

unusual adaptability.

The high interest of this question is that *H. sapiens* differs from the great apes (including the orang-utan of Southeast Asia, no longer counted as a close relative) in having 46 rather than 48 chromosomes. The genes of the missing ape chromosome have now been identified as a single block located at one end of human chromosome 2. It follows that at some stage in the evolutionary process, there was a major chromosomal translocation, as a consequence of which an entire ape chromosome was incorporated into the human chromosome 2.

It is not unreasonably soon to ask when, in human evolution, this translocation occurred, and even to guess what its genetic consequences would have been.

On the face of things, it would explain the lack of correlation, in human history, of adaptations with external events, but this may be to say no more than that the evidence so far of the environment in which the australopithecines evolved is entirely insufficient to make a judgement. That is yet another reason for hoping that the study of the comparative evolution of apes and people will soon be possible.

Meanwhile, it is possible that something could be learned from the study of the genomes concerned. What are the genes translocated onto human chromosome 2? Is there any reason to believe that their presence there is advantageous, perhaps because it is plausibly linked with the known progressive increase of the size of the brain-case of the australop-

ithecines, and thus presumably with a progressive increase of the sophistication of the nervous system?

That is one way in which the human genome projects may assist the cause of palaeoanthropology. Another will be possible when the nucleotide sequences of the non-coding regions of the human and ape genomes are known. But a great-ape genome project (for which there appear to be no present plans) would be of great interest in its own right, if only as a means of cataloguing the inter-specific differences between two closely related lineages, at least one of which has evolved at remarkable speed. □

1. Cann, R. L., Stoneking, M., Wilson, A. C. *Nature* **325**, 31–36 (1987).
2. WoldeGabriel, G. et al. *Nature* **371**, 330–333 (1994).

## Our ancestors' ancestors

WHATEVER the uncertainties remaining about the course of evolution of the australopithecines, the question of where their ancestors came from and what they were like is even more obscure. Technically, they are known as hominoids. As a group, they include the great apes and human beings (the Hominae), the Ponginae (the orang-utan and its presumed ancestors) and the predecessors of extant creatures such as gibbons<sup>1</sup>.

Among the common attributes of hominoids are the flexibility of the forearms and their components — the elbow, wrist and so on. There is unambiguous evidence from Africa that the hominoids were established there 20 million years ago, alongside other primates, where they are represented by species of the genus *Proconsul*.

But what then is to be made of the unambiguous hominoids represented by fossils from Pakistan and elsewhere, with ages of the order of 10–20 million years? The issue is controversial. The simplest view is that they should be grouped with the genera such as *Sivapithecus*, amply represented by fossil specimens, and regarded as ancestors of the orang-utan, now exclusively Asian. But that is widely disputed.

Whatever the correct interpretation, these hominoids appear to share with the early australopithecines the flexibility of the forearms and the woodland or forest habitat that appears to have been the common cradle of human emergence. The trick of enabling the thumb and forefinger to act in concert is common among them. The anatomical evidence suggests that they could walk with the help of their forearms, but that bipedalism awaited the emergence of *Homo erectus* in the human lineage. □

1. Andrews, P. *Nature* **360**, 641–646 (1992).

## Migration out of Africa

IN 10,000 generations or thereabouts, human beings have migrated from Africa to populate almost the entire surface of the Earth. It is known that there were people in Australia 50,000 years ago, and that the Americas were occupied less than 25,000 years ago by land migration from Asia. But there are limits to what can be learned by archaeology. Yet the cultural history of *H. sapiens* is presumably faithfully recorded in the genes of people still alive. Unfortunately, the attention given to deciphering these records does not match the intrinsic interest of a successful outcome.

Most attention has so far been given to the genes of mitochondrial DNA, largely as a result of the urging (and the example) of the late A.C. Wilson (Berkeley). Mitochondrial DNA (mtDNA) is especially convenient as a marker of genetic relatedness because it replicates simply, whenever mitochondria divide, without the complications of recombination between autosomal chromosomes, and because it is inherited only maternally.

Usable material can often be extracted from the single hairs of people long since dead. Most investigations use the 1,000-plus base-pair region of mtDNA (which has nearly 17,000 base-pairs altogether) that includes no coding genes, in the expectation that most of them will be subject to mutation without affecting function.

Language is another possible indicator of ancestral relatedness, but is intrinsically a less reliable one. Although language may be one of the distinctive attributes of human beings, it is acquired by newborns from their parents. Nevertheless, by breeding true, and by causing linguistic isolation of population groups, it may be mimical to the Mendelian inheritance of strictly genetic traits.

Luckily, enough has been done in the

past few years to confirm the promise of these lines of investigation. There does appear to be a correlation between genetic traits and language, with occasional glaring exceptions.

Thus Papua New Guinea (PNG), with its 1,000 languages notoriously the world's citadel of linguistic diversity, appears to share with many primitive African populations a deletion of a tract of mtDNA not now found in Asian populations. Is that a sign that PNG was occupied by migration from Africa across the Indian Ocean, that the original migrants travelled by land but that the traces of their journey through Asia have been eliminated by later arrivals, or even that the deletion has been separately acquired by the two widely separated populations?

Whatever the truth, there seems little chance that such ambiguities will be resolved without more extensive investigations of the nuclear as well as mitochondrial genomes of the people concerned. The investigations so far involve such small numbers of people that they can be regarded only as pilot projects.

There is now an urgent need for fresh data, as well as for a project to collect and store DNA from small primitive populations still living in circumstances similar to those they would have occupied immediately after the great migration out of Africa. Already there is evidence that the genetic diversity of !Kung people of Africa (numbering a maximum of 10,000 people) is much greater than would be expected from the size of the population, suggesting a recent decline of numbers.

The prize offered by programmes of this kind is nothing less than a reconstruction of the cultural history of mankind. Is that not a benefit comparable in magnitude with some of the intended outcomes of the human genome projects? □