

FOR THE RECORD

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Allele Frequencies of 13 STR Loci and the D1S80 Locus in a Tamil Population from Madras, India

Population: Tamil population (Tamil Nadu, India, $n=103$)

Keywords: forensic science, DNA typing, Tamil population, short tandem repeat, polymerase chain reaction population genetics, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX, CSF1PO, D1S80

Whole blood obtained by venipuncture was collected from unrelated individuals residing in Madras, Tamil Nadu, India. The DNA was extracted using standard phenol-chloroform method and purified by ethanol precipitation. The quantity of recovered DNA was estimated using a slot-blot procedure using commercial kits (PE-Biosystems, Foster City, CA and/or Gibco-BRL, Gaithersburg, MD). PCR amplification of the thirteen STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX, and CSF1PO) was performed using the AmpF ℓ STR Profiler plus and AmpF ℓ STR Cofiler kits (PE-Biosystems, Foster City, CA) following the manufacturer's protocol. The amplified products were separated and detected using the ABI PrismTM 377 DNA sequencer and/or ABI PrismTM 310 genetic analyzer (PE-Biosystems, Foster City, CA). The D1S80 locus was amplified using the D1S80 AmpliFLPTM kit following the manufacturer's protocol. Alleles were separated by a SA32 vertical gel electrophoresis unit (Gibco-BRL, Gaithersburg, MD) using GeneAmpTM detection gel (PE-Biosystems, Foster City, CA).

The data were analyzed using a program written by Chakraborty and Zhong. Allele frequencies and other pertinent information from analysis of the D1S80 locus and the thirteen STR loci are given in Tables 1 and 2.

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TABLE 1—D1S80 allele frequencies in 103 unrelated Tamil individuals.

| Allele | Frequency |
|------------------|-----------|
| 16 | 0.0388 |
| 18 | 0.3204 |
| 19 | 0.0097 |
| 21 | 0.0049 |
| 22 | 0.0340 |
| 23 | 0.0049 |
| 24 | 0.3398 |
| 25 | 0.0437 |
| 26 | 0.0243 |
| 27 | 0.0146 |
| 28 | 0.0340 |
| 29 | 0.0194 |
| 30 | 0.0049 |
| 31 | 0.0777 |
| 32 | 0.0049 |
| 38 | 0.0097 |
| 39 | 0.0049 |
| 41 | 0.0097 |
| Total | 1.00 |
| <i>p*</i> | 0.860 |
| PD | 0.925 |
| PE | 0.577 |
| Observed | 23.3 |
| Homozygosity (%) | |
| Expected | 22.8 |
| Homozygosity (%) | |

The complete data set is available upon request from corresponding author George Duncan, Ph.D., at: george_duncan@sheriff.org

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TABLE 2—STR allele frequencies of the 13 loci in the Tamil population.

