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## FOR THE RECORD

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# Genotype Distribution of DYS385 and D10S676 in Chinese Han Population of Yunnan Province

**POPULATIONS:** Chinese Han Population ($n = 103$)

**KEYWORDS:** forensic science, DNA typing, short tandem repeat, polymerase chain reaction, multiplex, population genetics, Yunnan Province, DYS385, D10S676

TABLE 1—*STR allele frequency for Chinese Han people of Yunnan Province.*

| Allele | DYS385 $n = 95$ | D10S676 $n = 103$ | Statistical Parameter | DYS385 | D10S676 |
|---|---|---|---|---|---|
| 9 | 0.005 | | HO | 0.126 | 0.252 |
| 10 | 0.037 | | HE | 0.874 | 0.748 |
| 11 | 0.258 | 0.010 | PE | 0.742 | 0.521 |
| 12 | 0.158 | 0.058 | PIC | 0.850 | 0.691 |
| 13 | 0.111 | 0.194 | PD | 0.954 | 0.877 |
| 14 | 0.058 | 0.408 | | | |
| 15 | 0.058 | 0.248 | | | |
| 16 | 0.037 | 0.078 | | | |
| 17 | 0.095 | 0.010 | | | |
| 18 | 0.047 | | | | |
| 19 | 0.100 | | | | |
| 20 | 0.026 | | | | |
| 21 | 0.005 | | | | |
| 22 | 0.005 | | | | |

HWE DYS385: $\chi^2 = 51.4$ df $= 37$ $P > 0.10$. D10S676: $\chi^2 = 18.12$ df $= 15$ $P > 0.25$.

Whole blood was obtained from 103 unrelated Chinese Han people from Yunnan Province. DNA was extracted by the standard phenol/chloroform extraction produre (1). PCR amplifications were performed as duplex in a 25 μL reaction mixture. The primers for D10S676 and DYS385 were designed according to (1). The PCR amplification was performed in a Perkin-Elmer 9600 and electrophoretic separation of the amplified product was performed in a vertical, denaturing (6M, urea), polyacrylamide gel (5%) using BRL SA32 and silver staining was performed as described previously (2). The alleles of the sample were identified by comparison with the allelic ladders in adjacent lanes in the gel and a 50 bp DNA molecular marker (Promega). The ladders contain the alleles 9 to 22 for locus DYS385 and 11 to 17 for locus D10S676. The alleles were assigned according to previous methods (1). Statistical analysis of the results was performed using the exact test that detected the Hardy-Weinberg equilibrium (HWE). The Homozygotes (HO), Heterozygotes (HE), Power of Exclusion (PE), power of discrimination (PD), polymorphism information (PIC) was performed using the Promega software (internet site at http://www.promega.com/geneticidtools/powerstats/).This simple method can provide a highly discriminatory value for those laboratories without the more expensive fluorescent detection equipment and for those laboratories familiar with manual gel electrophoresis and silver staining technology.

The complete dataset are available to any interested researcher upon requesty to the corresponding author Chun Jie Xiao.

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