



Population Genetics for 15 STR loci of Liaoning Han in Northeastern China

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Abstract

Allele frequencies for the 15 autosomal STR loci D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, and FGA (PowerPlex® 16 system™, Promega corporation) were determined in a population sample of 538 unrelated individuals from northeastern China Han (Liaoning).

Keywords: STR; Allele frequencies; Northeastern China Han; PowerPlex® 16 system™

Population

Blood samples were collected from 538 unrelated individuals from the northeastern China Han (Liaoning).

Extraction

DNA was extracted from whole blood using the Chelex-100 extraction method [1].

PCR

PCR amplification was performed using 1.0 ng genomic DNA template according to manufacturer's protocol (PowerPlex® 16 system™, Promega Corporation) [2].

Typing

PCR products were separated on an ABI Prism 3100 Genetic Analyzer (Applied Biosystems) using the recommended protocol. The results were analyzed by Data Collection (Version 1.1), GeneScan (Version 3.7), and Genotyper (Version 3.6) softwares (Applied Biosystems).

Analysis of Data

Allele frequencies and summary statistics were calculated with "PowerStats V 12" program (Promega home page: <http://www.promega.com/geneticidtools/>). Estimations of Hardy-Weinberg equilibrium according to Guo and Thompson [3]. To compare our data to those from other group samples, Arlequin 2.0 was used to calculate pairwise differences for each locus [4].

Quality control

Laboratory Internal Control Standards and Kit controls.

Access to the data

Via electronic mail from communicating author: zhangyj@ybu.edu.cn.

Results

Allele frequencies for each locus are presented in Table 1. Forensic statistics for the 15 loci are summarized in Table 2.

Other Remarks

No significant deviation from Hardy-Weinberg expectations ($p > 0.05$) for 15 STR loci. A comparative analysis between our data and previously published data for the same loci has been done using the statistical method of pairwise differentiation test. The comparative results showed that northeastern China (Liaoning) Han population has significant differences from Caucasian at 10 locus (except D3S1358, D18S51, Penta D, D8S1179 and FGA) [5], African at 13 locus (except D3S1358 and D16S539) [6], respectively. And there were no significant difference between the studied population and Beijing Han [7], Sichuan Han (except D18S51) [8], Hongkong Han (except TH01 and D18S51) [9], Southeastern Han [10], Northwestern Han (except D18S51) [11], South Korean (except TH01) [12], and Japanese (except TH01) [13, 14]. The combined MP (Matching Probability) and PE (power of exclusion) for 15 STR loci were 5.76×10^{-18} and 0.999998, respectively.

This paper follows the guidelines for publication of population data requested by the journal [15].

