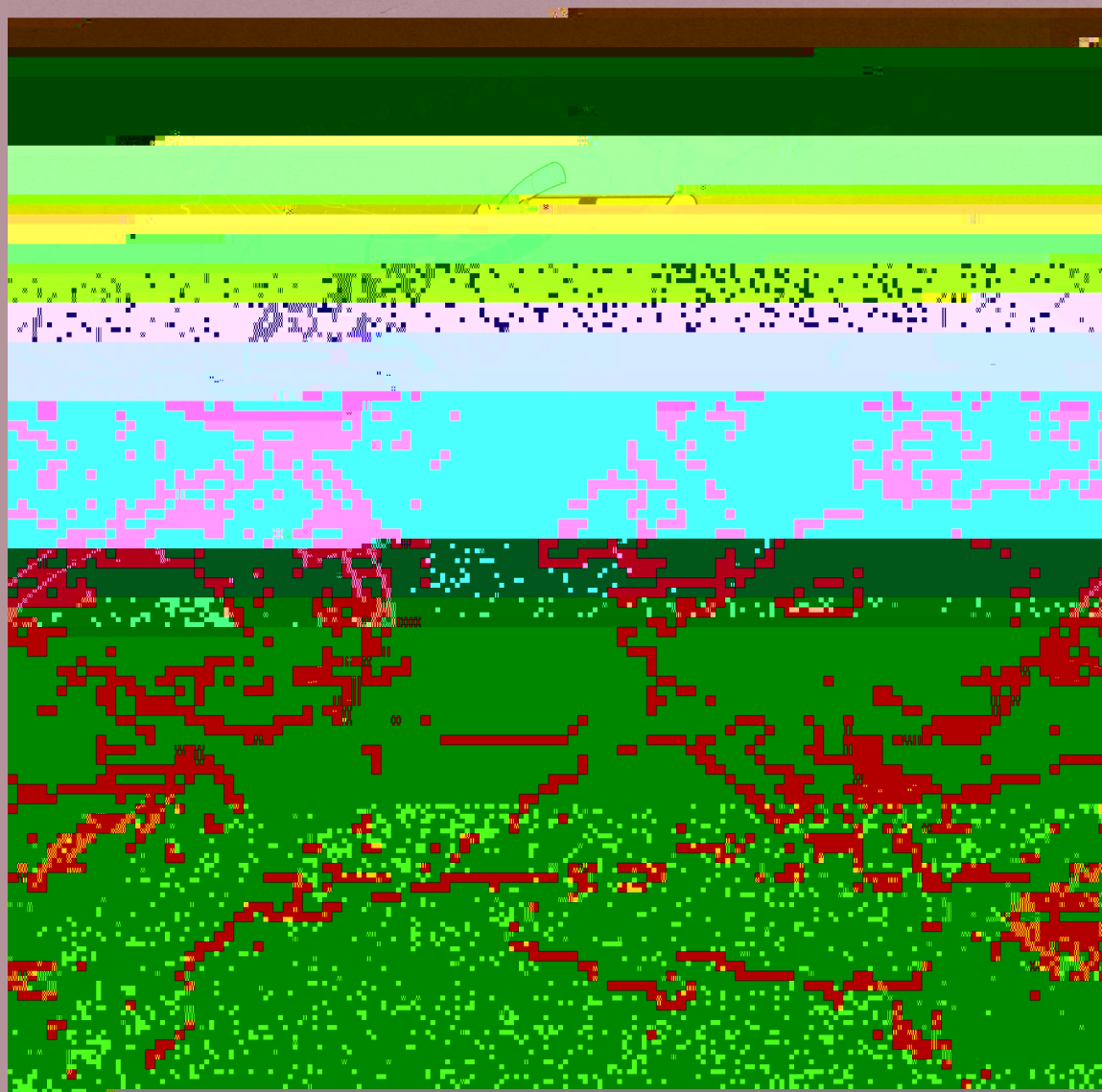




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Chapter 31

An Indian Ancestry: a Key for Understanding Human Diversity in Europe and Beyond

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nic diversity make it clear that to comprehend the richness of the gene pool of Indians long-lasting sys-

ants of India, and the question of their contribution to the gene pool of the contemporary Indians. Were they largely replaced by much more recent immigrants or alternatively, was the result of the recent migrations insignificant genetically while perhaps still profound culturally? There are currently about 500 tribal populations scattered over the Indian peninsula and generally thought of as the survivals of the pre-Neolithic Indians (Cavalli-Sforza *et al.* 1994; Papiha 1996). These tribal populations make up only a minor fraction of the total population of the present-day Indians. Study of their genetic identity would allow one to ask an important question: Do the tribal populations possess genetic lineages absent or rare among the other Indian populations or are they largely genetically identical to the latter, particularly if the differences attributable to drift can be clearly distinguished?

