

Southward Ho!

It is now established beyond reasonable doubt that anatomically modern humans evolved in Africa between 200,000 and 150,000 years ago. A small population of about 1,000 individuals, most probably from East Africa, expanded and spread throughout much of Africa about 100,000 years ago. Genetic data indicate further migration into Asia, and later to other parts of the world. Which route did the first humans take when they moved out of Africa? The easiest would have been a walking trail along the river Nile, across the Sinai Peninsula ('northern exit route'). Then, modern humans could have gone towards Europe or into India. Modern humans from East Africa could have taken an alternate route – across the Red Sea and along the shoreline of Saudi Arabia ('southern exit route'): to the best of my knowledge, this possibility was first proposed by Masatoshi Nei and Arun Roychoudhury in 1999. Or, they may have used both routes.

It is now clear that the northern exit route was used and that this exit took place around 45,000 years ago (Lahr and Foley 1994, 1998; Mountain 1998). On the other hand, fossil evidence indicates that southern Australia was definitely inhabited by anatomically modern humans 45,000 years ago; northern Australia and southeast Asia were perhaps inhabited even earlier (Tattersall 2002). There is no conceivable way that modern humans could have reached Australia at about the same time that they exited through the northern route.

Was the southern exit route used prior to the northern exit route? Could humans have moved along the shoreline of Saudi Arabia into India, and reached Australia along the shorelines of the Arabian Sea and the Bay of Bengal through northeast India, southeast Asia and Borneo? This would have been a more difficult route, as it would require crossing of straits and seas. Of course, tree trunks could have been used as rafts and as primitive boats. There have been no appropriate fossil finds to answer whether a southern exit route was used and existing genetic evidence has only been suggestive (Forster *et al* 2001; Endicott *et al* 2003; Kivisild *et al* 2003). Indeed, some have interpreted the genetic evidence as indicating the absence of a southern exit route (Cordaux and Stoneking 2003).

Since genes move as people move, the commonly used method to trace trails of human migration is to identify specific genetic signatures in the source population and look for these signatures in extant populations along the suspected migration route. This has not yet been possible in respect of the putative southern exit route. However, two recent studies (Thangaraj *et al* 2005; Macaulay *et al* 2005) have found some ancient genetic signatures in population isolates residing in the Andaman and Nicobar Islands and in southeast Asia. The individuals belonging to these populations possess Negrito morphological features (frizzly hair, thick everted lips, dark complexion, for example). These populations are therefore candidate relics of the ancient humans who moved out of Africa and populated other global regions. If anatomically modern humans had indeed used the southern exit route as they moved to populate Australia, then the Andaman Islands and Southeast Asia could have lain on their trail. Thangaraj *et al* (2005) have found two mitochondrial DNA (mtDNA) 'signatures' – sub-haplogroups that they have termed M31 and M32 – among the Ongge and Great Andamanese of the Andaman and Nicobar Islands. These sub-haplogroups arose from haplogroup M – found in high frequencies among extant populations of Ethiopia and mainland India – about 65,000 years ago. They did not find the M31 and M32 sub-haplogroups in mainland India. At the same time, Macaulay *et al* (2005) report two mtDNA sub-haplogroups that they have termed as M21 and M22, in the Orang Asli population of southeast Asia. These sub-haplogroups also branched off from the M haplogroup about 60,000 years ago.

Mitochondrial DNA evidence indicates that the macrohaplogroup L3 arose in East Africa about 85,000 years ago, from which arose the haplogroups M, N and R that are widely co-distributed throughout

Asia. Various sub-haplogroups, including M21, M22, M31 and M32, branched off from these ubiquitous haplogroups. The time estimates of these sub-haplogroups are consistent with the southern exit route hypothesis, and indicate that the southern exit route may have been used before the northern exit route.

Do the data presented in the two studies provide convincing evidence in support of the southern exit route hypothesis? I think that the data are consistent, but not necessarily clinching. Ideal evidence would comprise identification of a specific genetic signature (or, a set of signatures) in the source population and finding it in extant populations along the postulated southern exit route. Can we reasonably expect to find such evidence? For two reasons, I think not. First, the source-specific genetic signatures may have been lost during the time course of evolution by the accumulation of mutations and because of genetic drift. We may, therefore, never find such signatures in extant populations. It may, of course, be possible to identify some signatures among extant populations that were early derivatives of the 'original' signatures. If it is found that the frequencies of these derived signatures decrease from around the exit point as one moves towards Australia along the postulated trail, then such a pattern (a frequency cline) would comprise strong evidence in favour of the southern exit route hypothesis. Second, albeit unlikely, it could be that the modern humans who took the southern exit route did not leave any genes along their trail. This is unlikely because even if they were moving in a band, some members would surely have been left behind at various points on their march towards Australia from out of Africa. The search for genetic evidence to test the southern exit route hypothesis will continue and will continue with greater vigour stimulated by the remarkable findings of Thangaraj *et al* (2005) and Macaulay *et al* (2005).

References

- Cordaux R and Stoneking M 2003 South Asia, the Andamanese, and the genetic evidence for an "early" human dispersal out of Africa; *Am. J. Hum. Genet.* 72 1586–1590
- Endicott P, Gilbert M T, Stringer C, Lalueza-Fox C, Willerslev E, Hansen A J and Cooper A 2003 The genetic origins of the Andaman Islanders; *Am. J. Hum. Genet.* 72 178–184
- Forster P, Torroni A, Renfrew C and R66l A 2001 Phylogenetic star contraction applied to Asian and Papuan mtDNA evolution; *Mol. Biol. Evol.* 18 1864–1881
- Kivisild T, Rootsi S, Metspalu M, Mastana S, Kaldma K, Parik J, Metspalu E, Adojaan M, Tolk H V, Stepanov V, Golge M, Usanga E, Papiha S S, Cinnioglu C, King R, Cavalli-Sforza L, Underhill P A and Villems R 2003 The genetic heritage of the earliest settlers persists both in Indian tribal and caste populations; *Am. J. Hum. Genet.* 72 313–332
- Lahr M M and Foley R A 1994 Multiple dispersals and modern human origins; *Evol. Anthropol.* 3 48–60
- Lahr M M and Foley R A 1998 Towards a theory of modern human origins: geography, demography and diversity on recent human evolution; *Yearb. Phys. Anthropol.* 41 137–176
- Macaulay V, Hill C, Achilli A, Renno C, Clarke D, Meehan W, Blackburn J, Semino O, Scozzari R, Cruciani F, Taha A, Shaari N K, Raja J M, Izmail P, Zainuddin Z, Goodwin W, Bulbeck D, Bandelt H-J, Oppenheimer S, Torroni A and Richards M 2005 Single, rapid coastal settlement of Asia revealed by analysis of complete mitochondrial genomes; *Science* 208 1034–1036
- Mountain J L 1998 Molecular evolution and modern human origins; *Evol. Anthropol.* 7 21–37
- Nei M and Roychoudhury A K 1993 Evolutionary relationships of human populations on a global scale; *Mol. Biol. Evol.* 10 921–943
- Tattersall I 2002 The case for saltational events in human evolution; in *The speciation of modern Homo sapiens* (ed.) T J Crow (Oxford: Oxford University Press) pp 192–218
- Thangaraj K, Chaubey G, Kivisild T, Reddy A G, Singh V K, Rasalkar A A and Singh I. 2005 Reconstructing the origin of Andaman Islanders; *Science* 308 996

PARTHA P MAJUMDER
Human Genetics Unit,
Indian Statistical Institute,
203, BT Road,
Kolkata 700 108, India
(Email, ppm@isical.ac.in)