

## FOR THE RECORD

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# Allelic Frequencies of Three X-Y Homologous STR Loci in Chinese Population

**POPULATION:** We have analyzed the distribution of allele frequencies at three X-Y homologous short tandem repeat (STR) loci (DXS9900, DXS9905, DXS9906) among individuals ( $n = 385$ ) in Chengdu, China

**KEYWORDS:** forensic science, DNA typing, population genetics, short tandem repeat (STR), X-Y homologous, DXS9900, DXS9905, DXS9906, Han population

Blood samples for database studies were obtained from 385 healthy unrelated individuals (200 women and 185 men) from the Han ethnic group in Chengdu of China.

The DNA was extracted by using Chelex 100 protocol as described by Walsh et al. (1). The allelic variation at the three X-STR loci, named as DXS9900, DXS9905, DXS9906, were analyzed by PCR amplification system. Each PCR reaction was performed in a 37.5  $\mu$ L containing 2–10 ng DNA, 1  $\times$  Taq buffer, 1.5 mM MgCl<sub>2</sub>, 200  $\mu$ M each dNTP (Pharmacia Biotech, Sweden), 1.5 U Taq polymerase (NEB, UK), 0.3  $\mu$ M each primer. The amplification conditions were the same for the three X-STRs markers and consisted of initial denaturation at 94°C for 3 min, followed by 32 cycles at 94°C for 30 s, 54°C for 1 min, 72°C for 50 s and final extension step at 72°C for 7 min, in a Perkin-Elmer 9600 thermocycler. The PCR products were separated in a vertical, non-denaturing polyacrylamide gel electrophoresis and visualized by silver staining (2). Fragment size was typed by comparison with sequenced allelic ladders. Alleles were classified according to the recommendations of the ISFH (3).

The amplification of these three X-STR loci, using the primers described in the Genome Data Base, shows not only a band to the X-specific one in males, but also an additional band in Y-specific in the same size range as the observed in females. The pattern in families reflects a X-specific linked loci and also a polymorphic Y loci with an Y-linked pattern of inheritance. From the results, it may be concluded that these three STR loci are X-unspecific and comply with the inheritance pattern as autosomal STR. Allele frequencies and others statistics parameters for

TABLE 1—Allele frequencies of the STR loci DXS9900, DXS9905, and DXS9906 in the Chinese Han population.

| Allele   | DXS9900<br>( $n = 165$ ) | DXS9905<br>( $n = 385$ ) | DXS9906<br>( $n = 385$ ) |
|----------|--------------------------|--------------------------|--------------------------|
| 6        | 0.3517                   |                          |                          |
| 7        | 0.4533                   |                          |                          |
| 8        | 0.1950                   |                          |                          |
| 9        |                          | 0.1405                   | 0.0289                   |
| 10       |                          | 0.1631                   | 0.0540                   |
| 11       |                          | 0.2936                   | 0.1784                   |
| 12       |                          | 0.2165                   | 0.2079                   |
| 13       |                          | 0.1509                   | 0.0712                   |
| 14       |                          | 0.0354                   | 0.1288                   |
| 15       |                          |                          | 0.1096                   |
| 15.3     |                          |                          | 0.0981                   |
| 16       |                          |                          | 0.0752                   |
| 17       |                          |                          | 0.0315                   |
| 18       |                          |                          | 0.0164                   |
| <i>p</i> | 0.4623                   | 0.5796                   | 0.7213                   |
| H        | 0.5404                   | 0.7673                   | 0.8456                   |
| PD       | 0.6271                   | 0.9151                   | 0.9542                   |
| PE       | 0.4484                   | 0.6489                   | 0.7039                   |

*n*: number of unrelated individuals; *p*: Hardy-Weinberg equilibrium exact test; H: heterozygosity; PD: power of discrimination; PE: probability of exclusion.

forensic and paternity were determined for each locus by the PowerStats software packages (4). The Hardy-Weinberg equilibrium test (HWE) was performed by an exact test (5). 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 corresponding author, Professor Hou Yiping.

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