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Genetic Affinity Among Eight Ethnic Populations of West Bengal and Manipur, India: A Study Based on Six Polymorphic Functional Loci (HLADQA1, LDLR, GYPA, HBGG, D7S8 and GC)

P. Chattopadhyay¹, T.S. Vasulu² and V.K. Kashyap¹

1. DNA Typing Unit, Central Forensic Science Laboratory, Kolkata,
West Bengal, India

2. AHGU, Indian Statistical Institute, Kolkata, West Bengal, India

KEY WORDS HLADQA1; LDLR; GYPA; HBGG; D7S8; GC; reverse dot blot; genetic variation; Tribes of Manipur, castes of Bengal, and population affinities

ABSTRACT Extent of genetic variation at six DNA loci: HLADQA1, LDLR, GYPA, HBGG, D7S8 & GC, which are widely used in forensic testing, were investigated, using allele specific oligonucleotide (ASO) probes and reverse dot blot methodology, in three castes, four tribal and one religious group from West Bengal and Manipur. All studied loci were found polymorphic in the studied populations. No departure from Hardy-Weinberg expectations among the selected loci was observed. The Power of Discrimination for the six loci in the eight population groups ranged between 0.925 and 0.494. Heterozygosity values for the six loci ranged between 0.430 and 0.841. The average heterozygosity for the eight populations range from 0.466 in Naga to 0.644 in Brahmin. The gene differentiation among the studied loci is high ($G_{ST} = 0.046$). The dendrograms based on UPGMA method by six PCR based markers show good correspondence with the spatial and ethnic affiliations of the tribal and caste populations. The UPGMA based phylogenetic tree constructed on the basis of the generated data shows very low genetic distance between the Brahmin and Kayastha communities in relation to the Garo. Genetic affinities among the populations of Manipur reveal very close association between the Meitei, Naga, Hmar and Kuki. Our study suggests that the six PCR based loci, used so far mostly for forensic investigations, can be used fruitfully for micro evolutionary studies as well

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