

Comment on “Reconstructing the Origin of Andaman Islanders”

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On the basis of mitochondrial DNA sequence analyses, Thangaraj *et al.* (Brevia, 13 May 2005, p. 996) proposed that Andaman islanders descended from the first humans to migrate out of Africa. We identified mitochondrial DNA from two northeast Indian Rajbanshi individuals that shares three specific mutations with the M31a lineage observed in the Great Andamanese, which suggests that the predecessor of haplogroup M31 originated on the Indian subcontinent.

The origin of Andaman islanders has been the subject of recent debate (1, 2). On the basis of analyses of complete mitochondrial DNA (mtDNA) sequences, Thangaraj *et al.* (3) concluded that two Andaman populations, the Onge and the Great Andamanese, are the direct descendants of the first emigrants from the out-of-Africa migration ~50,000 to 70,000 years ago. This inference, however, is largely based on the observation of two specific mitochondrial lineages in these populations, referred to as M31 and M32. Our genome screening for both control and partial coding regions in 1200 Indian individuals (4–6) identified two Rajbanshi individuals from West Bengal who belong to the same haplotype and show genetic similarity with the hitherto Andaman islanders–

specific haplogroup M31. They share three coding-region mutations at nucleotide positions 4907, 11176, and 15530 (Fig. 1). The complete sequencing data illustrate that the Rajbanshi mtDNA differs markedly from the Andaman islanders–specific haplogroup M31 (here renamed M31a to distinguish the Rajbanshi branch, which we name M31b) by 11 specific coding-region mutations. This provides new phylogeographic evidence for an early divergence of these lineages on the Indian subcontinent and reduces the estimated time of isolation of the Andamanese (3).

It is therefore most plausible that the predecessor of haplogroup M31 (defined by the motif 4907-11176-15530) originated on the Indian subcontinent rather than in East Africa or East Asia and that the subsequent isolation of the Great Andamanese eventually gave rise to the M31a haplogroup. More population data from India are necessary to confirm this theory. Mapping out the distribution of the newly identified and rare M31b branch among the heavily structured populations of South Asia, as well as identifying relatives of the M32 lineage, will provide further insight into the origin of Andaman islanders.

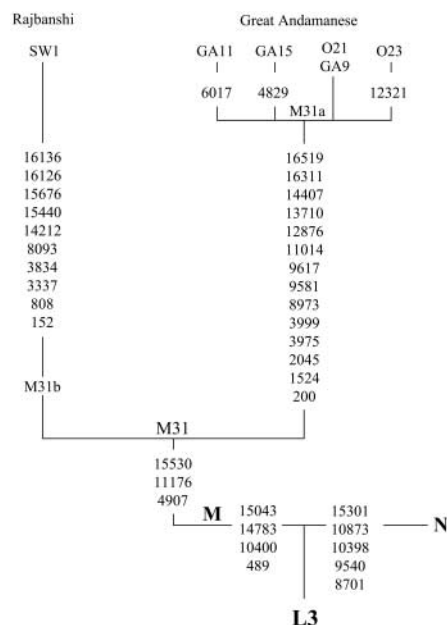


Fig. 1. Phylogenetic tree reconstructed on the basis of complete M31 mtDNA sequences from the Great Andamanese and Rajbanshi.

References and Notes

1. K. Thangaraj *et al.*, *Curr. Biol.* **13**, 86 (2003).
2. P. Endicott *et al.*, *Am. J. Hum. Genet.* **72**, 178 (2003).
3. K. Thangaraj *et al.*, *Science* **308**, 996 (2005).
4. M. G. Palanichamy *et al.*, *Am. J. Hum. Genet.* **75**, 966 (2004).
5. M. G. Palanichamy *et al.*, unpublished data.
6. The 1200 analyzed mtDNA sequences include 521 south Indians (Reddy and Thogataveera from Andhra Pradesh and a mixed group from Tamil Nadu), 568 north Indians (Bhargava, Chaturvedi, and mixed Brahmin from Uttar Pradesh), and 111 northeast Indians (Rajbanshi from West Bengal and Khasi from Meghalaya).
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