

For the Record

Population Data for Nine Fluorescent Based STR Loci Among Four Important Tribal Populations of India*

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Population: Four major Indo Mongoloid tribal populations, namely, Garo ($N = 110$), Naga ($N = 106$), Kuki ($N = 105$) and Hmar ($N = 101$), practicing very high degree of endogamy. These populations are found in the Eastern and North Eastern part of Indian subcontinent.

DNA extraction was carried out using protocols of organic extraction (phenol/chloroform/isoamyl alcohol) followed by ethanol precipitation (1), from the blood samples. Quantitation of DNA was carried out using the Quantiblot kit (PE Biosystems).

PCR amplification was performed using the AmpF ℓ STR Profiler Plus™ PCR amplification Kit following manufacturer's instructions (2). The amplified products were detected using the ABI Prism™ 377 DNA Sequencer and reference sequenced ladders (PE Applied Biosystems).

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Access to Data: Via electronic mail from communicating author.

Analysis of Data: DNA type, (Windows 95/NTVer. Chakraborty and Zhong, CHG, University of Texas). PE & PD (3).

The maximum allele occurrence among the populations was consistent with other published world population data at these loci. Significant variations in allele frequencies were observed among the less frequent alleles among the studied and compared populations. Significant interclass correlation value ($p < 0.05$) was obtained at D5S818/D8S1179 (Garo), at D5S818/D18S51 (Naga, Hmar), at vWA/D21S11 (Kuki, Hmar) and D5S818/D18S51 (Garo, Hmar).

References

1. Sambrook J, Fritsch EF, Maniatis T. Molecular cloning. A laboratory manual. 2nd ed. Cold Spring Harbor NY: Cold Spring Harbor Laboratory Press, 1989.
2. Perkin Elmer/ABI AmpF ℓ STR Users Manual. 1998.
3. Garber RA, Morris JW. General equations for the average power of exclusion for genetic systems of N codominant alleles in one-parent cases of disputed parentage. In: Walker RH, editor. Inclusion probabilities in parentage testing. American Association of Blood Banks. Arlington VA; 1983: 277-80.

TABLE 1—Allele frequencies for the AmpFLSTR Profiler Plus loci in Garo population of Eastern India.

| Allele | D3S1358 N: 110 | vWA N: 110 | FGA N: 110 | D8S1179 N: 110 | D21S11 N: 110 | D18S51 N: 110 | D5S818 N: 110 | D13S317 N: 110 | D7S820 N: 110 |
|--------|-------------------|---------------|---------------|-------------------|------------------|------------------|------------------|-------------------|------------------|
| 6 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 7 | ... | ... | ... | ... | ... | ... | 0.010 | ... | ... |
| 8 | ... | ... | ... | ... | ... | ... | 0.010 | ... | 0.281 |
| 9 | ... | ... | ... | 0.076 | ... | 0.065 | 0.152 | 0.019 | 0.229 |
| 10 | ... | ... | ... | 0.141 | ... | 0.032 | 0.108 | 0.501 | 0.104 |
| 11 | ... | ... | ... | 0.217 | ... | 0.178 | 0.174 | 0.121 | 0.125 |
| 12 | ... | ... | ... | 0.152 | ... | 0.076 | 0.206 | 0.061 | 0.145 |
| 13 | 0.010 | ... | ... | 0.260 | ... | 0.076 | 0.173 | 0.204 | 0.104 |
| 13.2 | ... | ... | ... | ... | ... | 0.108 | ... | ... | ... |
| 14 | 0.065 | 0.087 | ... | 0.065 | ... | 0.076 | 0.076 | 0.092 | ... |
| 15 | 0.337 | 0.032 | ... | 0.054 | ... | 0.189 | 0.043 | ... | 0.010 |
| 15.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 16 | ... | 0.282 | ... | 0.021 | ... | 0.043 | 0.042 | ... | ... |
| 17 | 0.347 | 0.250 | ... | 0.010 | ... | 0.097 | ... | ... | ... |
| 18 | 0.217 | 0.152 | 0.056 | ... | ... | 0.010 | ... | ... | ... |
| 19 | 0.021 | 0.173 | 0.017 | ... | ... | 0.010 | ... | ... | ... |
| 20 | ... | 0.010 | 0.057 | ... | ... | ... | ... | ... | ... |
| 21 | ... | 0.010 | 0.167 | ... | ... | 0.021 | ... | ... | ... |
| 21.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 22 | ... | ... | 0.022 | ... | ... | ... | ... | ... | ... |
| 22.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 23 | ... | ... | 0.219 | ... | ... | ... | ... | ... | ... |
| 23.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 24 | ... | ... | 0.257 | ... | ... | ... | ... | ... | ... |
| 25 | ... | ... | 0.135 | ... | ... | 0.010 | ... | ... | ... |
| 26 | ... | ... | 0.051 | ... | ... | ... | ... | ... | ... |
| 26.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 27 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 27.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 28 | ... | ... | ... | ... | 0.062 | ... | ... | ... | ... |
| 28.2 | ... | ... | ... | ... | 0.020 | ... | ... | ... | ... |
| 29 | ... | ... | ... | ... | 0.229 | ... | ... | ... | ... |
| 29.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 30 | ... | ... | ... | ... | 0.250 | ... | ... | ... | ... |
| 30.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 31 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31.2 | ... | ... | ... | ... | 0.061 | ... | ... | ... | ... |
| 32 | ... | ... | ... | ... | 0.104 | ... | ... | ... | ... |
| 32.2 | ... | ... | ... | ... | 0.187 | ... | ... | ... | ... |
| 33 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 33.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 36 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| H | 0.631 | 0.798 | 0.826 | 0.674 | 0.888 | 0.778 | 0.783 | 0.797 | 0.696 |
| PD | 0.812 | 0.876 | 0.906 | 0.739 | 0.954 | 0.854 | 0.859 | 0.874 | 0.764 |
| PE | 0.330 | 0.605 | 0.594 | 0.389 | 0.770 | 0.559 | 0.567 | 0.594 | 0.422 |
| P | 0.835 | 0.118 | 0.136 | 0.002 | 0.119 | 0.217 | 0.117 | 0.325 | 0.214 |

