

Genetic Imprints of Pleistocene Origin of Indian Populations: A Comprehensive Phylogeographic Sketch of Indian Y-Chromosomes

R. Trivedi¹, Sanghamitra Sahoo^{1,2}, Anamika Singh¹, G. Hima Bindu¹, Jheelam Banerjee¹,
Manuj Tandon¹, Sonali Gaikwad¹, Revathi Rajkumar¹, T. Sitalaximi¹, Richa Ashma¹,
G.B.N. Chainy³ and V.K. Kashyap^{*1,2}

1. *National DNA Analysis Centre, Central Forensic Science Laboratory, 30, Gorachand Road, Kolkata 700 014, West Bengal, India*
2. *National Institute of Biologicals, A-32, Sector 62, Institutional Area, Noida 201307, Uttar Pradesh, India*
3. *PG Department of Biotechnology, Vani Vihar, Utkal University, Bhubaneswar 751 004, Orissa, India*

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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 20 microsatellite and 38 binary polymorphisms on the non-recombining part of the uniparental, haploid Y-chromosome was examined in 1434 male individual of 87 different populations of India to investigate various hypothesis of migration and peopling of South Asia Sub-continent. This study revealed a total of 24 paternal lineages, of which haplogroups H, R1a1, O2a and R2 portrayed 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 signified an early settlement of the subcontinent by modern humans. Haplogroup frequency and AMOVA results provide similar evidence in support of a common Pleistocene origin of Indian populations, with partial 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 most likely 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 propose 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.