FOR THE RECORD

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Polymorphism Data of Two STR Loci DYS632 and DYS634 in a Chinese Han Population

POPULATION: Chinese population.

KEYWORDS: forensic science, DNA typing, short tandem repeat, polymorphism chain reaction, Chinese population, DYS632, DYS634

 TABLE 1—Y-STR allele frequencies of Han ethnic group in Chengdu of China.

| Allele | DYS632 | DYS634 |
|----------------|--------|--------|
| 7 | 0.950 | 0.130 |
| 8 | 0.050 | 0.720 |
| 9 | | 0.070 |
| 10 | | 0.080 |
| Gene diversity | 0.096 | 0.458 |
| SE | 0.028 | 0.039 |

Blood samples were collected from 100 unrelated healthy males of the Chinese Han ethnic group in Chengdu of China. DNA was extracted using the Chelex method (1). The allelic variation at the two Y-STR loci named as DYS632 and DYS634 were analyzed by PCR amplification system. PCR amplification conditions can be accessed at: http://www.legalmed.org/dna/DYS632.htm. The volume of PCR reaction for each locus was 37.5 μ L. The PCR products were analyzed by horizontal non-denaturing polyacrylamide gel electrophoresis with discontinuous buffer system and visualized by silver staining (2). Alleles were designated according to the recommendation of the International Society of Forensic Genetics (3). The gene diversity, the haplotype diversity, and the standard errors of diversity were calculated in accordance with Hou's method (4).

The complete data can be accessed at: http://www.legalmed. org/dna/DYS632.htm.

| TABLE 2—Y-STR | haplotype of I | Han ethnic group | in Chengdu of China. |
|---------------|----------------|------------------|----------------------|
|---------------|----------------|------------------|----------------------|

| _ | Haplotype | DYS632 | DYS634 | n | F |
|---|--------------------|--------|--------|----|-------|
| | H1 | 7 | 7 | 12 | 0.120 |
| | H2 | 7 | 8 | 69 | 0.690 |
| | H3 | 7 | 9 | 6 | 0.060 |
| | H4 | 7 | 10 | 8 | 0.080 |
| | H5 | 8 | 7 | 1 | 0.010 |
| | H6 | 8 | 8 | 3 | 0.030 |
| | H7 | 8 | 9 | 1 | 0.010 |
| h | aplotype diversity | | | | 0.503 |
| | SE | | | | 0.040 |
| | | | | | |

n: individuals observed for each haplotype; F: frequency for each haplotype in 100 individuals; SE: standard errors of diversity.

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