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Anthropologist Special Issue No. 3: 393-414 (2007)

High Resolution Phylogeographic Map of Y-Chromosomes Reveal the Genetic Signatures of Pleistocene Origin of Indian Populations

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KEYWORDS Population Genetics. People of India. Linguistic Groups. Migration

ABSTRACT Paleoanthropological evidence indicates that modern humans reached South Asia in one of the first dispersals out of Africa, which were later followed by migrations from different parts of the world. The variation of 38 binary and 20 microsatellite polymorphisms on the non-recombining part of the Y-chromosome was examined in 1434 male subjects of 87 different populations of India to investigate various hypothesis of migration and peopling of South Asia. This survey revealed a total of 24 paternal lineages, of which haplogroups H, R1a1, O2a and R2 accounted for approximately 70% of the Indian Y-Chromosomes. The high NRY diversity value (0.893) and coalescence age of approx. 45-50 KYA for H and C haplogroups indicated an early settlement of the subcontinent by modern humans. Haplogroup frequency and AMOVA results provide congruent evidence in support a common Pleistocene origin of Indian populations, with limited influence of Indo-European gene pool on the Indian society. The differential Y-chromosome and mt DNA pattern in the two Austric speakers of India signaled that an earlier male-mediated exodus from South East Asia largely involved the Austro-Asiatic tribes, while the Tibeto-Burman males migrated with females through two different routes; one from Burma probably brought the Naga-Kuki-Chin language and O3e Y-chromosomes and the other from Himalayas, which carried the YAP lineages into northern regions of subcontinent. Based on distribution of Y-chromosome haplogroups (H, C, O2a, and R2) and deep coalescing time depths for these paternal lineages, we suggest that the present day Dravidian speaking populations of South India are the descendants of earliest Pleistocene settlers while Austro-Asiatic speakers came from SE Asia in a later migration event.