

FOR THE RECORD

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Allele Frequencies and Statistic Parameters for Penta D and Penta E Loci in Chinese Han Population

POPULATION: Chinese Han population

KEYWORDS: forensic science, DNA typing, population genetics, Penta D, Penta E, Han population

EDTA whole blood samples were collected from 281 unrelated individuals of Han population living in Wuhan, China. DNA was extracted using Cheles-100 method (1). Hot-start PCR was performed in a total volume of 10 μ L containing 10 ng genomic DNA, 0.2 μ M each primer, 10 mM Tris-HCl buffer (pH8.3), 50 mM KCl, 1.5 mM MgCl₂, 200 μ M each dNTP, and 0.3 U Taq DNA polymerase (BioStar, Canada) was added when the temperature reaches 92°C. The primer sequences newly designed by us were: Penta D: 5'-cagagcaagacacatctcaa-3', 5'-ttgcctaacctatggcataacg-3'; Penta E: 5'-agatcagccattgcactcc-3', 5'-gggttattaattgagaaaactcctacaat-3'. PCR cycling conditions: 95°C for 2 min soak, 32 cycles of 30 s at 94°C, 30 s at 62°C for Penta D and 60°C for Penta E, 35 s at 72°C followed by a 5 min extension period at 72°C. The amplification products were separated in a vertical, native polyacrylamide gel (6% T; 5% C) and visualized by silver staining (2). Allele frequencies and other statistics parameters for forensic and paternity were determined for these two loci by the PowerStats software packages (3). The Hardy-Weinberg equilibrium test (HWE) was performed by an exact test (4). None of the analyzed loci showed deviations from HWE ($P > 0.05$) in the population studied.

The complete dataset is available to any interested researcher upon request to the authors.

TABLE 1—Allele frequencies and statistic parameters of Penta D and Penta E loci in the Chinese Han population.

Allele	Penta D (n = 230)	Penta E (n = 281)
5		0.0516
6		
7	0.0065	0.0018
8	0.0696	0.0089
9	0.3587	0.0124
10	0.1130	0.0552
11	0.1261	0.1139
12	0.1826	0.1263
13	0.1087	0.0480
14	0.0261	0.0783
15	0.0065	0.1068
16	0.0022	0.0694
17		0.0658
18		0.0676
19		0.0712
20		0.0498
21		0.0338
22		0.0196
23		0.0107
24		0.0036
25		0.0018
26		0.0036
H _{ob}	0.8348	0.9181
H _{ex}	0.7988	0.9240
P _m	0.0738	0.0140
PD	0.9262	0.9860
PE	0.6651	0.8325
PIC	0.7668	0.9184
HWE-exact test	$P = 0.0893$	$P = 0.7084$

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H_{ob}: Observed heterozygosity; H_{ex}: Expected heterozygosity; P_m: Probability of match; PD: Power of discrimination; PE: Probability of exclusion; PIC: Polymorphism information content.

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