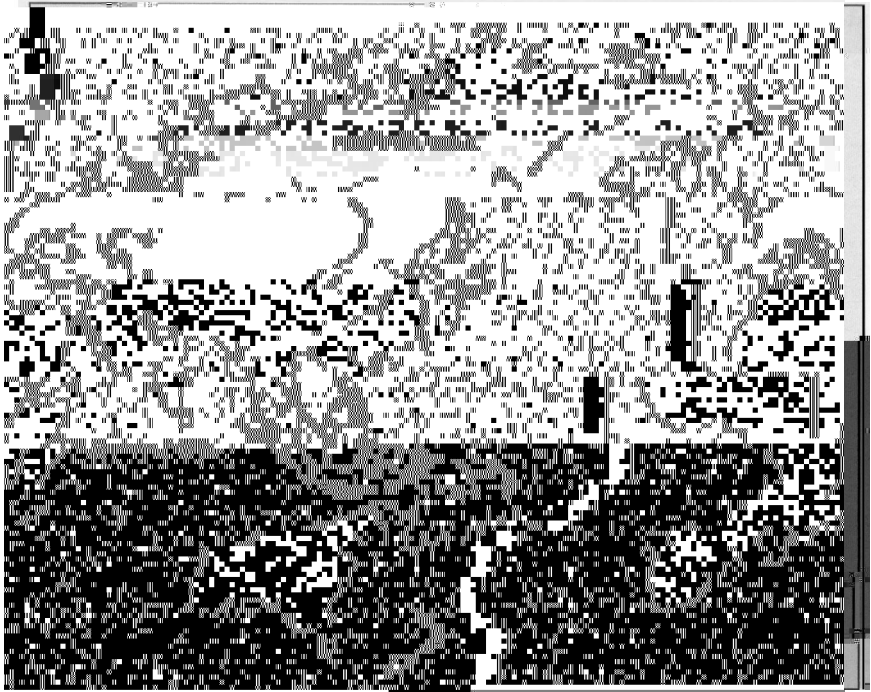


Figure 31.1. *Two alternative routes for out-of-Africa migration.*

Our work: questions, populations and methods

The hypotheses set out above are the basis of our research in the form of two questions. The first is in the placement of the genetic lineages of Indians in the global context. We are trying to understand, in both qualitative and quantitative terms, the extent of the overlap of the genetic lineages found in India with those found elsewhere. Second, provided that such lineage clusters can be reliably reconstructed, can we establish when they diverge from those found elsewhere? Clearly the two questions are connected and the answers we look for depend on a detailed general knowledge about the genetic structure of the other Eurasians as well, and, at least partially, of the Africans.

So far we have analyzed 19

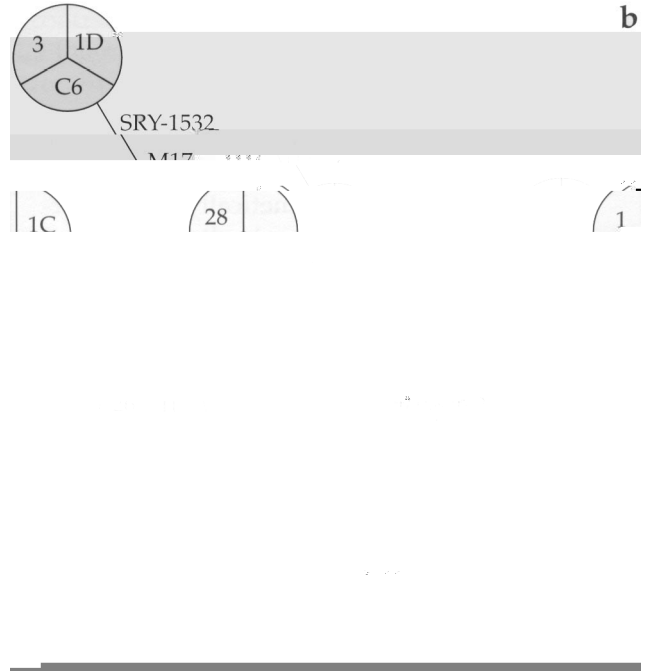
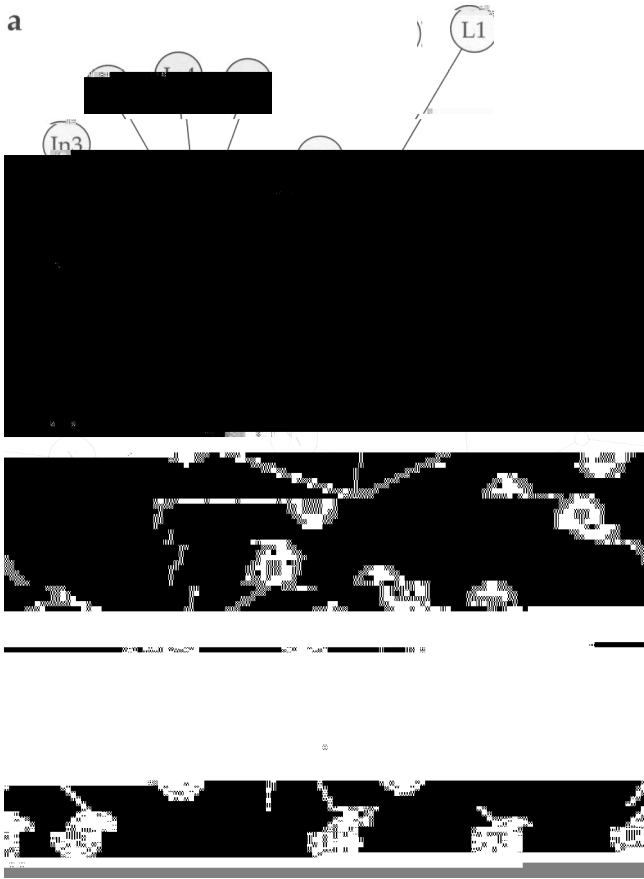


