

Population genetic study of three VNTR loci (D2S44, D7S22, and D12S11) in five ethnically defined populations of the Indian subcontinent

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Abstract

Using RFLP (restriction fragment length polymorphism) analysis, we have characterized the genotypic variation of three VNTR (variable number of tandem repeat) loci (D2S44, D7S22, and D12S11) with probes YNH24, g3, and MS43a, respectively, for 288 individuals from 5 genetically well-defined ethnic groups (Brahmins, Maratha, Gujarati Patel, Sinhalese, and Moors) of the Indian subcontinent. The distributions of VNTR alleles at the binned level were examined among the five populations, and the genetic affinities obtained using the VNTR data were compared with serogenetic data on 22 blood group and protein loci previously reported from our laboratory. For classical genetic markers the Sinhalese show slight affinity with the populations of western India. However, the genetic affinity results considerably parallel the results for VNTR loci and 25 combined VNTR/blood group/protein loci, suggesting that the Sinhalese show the least affinity with the populations of western India. These results confirm the findings of a recent study of genetic relationships of the populations of Sri Lanka based on admixture analysis. The concerns regarding whether or not the pattern of genetic variation of VNTR loci at the bin level can be studied using classical population principles are addressed.