

FOR THE RECORD

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Population Genetics of Two STR Loci D2S1346 and D2S1353 in a Han Population of Chinese

POPULATION: Chinese.

KEYWORDS: forensic science, Han ethnic group, China, DNA typing, short tandem repeats, population genetics, D2S1346, D2S1353

Blood samples were collected from unrelated healthy individuals of the Chinese Han ethnic group in the Chengdu city of Sichuan. Genomic DNA samples were extracted using the Chelex-100 method (1). And polymerase chain reaction (PCR) amplification conditions can be accessed at <http://www.legalmed.org/dna/D2S1346> and [D2S1353.htm](http://www.legalmed.org/dna/D2S1353). The volume of PCR reaction for each locus was 20 μ L. The PCR products were analyzed by horizontal nondenaturing polyacrylamide gel electrophoresis with a discontinuous buffer system and then visualized by silver staining (2). Data of population genetics and forensic science of the loci D2S1353 and D2S1346 were analyzed using POWERSTATS program (3). The genotype distributions of the two loci were analyzed for Hardy–Weinberg equilibrium according to Hou's method (4). No deviation from Hardy–Weinberg equilibrium was observed.

The complete data can be accessed at both <http://www.legalmed.org/dna/D2S1346.htm> and <http://www.fayi.cn/dna/D2S1346.htm>

TABLE 1—Allele frequencies of D2S1346 and D2S1353 in a Chinese population.

| Allele | Frequency | |
|--------|-------------------|------------------|
| | D2S1346 (N = 100) | D2S1353 (N = 98) |
| 10 | 0.005 | |
| 11 | 0.030 | 0.036 |
| 12 | 0.565 | 0.235 |
| 13 | 0.185 | 0.281 |
| 14 | 0.010 | 0.199 |
| 15 | 0.160 | 0.133 |
| 16 | 0.045 | 0.082 |
| 17 | | 0.036 |
| Total | 1.000 | 1.000 |
| HWE* | $p > 0.05$ | $p > 0.05$ |

*Test for Hardy–Weinberg equilibrium.

TABLE 2—Population genetics and forensic data of D2S1346 and D2S1353.

| Locus | PIC | DP | P_m | EP | H_o | H_e |
|---------|------|-------|-------|-------|--------|--------|
| D2S1346 | 0.58 | 0.800 | 0.200 | 0.444 | 0.2900 | 0.7100 |
| D2S1353 | 0.77 | 0.929 | 0.071 | 0.536 | 0.2350 | 0.7650 |

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

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