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Molecular Genetic Perspectives on the Origin of the Lyngngam Tribe of Meghalaya, India

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Author(s)

Banrida T. Langstieh, Vikrant Kumar, Meka Aruna, Alla Govardhan Reddy, Shilpi Dasgupta, Alla Nirmala, Kumarasamy Thangaraj, Lalji Singh, Battini Mohan Reddy

ABSTRACT

Meghalaya, one of the Northeast Indian states, is inhabited by two major tribal clusters, Khasi and Garo. The disputed origin of the Lyngngam tribe of Meghalaya is a result of their geographic distribution, which is sandwiched between that of the above two major tribal clusters. Our earlier analysis of ethnohistoric, linguistic and demographic data suggested the neighbouring Khasi and Garo as the putative parental population(s) of Lyngngam. In this paper, we have investigated the Lyngngam, Garo and all the 7 subtribes of Khasi of Meghalaya using molecular genetic markers-autosomal, Y-chromosome and mtDNA-to explore the possible origin of the Lyngngam tribe. We obtained admixture estimates for Lyngngam versus the putative parental populations. While autosomal STRs and mtDNA results clearly suggest Khasi origin of the Lyngngam, Y-STR distances show greater proximity of Lyngngam to the Garo. Further, the comparative analysis of the Y-Chromosome and mtDNA haplogroup data on relevant Austro-Asiatic and Tibeto-Burman populations from South and Southeast Asia, published by us earlier, clearly exclude the possibility of Lyngngam origin from outside Meghalaya. The molecular genetic evidence in conjunction with the linguistic, demographic and ethno-historic information clearly suggests Khasi origin of the Lyngngam tribe.

KEYWORDS

Austro-Asiatics; Admixture; Autosomal STRs; Y-Chromosome Markers; MtDNA HVS-I and II Sequences

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