β-globin gene cluster[2].

Of course, the data on the β-haplotypes taken by themselves do not prove an African origin for modern man. Nevertheless, this hypothesis is consistent not only with fossil evidence[3], but also with the available molecular data. The two lines of evidence that are emerging from DNA analysis of human populations are, firstly, genetic distance analyses, based on allele and haplotype frequencies, which show a distinct African lineage[1,4], and second, data indicating a greater nucleotide sequence diversity at particular loci in African populations[4,5]. Our β-haplotype data and more recent population data on a α-globin haplotypes[6] both suggest greater diversity in African populations, making an African origin for man more likely than one in Eurasia.

These observations are preliminary and will require confirmation by analysis of other world populations and investigation of many other loci. Nevertheless, if they are corroborated, it would be very difficult to postulate that Eurasian populations were ancestral to African populations. Much more likely, as Giles and Ambrose put it, "Out of Africa".

J.S. WAINSCOAT
A.V.S. HILL
S.L. THEIN
J.B. CLEGG
Department of Haematology and
MRC Molecular Haematology Unit,
John Radcliffe Hospital,
Oxford OX3 9DU,
UK

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