Abstract

Analyses of the DNA flanking the hypervariable minisatellite MS32 (locus D1S8) were carried out on 210 healthy, unrelated Malaysian individuals (70 Chinese, 70 Indians, and 70 Malays). Genomic DNA from each blood sample was extracted by using the rapid mini-preparation of genomic DNA protocol.

Five polymorphic sites (O2, *Hin*fI, Hump1, O1, and Hump2) were assayed for each DNA sample by using the PCR-based tests, restriction enzyme digestions, and gel electrophoresis. Of the 5 sites, only the *Hin*fI, Hump1, and Hump2 were polymorphic, whereas the O1 and O2 were monomorphic. For the *Hin*fI, Hump1 and Hump2 sites, each appeared to be at Hardy-Weinberg equilibrium, and their allele frequencies, power of discrimination (Pd), and heterozygosity (h) were calculated. Based on the data of *Hin*fI, Hump1, and Hump2 assays, approximately 67% of the Malaysian individuals were heterozygous at one or more of the flanking polymorphic sites, which can therefore have their single alleles mapped by the allele-specific minisatellite variant repeat mapping by polymerase chain reaction (MVR-PCR).

Haplotype assays were tested out only on the double heterozygous (*Hin*fI-Hump1, *Hin*fI-Hump2, and Hump1-Hump2) individuals by using the PCR-based tests, restriction enzyme digestions, and gel electrophoresis. Statistical analyses for all haplotypes of *Hin*fI, Hump1, and Hump2 in the Malaysian and each ethnic group showed that a significant association existed among these three sites. Significant association was also observed between each pair of the polymorphic sites (*Hin*fI-Hump1, *Hin*fI-Hump2, and Hump1-Hump2). Haplotype G+C appeared to be at the highest frequency, whereas haplotypes C-T and C-C, C+T did not exist in all samples and the Chinese, respectively.

Pairwise comparisons of the distributions of 8 haplotypes between different population samples showed that the Chinese, Indians, and Malays were closely related to each other genetically. The results also indicated that the Chinese shared great degree of genetic affinity with the Japanese, whereas the other races were not.

Direct DNA sequencing method with an allele-specific primer 32-H1C and a

universal primer 32-O was used to sequence the 5' flanking region in 12 samples. A total length of 244 bases was obtained by this approach, in which the allele-specific primer 32-H1C was used to amplify the DNA strand with $H1^C$, and then separated from the DNA strand with $H1^G$ in the homologous chromosome. The known polymorphic sites (*Hin*fI, Hump1 and Hump2) remained the same and no new polymorphic sites were detected.