Table 31.1. *MtDNA haplogroup U and M frequencies worldwide.*

	n	U (%)	M (%)	Reference
W-Europe	172	23.9	0.6	(our data)
E-Europe	329	23.7	0.6	(our data)
The Caucasus	532	23.6	1.5	(our data)
Anatolia	379	24.5	3.9	(our data)
C-Asia	195	8.7	4.1	(deduced from Comas <i>et al.</i> 1998)
India	1061	1.3	60.1	(our data)
S-China	69	0	37.7	(our data)
NW-Africa	268	13.7	0.6	(Rando <i>et al.</i> 2007)
E-Africa	199	2.5	8	



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differences are due to differential migrational patterns or, rather, due to profound differences in the demographic histories of the sex-specific genes, where the survival of the male lineages have undergone severe bottlenecks in some lineages and rapid bursts in others.

Returning now to the expansion of modern humans out of Africa, we suggest a scheme as shown in Figure 31.3. We regard it as minimalist, because many aspects known already are omitted, such like the sharing of mtDNA haplogroup U7 between Indian and Anatolian populations, lack of YAP+ Y chromosomes in India etc. However, data are lacking from such critically important regions as Afghanistan, Iran, Iraq, Myanmar, Thai etc. The ever-improving selection of genetic markers, combined with improvements in the understanding of the driving forces of demographic behaviour of humans and their pre-history and history in general, allow us to expect further progress in our reconstructions of the past. However, despite its shortcomings, we hope that this article shows that study of the Indian, mtDNA and Y-chromosomal lineages sheds new light on the general problem of the peopling of the

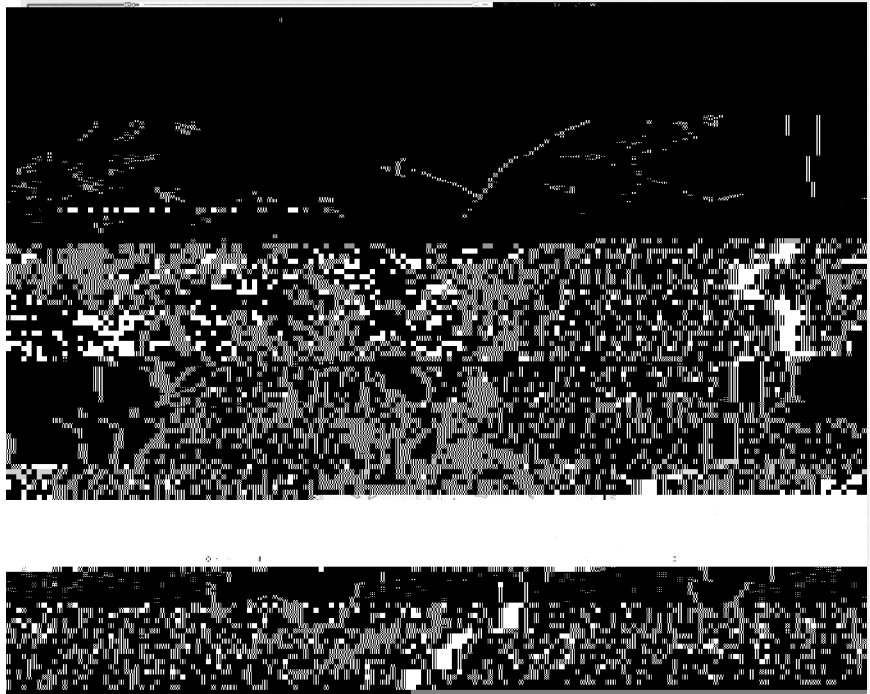


Figure 31.3. Scheme combining the routes and expansions of modern human early dispersals.

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