

Response to Comment on “Reconstructing the Origin of Andaman Islanders”

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The mitochondrial DNA coding region substitutions shared by the Andamanese and two Rajbanshi individuals suggests the early split of M31 from some continental Indian mitochondrial DNA lineages at the time depth 11/14 of the age of haplogroup M. This is still consistent with the ancient isolation of these gene pools, albeit not as early as the initial phase of human migration out of Africa.

Our recent study on Andaman and Nicobar islanders identified two more mitochondrial DNA (mtDNA) lineage groups, M31 and M32, present in Andaman islanders and absent in 6500 samples from the Indian subcontinent (1). The Andamanese sequences of these two haplogroups shared their most recent common ancestor (MRCA) within these haplogroups at time depths 3000 years [confidence interval (CI) 2] and 12,000 years (CI 4), respectively, while sharing the MRCA with continental Indian mtDNA lineages nested within haplogroup M at a time depth of 65,000 years (CI 7). Given these data, the settlement of the Andaman islanders by a population carrying M31 and M32 founders could have happened any time after the out-of-Africa migration of modern humans. The lack of related lineages in the Indian subcontinent, as well as elsewhere in the world, led us to suggest that the initial settlement of the Andaman islanders could have taken place at the time of coastal migration.

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Further screening of Indian populations by Palanichamy *et al.* (2) has revealed two individuals of the Rajbanshi population from West Bengal sharing 3 out of 14 mtDNA coding region substitutions specific for the Andamanese haplogroup M31 (Fig. 1). With very broad error limits, this finding suggests that the Andamanese M31 lineages share a common ancestor with some continental Indian mtDNA lineages at the time depth 11/14 of the age of haplogroup M (approximately 50,000 years, assuming 65,000 years for the age of M), which is still consistent with an ancient isolation of these gene pools but not as early as the initial phase of the out-of-Africa migration.

Taken together, the finding of M31-related lineages in continental India (2) clearly demonstrates that the absence of evidence for a clade is not the evidence of absence of that clade, even when the sample size exceeds 6000 for a population with the genetic structure of India. We note as well that our sample of 107 Rajbanshi (3) did not include any M31-related samples.

References

1. K. Thangaraj *et al.*, *Science* **308**, 996 (2005).

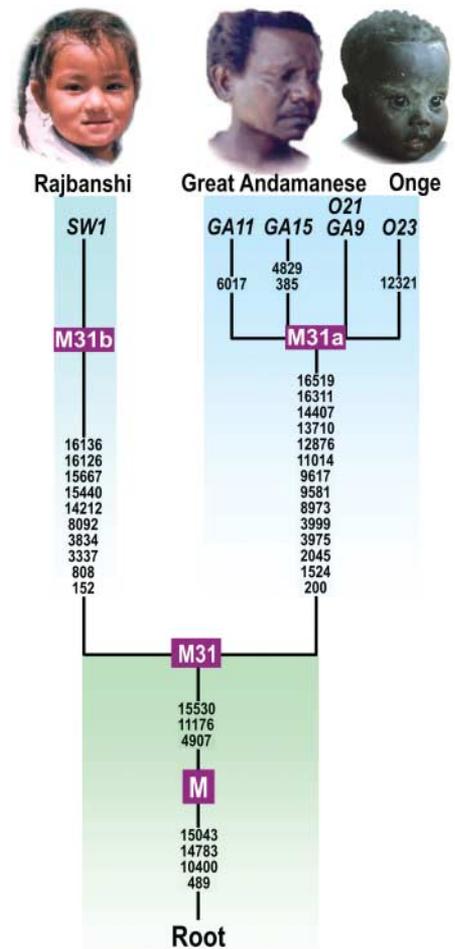


Fig. 1. Maximum parsimonious tree of Great Andamanese, Onge, and Rajbanshi reconstructed on the basis of complete mtDNA sequences from the M31 lineage. The Rajbanshi sequence was taken from Palanichamy *et al.* (2).

2. M. G. Palanichamy *et al.*, *Science* **311**, 470 (2005); www.sciencemag.org/cgi/content/full/311/5760/470a.
3. K. Thangaraj *et al.*, unpublished data.

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