

Y-CHROMOSOMAL VARIATION IN SOUTHERN INDIA: GENETIC INSIGHTS INTO THE ORIGIN(S) OF LINGAYAT AND VOKKALIGA POPULATIONS. Shilpa

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The Indian subcontinent has served as a major corridor for the dispersal of modern humans out of Africa. Although several genetic studies have been published, they fail to reach a consensus on the genetic origin of Indian populations. In the present study, we examined more than 60 SNPs on the non-recombining region of the Y-chromosome (NRY) in two Dravidian Kannada-speaking populations: Lingayat (101) and Vokkaligas (102) from Karnataka state in southern India. Of the eight major Y-haplogroups observed, three (R, L and H) of them constitute about 78% of the paternal gene pools of both groups. While the frequency of Indian-specific haplogroup H (~25%) is equivalent in both Lingayats and Vokkaligas, they exhibit contrasting distributions of R (35.6% and 21.5%, respectively) and L (17.8% and 32.3%) lineages. A median-joining network based on 15 Y-STR loci showed no shared haplotypes, indicating absence of recent gene flow between the two Dravidian collections.