

FOR THE RECORD

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Allele Frequency Distribution of Short Tandem Repeat D13S1493 in Two Populations

POPULATION: 157 unrelated healthy Japanese donors, 138 unrelated healthy German donors.

KEYWORDS: forensic science, D13S1493, short tandem repeat, Japanese, German, DNA typing, population genetics

Blood specimens were obtained from 157 unrelated healthy Japanese volunteer donors from western Japan and 138 unrelated healthy German volunteer donors from the Munich area. DNA was extracted from blood specimens by a salting-out method (1). PCR of D13S1493 (2) was performed in a PE9700 cycler using HotStarTaq polymerase, as recommended by the supplier (Qiagen, Hilden, Germany). A 25 μ L reaction mixture contained DNA 20 ng and 5 pmol of primers F (5'-acctgtgtatggcagcagt-3') and R (5'-ggttgactcttcccaact-3'). Cycle conditions were 95°C for

15 min, then 30 cycles of 94°C for 30 sec, 55°C for 30 sec, 72°C for 60 sec, with a final extension step of 10 min at 72°C. The amplified products were analyzed in a 4% denaturing polyacrylamide gel electrophoresis by using allelic ladders as size markers, followed by silver staining. Allele designation was established following the recommendation of the DNA commission of the ISFH (3). Genetic data were analyzed using programs POWERSTATS (4) and Arlequin (5).

D13S1493 locus is tetranucleotide, GGAA (2). It exhibited 10 clearly distinguishable alleles ranging from 214 bp to 250 bp. Table 1 contains the summary of allele frequencies and forensic values.

The complete data set is available upon request at e-mail: yuasai@grape.med.tottori-u.ac.jp.

TABLE 1—Allele frequency distributions of D13S1493 in two populations.

Allele	Size (bp)	Populations	
		Japanese (n = 157)	German (n = 138)
8	214	0.013	—
9	218	—	0.004
10	222	0.041	0.062
11	226	0.280	0.156
12	230	0.185	0.315
13	234	0.242	0.152
14	238	0.143	0.246
15	242	0.080	0.054
16	246	0.006	0.011
17	250	0.010	—
DP	—	0.933	0.921
P_m	—	0.067	0.079
PIC	—	0.77	0.75
PE	—	0.569	0.554
H_o	—	0.783	0.775
H_e	—	0.802	0.788
HWE	—	0.990	0.544

DP, power of discrimination; P_m , probability of match; PIC, polymorphism information content; PE, power of exclusion; H_o , observed heterozygosity; H_e , expected heterozygosity; HWE, probability value.

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