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SHORT COMMUNICATION

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Amplification and detection of the VNTR locus D4S95 in a Japanese population

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Abstract The D4S95-VNTR locus was amplified and the polymorphism analysed in a population sample of 169 randomly selected Japanese individuals. A total of 14 alleles containing 850–1360 base pairs were distinguished by agarose gel electrophoresis. The distribution of alleles was symmetrical with respect to one peak at 1030 bp. The mean exclusion chance and discrimination power were calculated as 0.604 and 0.876 respectively.

Key words Forensic identification · VNTR polymorphisms · D4S95 · PCR · Population genetics

Introduction

Here, we report the VNTR polymorphism at locus D4S95 which is closely linked to the Huntington's disease (HD) locus (Wasmuth et al. 1988; Norremolle et al. 1992) and the allelic distribution of D4S95 using samples collected from 169 unrelated healthy Japanese individuals.

Materials and methods

Genomic DNA was extracted from whole blood by a standard procedure (Maniatis et al. 1982).

Amplification mixture: 400 ng DNA (template), 2.5 units Taq-Polymerase (Promega), 0.5 µM each primer (5′-GCATAAAATGGGGATAACAGTAC-3′, and 5′-GACATTGCTTTATAGCTGTGCCTCAGTTT-3′) (Allitto et al. 1992), 200 µM d-NTPs, 50 mM Tris-HCl (pH 8.3), 1.25 mM $MgCl_2$, 0.025% BSA (bovine serum albumin).

temp	95/60/72° C
time	1/2/3 min
cycles	30

The size of amplified fragments was determined in 1.5% agarose gel (MetaPhor Agarose, FMC) with a size marker (100 bp ladder, Pharmacia)

Results and discussion

Fourteen different alleles containing 850–1360 base pairs were distinguished. The distribution of alleles in Japanese samples is symmetrical with respect to one peak at 1030 bp (Table 1).

No deviation of Hardy-Weinberg disequilibrium was observed using a four-allele-model (850–1000, 1030, 1060, 1090–1360: $\chi 2 = 13.04$; df = 9, p = 0.1609).

Compared to the findings obtained in 41 Caucasians by Allitto et al. (1991), we detected a smaller allele distribution range (850–1360 bp in Japanese; 990–1600 bp in Caucasians) with different peaks of allele (1030, 1060 bp

Table 1 Allele frequency distribution at the D4S95 locus in Japanese. The mean exclusion chance and discrimination power were calculated as 0.604 and 0.876 respectively. The most common genotype was the combination of the most frequent 2 alleles (20.71%)

Allele (bp)	n	%
850	7	2.1
880	7	2.1
910	6	1.8
940	7	2.1
970	15	4.4
1000	48	14.2
1030	105	31.1
1060	87	25.7
1090	29	8.6
1120	16	4.7
1180	4	1.2
1270	3	0.9
1330	2	0.6
1360	2	0.6
14 alleles	338	E_{max} 100

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in Japanese; 1090, 1150 bp in Caucasians). The reason for the differences was presumed to be a racial difference.

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