

FOR THE RECORD

H. J. Zhang,¹ M.D.; Y. H. Shen,¹ M.D.; Q. F. Zhu,² M.D.; Q. H. Wang,¹ M.D.; Q. Ji,² Ph.D.; J. P. Tang,² Ph.D.; J. Liao,¹ M.D.; Y. G. Lin,¹ B.D.; and Y. P. Hou,² M.D.

Distributions of Allelic Frequencies and Haplotypes of Three New Y-STR Loci in a Chinese Han Population

POPULATION: Chinese Han

KEYWORDS: forensic science, Y-chromosome, DYS588, DYS594, DYS557, STRs, population genetics, Chinese Han population

Whole blood samples were collected from 109 unrelated males of Han ethnic group in Sichuan of China. DNA was extracted using Chelex method (1). The volume of PCR reaction for each locus was 25 μ L, which contained 1–5 ng human genome, 1 \times Taq buffer, 1.5 mM MgCl₂, 200 μ M each dNTP (Pharmacia Biotech, Sweden), 1 U Taq polymerase (Applied Biosystems, Foster City, CA), 0.25 μ M each primer (Each forward primer was 5' FAM labeled). PCR amplifications were carried out in a GeneAmp PCR System 9600 (Perkin-Elmer, Foster City, CA). The cycling protocols were: 94°C for 1 min, followed by 30 cycles of 94°C for 30 s, 59°C for 30 s, 72°C for 40 s, and extension at 72°C for 30 min. Typing were performed using denaturing capillary gel electrophoresis on an ABI PRISM 310 Genetic Analyzer with laser-induced fluorescence detection. Alleles were designated according to recommendation of the DNA commission of the International Society of Forensic

Genetics (2). Data of population genetics and forensic science were analyzed according to Hou's method (3).

The complete dataset can be accessed at: <http://www.legalmed.org/dna/DYS588.htm>

References

1. Walsh BS, Petzger DA, Higuchi R. Chelex-100 as medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 1991;10:506–10.
2. Gill P, Brenner C, Brinkmann B, Budowle B, Carracedo A, Jobling MA, et al. DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. *Int J Legal Med* 2001;114:305–9.
3. Hou YP, Zhang J, Li YB, Wu J, Zhang S, Prinz M. Allele sequences of six new Y-STR loci and haplotypes in the Chinese Han population. *Forensic Sci Int* 2001;118:147–52.

Additional information and reprint requests:

Professor Yi Ping Hou

Institute of Forensic Medicine

Sichuan University (West China University of Medical Sciences)

Chengdu 610041, Sichuan

P. R. China

E-mail: rechtsme@wcums.edu.cn

¹ Center of Forensic Sciences, Bureau of Public Security of Sichuan Province, Chengdu, 610041, Sichuan, P. R. China.

² Institute of Forensic Medicine, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, P. R. China.

TABLE 1—*Allele frequencies at three Y-STR loci in a Chinese Han population.*

| DYS594 | | DYS588 | | DYS557 | |
|----------------|-----------|--------|-----------|--------|-----------|
| Allele | Frequency | Allele | Frequency | Allele | Frequency |
| 8 | 0.0459 | 11 | 0.0182 | 21 | 0.0273 |
| 9 | 0.00917 | 12 | 0.1091 | 22 | 0.3636 |
| 10 | 0.2477 | 13 | 0.7909 | 23 | 0.1818 |
| 11 | 0.6330 | 14 | 0.0363 | 24 | 0.1727 |
| 12 | 0.0642 | 15 | ... | 25 | 0.1364 |
| | | 16 | 0.0091 | 26 | 0.0545 |
| | | 17 | 0.2727 | 27 | 0.0364 |
| | | 18 | 0.0091 | 28 | 0.0182 |
| | | | | 29 | 0.0091 |
| Gene diversity | 0.5365 | | 0.3633 | | 0.7880 |
| Standard error | 0.0302 | | 0.0398 | | 0.0160 |

TABLE 2—*Distribution of haplotypes of three Y-STR loci in a Chinese Han population.*

| Haplotype | DYS557 | DYS588 | DYS594 | Number |
|-----------|--------|--------|--------|--------|
| H01 | 21 | 19 | 8 | 1 |
| H02 | 21 | 19 | 11 | 2 |
| H03 | 22 | 17 | 8 | 1 |
| H04 | 22 | 18 | 10 | 1 |
| H05 | 22 | 19 | 8 | 3 |
| H06 | 22 | 19 | 10 | 9 |
| H07 | 22 | 19 | 11 | 19 |
| H08 | 22 | 19 | 12 | 2 |
| H09 | 22 | 22 | 10 | 1 |
| H10 | 22 | 23 | 9 | 1 |
| H11 | 22 | 23 | 10 | 1 |
| H12 | 22 | 23 | 11 | 1 |
| H13 | 23 | 19 | 10 | 6 |
| H14 | 23 | 19 | 11 | 13 |
| H15 | 23 | 20 | 11 | 1 |
| H16 | 24 | 17 | 11 | 1 |
| H17 | 24 | 19 | 10 | 5 |
| H18 | 24 | 19 | 11 | 11 |
| H19 | 24 | 19 | 12 | 1 |
| H20 | 24 | 24 | 10 | 1 |
| H21 | 25 | 18 | 11 | 3 |
| H22 | 25 | 19 | 10 | 2 |
| H23 | 25 | 19 | 11 | 5 |
| H24 | 25 | 19 | 12 | 3 |
| H25 | 25 | 20 | 10 | 1 |
| H26 | 25 | 20 | 11 | 1 |
| H27 | 26 | 18 | 11 | 3 |
| H28 | 26 | 18 | 12 | 1 |
| H29 | 26 | 19 | 11 | 2 |
| H30 | 27 | 18 | 11 | 1 |
| H31 | 27 | 19 | 11 | 2 |
| H32 | 27 | 20 | 11 | 1 |
| H33 | 28 | 18 | 11 | 2 |
| H34 | 29 | 18 | 11 | 1 |

Haplotype diversity 0.9332, Standard error 0.00790.