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| | D3S1358 | TH01 | D21S11 | D18S51 | Penta E | D5S818 | D13S317 | D7S820 | D16S539 | CSF1PO | Penta D | vWA | D8S1179 | TPOX | FGA |
|--------|---------|--------|--------|--------|---------|--------|---------|--------|---------|--------|---------|--------|---------|--------|--------|
| Allele | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 | n=538 |
| 5 | | | | | 0.0428 | | | | | | | | | | |
| 6 | | 0.1050 | | | | | | | | | 0.0028 | | | | |
| 7 | | 0.2416 | | | 0.0019 | 0.0093 | 0.0065 | | | 0.0019 | 0.0056 | | | 0.0009 | |
| 8 | | 0.0530 | | | 0.0037 | 0.0009 | 0.2630 | 0.1292 | 0.0065 | 0.0009 | 0.0436 | | 0.0009 | 0.5325 | |
| 9 | | 0.5437 | | | 0.0084 | 0.0594 | 0.1227 | 0.0799 | 0.2890 | 0.0604 | 0.2931 | | 0.0009 | 0.1125 | |
| 9.3 | | 0.0325 | | | | | | | | | | | | | |
| 10 | | 0.0214 | | 0.0019 | 0.0502 | 0.2189 | 0.1543 | 0.1599 | 0.1171 | 0.2128 | 0.1252 | | 0.0836 | 0.0251 | |
| 11 | | 0.0028 | | 0.0037 | 0.1199 | 0.3219 | 0.2388 | 0.3522 | 0.2574 | 0.2342 | 0.1753 | | 0.0846 | 0.3011 | |
| 12 | | | | 0.0381 | 0.0948 | 0.2347 | 0.1599 | 0.2435 | 0.2100 | 0.3931 | 0.1670 | | 0.1375 | 0.0270 | |
| 13 | | | | 0.1896 | 0.0455 | 0.1391 | 0.0372 | 0.0316 | 0.1041 | 0.0855 | 0.1494 | | 0.2184 | 0.0009 | |
| 14 | 0.0417 | | | 0.2165 | 0.0781 | 0.0102 | 0.0177 | 0.0037 | 0.0149 | 0.0102 | 0.0306 | 0.2649 | 0.1868 | | |
| 15 | 0.3813 | | | 0.1719 | 0.1152 | 0.0037 | | | 0.0009 | 0.0009 | 0.0056 | 0.0344 | 0.1812 | | |
| 16 | 0.3284 | | | 0.1301 | 0.0976 | 0.0009 | | | | | 0.0009 | 0.1691 | 0.0883 | | |
| 17 | 0.1837 | | | 0.0641 | 0.0939 | | | | | | | 0.2305 | 0.0139 | | 0.0009 |
| 18 | 0.0622 | | | 0.0595 | 0.0818 | 0.0009 | | | | | 0.0009 | 0.1989 | 0.0037 | | 0.0270 |
| 19 | 0.0028 | | | 0.0362 | 0.0586 | | | | | | | 0.0836 | | | 0.0465 |
| 20 | | | | 0.0279 | 0.0586 | | | | | | | 0.0158 | | | 0.0437 |
| 20.2 | | | | | | | | | | | | | | | 0.0019 |
| 21 | | | | 0.0279 | 0.0242 | | | | | | | 0.0028 | | | 0.1059 |
| 21.2 | | | | | | | | | | | | | | | 0.0028 |
| 22 | | | | 0.0186 | 0.0112 | | | | | | | | | | 0.1320 |
| 22.2 | | | | | | | | | | | | | | | 0.0084 |
| 22.3 | | | | | | | | | | | | | | | 0.0019 |
| 23 | | | | 0.0093 | 0.0084 | | | | | | | | | | 0.2212 |
| 23.2 | | | | | | | | | | | | | | | 0.0065 |
| 24 | | | | 0.0046 | 0.0019 | | | | | | | | | | 0.2138 |
| 24.2 | | | | | 0.0037 | | | | | | | | | | 0.0056 |
| 25 | | | | | | | | | | | | | | | 0.0967 |
| 25.2 | | | | | | | | | | | | | | | 0.0037 |
| 26 | | | | | | | | | | | | | | | 0.0576 |
| 26.2 | | | | | | | | | | | | | | | 0.0019 |
| 27 | | | | | | | | | | | | | | | 0.0186 |
| 28 | | | 0.0409 | | | | | | | | | | | | 0.0037 |
| 28.2 | | | 0.0046 | | | | | | | | | | | | |
| 29 | | | 0.2463 | | | | | | | | | | | | |
| 29.2 | | | 0.0009 | | | | | | | | | | | | |
| 30 | | | 0.3132 | | | | | | | | | | | | |
| 30.2 | | | 0.0130 | | | | | | | | | | | | |
| 30.3 | | | 0.0056 | | | | | | | | | | | | |
| 31 | | | 0.1022 | | | | | | | | | | | | |
| 31.2 | | | 0.0595 | | | | | | | | | | | | |
| 32 | | | 0.0297 | | | | | | | | | | | | |
| 32.2 | | | 0.1264 | | | | | | | | | | | | |
| 33 | | | 0.0084 | | | | | | | | | | | | |
| 33.2 | | | 0.0437 | | | | | | | | | | | | |
| 34 | | | 0.0028 | | | | | | | | | | | | |
| 34.2 | | | 0.0009 | | | | | | | | | | | | |
| 35 | | | 0.0009 | | | | | | | | | | | | |
| 35.2 | | | 0.0009 | | | | | | | | | | | | |

Table 1: STR allele frequencies of 538 individuals from northeastern China(Liao Ning) Han.

| | D3S1358 | TH01 | D21S11 | D18S51 | Penta E | D5S818 | D13S317 | D7S820 | D16S539 | CSF1PO | Penta D | vWA | D8S1179 | TPOX | FGA |
|-----|---------|--------|--------|--------|---------|--------|---------|--------|---------|--------|---------|--------|---------|--------|--------|
| He | 0.7075 | 0.6307 | 0.8065 | 0.8582 | 0.9199 | 0.7703 | 0.8076 | 0.7670 | 0.7813 | 0.7342 | 0.8146 | 0.8001 | 0.8435 | 0.6117 | 0.8588 |
| Ho | 0.6902 | 0.6450 | 0.7881 | 0.8662 | 0.9349 | 0.7774 | 0.8011 | 0.7602 | 0.7770 | 0.7435 | 0.7885 | 0.7714 | 0.8383 | 0.6059 | 0.8606 |
| PIC | 0.6558 | 0.5852 | 0.7813 | 0.8428 | 0.9121 | 0.7340 | 0.7801 | 0.7332 | 0.7470 | 0.6926 | 0.7900 | 0.7703 | 0.8241 | 0.5499 | 0.8438 |
| PE | 0.4132 | 0.3484 | 0.5772 | 0.7270 | 0.8672 | 0.5577 | 0.6011 | 0.5274 | 0.5570 | 0.4987 | 0.5779 | 0.5470 | 0.6719 | 0.2981 | 0.7159 |
| PD | 0.8657 | 0.8229 | 0.9392 | 0.9632 | 0.9852 | 0.9081 | 0.9348 | 0.9118 | 0.9126 | 0.8868 | 0.9400 | 0.9311 | 0.9556 | 0.7912 | 0.9636 |
| P | 0.6977 | 0.7612 | 0.2924 | 0.7479 | 0.0987 | 0.7173 | 0.7893 | 0.9609 | 0.1495 | 0.3675 | 0.1520 | 0.9558 | 0.1595 | 0.9817 | 0.2945 |

He: Expected heterozygotes, Ho: Observed heterozygotes, PIC: Polymorphism information content., PE: Power of exclusion, PD: power of discrimination, p: probability values of exact tests for Hardy-Weinberg equilibrium.

Table 2: Statistical parameters of the 15 STR loci for forensic interest in northeastern China(Liao Ning) Han.

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