| Allele | D3S1358 | VWA | FGA | D8S179 | D21S11 | D18S51 | D5S818 | D13S317 | D7S820 | D16S539 | TH01 | TPOX | CSF1PO |
|--------|---------|--------|--------|--------|--------|--------|--------|---------|--------|---------|--------|--------|--------|
| 6 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 0.2767 | ... | ... |
| 7 | ... | ... | ... | ... | ... | ... | 0.0097 | 0.0534 | ... | 0.1990 | 0.1456 | 0.2961 | 0.0049 |
| 8 | ... | ... | ... | ... | ... | ... | 0.0049 | 0.2282 | 0.2476 | 0.0388 | 0.1505 | 0.2718 | 0.0049 |
| 9 | ... | ... | ... | ... | ... | ... | 0.0437 | 0.0534 | 0.0388 | ... | 0.1019 | 0.1359 | 0.0146 |
| 9.3 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 10 | ... | ... | ... | ... | ... | 0.1845 | 0.0097 | 0.1359 | 0.1117 | 0.1165 | 0.0049 | 0.0777 | 0.1699 |
| 11 | ... | ... | ... | ... | ... | 0.0631 | 0.0340 | 0.4126 | 0.2767 | 0.2379 | 0.2621 | ... | 0.4369 |
| 12 | ... | ... | ... | ... | ... | 0.0728 | 0.0825 | 0.2573 | 0.2379 | 0.1748 | 0.2476 | ... | 0.0437 |
| 13 | ... | ... | ... | ... | ... | 0.1553 | 0.0971 | 0.1359 | 0.0728 | 0.0485 | 0.1553 | ... | 0.3884 |
| >13 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 0.0049 |
| 14 | 0.0146 | 0.1942 | 0.2330 | 0.2961 | 0.0097 | 0.0097 | 0.0097 | 0.2961 | 0.1553 | 0.1165 | 0.0049 | 0.0049 | 0.0049 |
| 15 | 0.3981 | 0.0971 | 0.1651 | 0.0971 | 0.0922 | 0.0971 | 0.0971 | 0.0971 | 0.0971 | 0.0971 | ... | ... | ... |
| 16 | 0.2961 | 0.1651 | 0.0922 | 0.0922 | 0.0340 | 0.0583 | 0.0583 | 0.0583 | 0.0583 | 0.0583 | ... | ... | ... |
| 17 | 0.2087 | 0.2573 | 0.0340 | 0.0777 | 0.0049 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | ... | ... |
| 18 | 0.0825 | 0.1990 | 0.0049 | 0.0049 | 0.0340 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | ... | ... |
| 18.2 | ... | ... | 0.0680 | 0.0049 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | 0.0437 | ... | ... |
| 19 | ... | ... | 0.0194 | 0.1262 | 0.1262 | 0.0049 | 0.0049 | 0.0049 | 0.0049 | 0.0049 | 0.0049 | 0.0049 | ... |
| 20 | ... | ... | ... | 0.1505 | 0.1505 | ... | ... | ... | ... | ... | ... | ... | ... |
| 21 | ... | ... | ... | 0.0146 | 0.0146 | ... | ... | ... | ... | ... | ... | ... | ... |
| 22 | ... | ... | ... | 0.1553 | 0.1553 | ... | ... | ... | ... | ... | ... | ... | ... |
| 22.2 | ... | ... | ... | 0.0049 | 0.0049 | ... | ... | ... | ... | ... | ... | ... | ... |
| 23 | ... | ... | ... | 0.1942 | 0.1942 | ... | ... | ... | ... | ... | ... | ... | ... |
| 23.2 | ... | ... | ... | 0.1117 | 0.1117 | ... | ... | ... | ... | ... | ... | ... | ... |
| 24 | ... | ... | ... | 0.0049 | 0.0049 | ... | ... | ... | ... | ... | ... | ... | ... |
| 25 | ... | ... | ... | 0.0291 | 0.0291 | ... | ... | ... | ... | ... | ... | ... | ... |
| 25.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 26 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

continues

TABLE 2—Continued.

| Allele | D3S1358 | VWA | FGA | D8S1179 | D21S11 | D18S51 | D5S818 | D13S317 | D7S20 | D16S539 | TH01 | TPOX | CSF1PO | |
|---------------------------|---------------|---------------|---------------|--------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|-----|
| 27 | ... | ... | ... | ... | 0.0097 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 28 | ... | ... | ... | ... | 0.1456 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 29 | ... | ... | ... | ... | 0.1893 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 29.2 | ... | ... | ... | ... | 0.0097 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 29.3 | ... | ... | ... | ... | 0.0049 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 30 | ... | ... | ... | ... | 0.1505 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 30.2 | ... | ... | ... | ... | 0.0194 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31 | ... | ... | ... | ... | 0.0583 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31.2 | ... | ... | ... | ... | 0.1262 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 32 | ... | ... | ... | ... | 0.0146 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 32.2 | ... | ... | ... | ... | 0.1893 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 33 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 33.2 | ... | ... | ... | ... | 0.0680 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 34 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 34.2 | ... | ... | ... | ... | 0.0049 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 35 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 35.2 | ... | ... | ... | ... | 0.0049 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| <i>p</i> * | | | | | | | | | | | | | | |
| Observed Homozygosity (%) | 0.530 34.0 | 0.952 21.4 | 0.412 12.6 | 0.638 6.8 | 0.433 15.5 | 0.224 17.5 | 0.077 31.1 | 0.062 26.2 | 0.993 18.4 | 0.699 16.5 | 0.407 21.4 | 0.916 27.2 | 0.761 31.1 | |
| Expected Homozygosity (%) | 29.3 | 18.1 | 13.8 | 15.5 | 13.6 | 14.8 | 27.2 | 20.2 | 19.1 | 18.9 | 21.8 | 30.2 | 29.5 | |
| PD | 0.861 | 0.939 | 0.953 | 0.941 | 0.958 | 0.956 | 0.878 | 0.923 | 0.931 | 0.928 | 0.909 | 0.855 | 0.862 | |
| PE | 0.448 | 0.631 | 0.712 | 0.682 | 0.718 | 0.708 | 0.495 | 0.596 | 0.614 | 0.619 | 0.563 | 0.453 | 0.451 | |

* Exact test based on 2000 shufflings.

Interclass correlations yielding $p < 0.05$ for pairwise comparisons: D3S1358/D8S1179, vWAD5S818, FGA/D8S1179, FGA/TPOX, D8S1179/D21S11, D8S1179/D7S820, D21S11/D18S51, D21S11/TPOX, D13S317/D7S820, D7S820/D7S820, D7S820/D18S51.

... allele not detected or not applicable; PD: Power of Discrimination; PE: Probability of Exclusion.