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Genomic Diversity in North-East, India: Genetic Relationship Among Five Ethnic Populations From Manipur Based on VNTR Polymorphism

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ABSTRACT Polymorphisms at four mini-satellite loci (D1S7, D4S139, D5S110 and D17S79) were examined to assess the genetic relationship among five contiguous and socio-culturally distinct ethnic populations (Meitei, Kuki, Naga, Hmar and Manipuri Muslim) in northeastern India. All the studied loci were highly polymorphic, with almost no departure from HW-equilibrium. Heterozygosity values among the five groups for the minisatellite range from 68% to 94%. The gene differentiation for the VNTR loci was moderate ($G_{ST} = 0.030$). Neighboring joining method of clustering suggests a close cluster for the tribal groups of Kuki, Naga and Hmar, while Manipuri Muslim is distinct from other populations. The results show that geographic proximity has the least influence on genetic variation and support the results obtained from the traditional markers that northeast Mongoloid populations show genetic affinity irrespective of their linguistic background and geographic proximity.

[Home](#)

[Back](#)