H: observed heterozygosity; PD: power of discrimination; PE: probability of exclusion; P: Hardy-Weinberg equilibrium; exact test based on 2000 shufflings.

TABLE 2—Allele frequencies for the AmpF Φ STR Profiler Plus loci in Naga population of Eastern India.

| Allele | D3S1358 N: 106 | vWA N: 106 | FGA N: 106 | D8S1179 N: 106 | D21S11 N: 106 | D18S51 N: 106 | D5S818 N: 106 | D13S317 N: 106 | D7S820 N: 110 |
|--------|-------------------|---------------|---------------|-------------------|------------------|------------------|------------------|-------------------|------------------|
| 6 | ... | ... | ... | ... | ... | ... | ... | ... | 0.125 |
| 7 | ... | ... | ... | ... | ... | ... | 0.020 | ... | 0.162 |
| 8 | ... | ... | ... | ... | ... | ... | 0.020 | 0.270 | ... |
| 9 | ... | ... | ... | 0.020 | ... | ... | 0.250 | 0.250 | 0.137 |
| 10 | ... | ... | ... | 0.145 | ... | ... | 0.145 | 0.104 | 0.075 |
| 11 | ... | ... | ... | 0.062 | ... | ... | 0.250 | 0.104 | 0.179 |
| 12 | ... | ... | ... | 0.145 | ... | 0.020 | 0.145 | 0.187 | 0.171 |
| 13 | ... | ... | ... | 0.354 | ... | 0.104 | 0.166 | 0.083 | 0.100 |
| 13.2 | ... | ... | ... | ... | ... | 0.145 | ... | ... | ... |
| 14 | 0.062 | 0.062 | ... | 0.125 | ... | 0.145 | ... | ... | 0.025 |
| 15 | 0.333 | 0.020 | ... | 0.083 | ... | 0.250 | ... | ... | 0.025 |
| 15.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 16 | ... | 0.291 | ... | 0.041 | ... | 0.083 | ... | ... | ... |
| 17 | 0.354 | 0.312 | ... | 0.020 | ... | 0.145 | ... | ... | ... |
| 18 | 0.229 | 0.145 | 0.042 | ... | ... | 0.020 | ... | ... | ... |
| 19 | 0.020 | 0.125 | 0.041 | ... | ... | 0.020 | ... | ... | ... |
| 20 | ... | 0.020 | 0.103 | ... | ... | ... | ... | ... | ... |
| 21 | ... | 0.020 | 0.145 | ... | ... | 0.041 | ... | ... | ... |
| 21.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 22 | ... | ... | 0.041 | ... | ... | ... | ... | ... | ... |
| 22.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 23 | ... | ... | 0.229 | ... | ... | ... | ... | ... | ... |
| 23.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 24 | ... | ... | 0.208 | ... | ... | ... | ... | ... | ... |
| 25 | ... | ... | 0.125 | ... | ... | 0.020 | ... | ... | ... |
| 26 | ... | ... | 0.041 | ... | ... | ... | ... | ... | ... |
| 26.2 | ... | ... | 0.020 | ... | ... | ... | ... | ... | ... |
| 27 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 27.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 28 | ... | ... | ... | ... | 0.062 | ... | ... | ... | ... |
| 28.2 | ... | ... | ... | ... | 0.020 | ... | ... | ... | ... |
| 29 | ... | ... | ... | ... | 0.229 | ... | ... | ... | ... |
| 29.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 30 | ... | ... | ... | ... | 0.250 | ... | ... | ... | ... |
| 30.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 31 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31.2 | ... | ... | ... | ... | 0.061 | ... | ... | ... | ... |
| 32 | ... | ... | ... | ... | 0.104 | ... | ... | ... | ... |
| 32.2 | ... | ... | ... | ... | 0.187 | ... | ... | ... | ... |
| 33 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 33.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 36 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| H | 0.584 | 0.667 | 0.792 | 0.792 | 0.885 | 0.869 | 0.792 | 0.700 | 0.667 |
| PD | 0.641 | 0.732 | 0.869 | 0.829 | 0.971 | 0.953 | 0.869 | 0.768 | 0.732 |
| PE | 0.332 | 0.584 | 0.379 | 0.584 | 0.765 | 0.733 | 0.584 | 0.428 | 0.379 |
| P | 0.152 | 0.235 | 0.140 | 0.717 | 0.166 | 0.250 | 0.708 | 0.050 | 0.434 |

H: observed heterozygosity; PD: power of discrimination; PE: probability of exclusion; P: Hardy-Weinberg equilibrium; exact test based on 2000 shufflings.

TABLE 3—Allele frequencies for the AmpF ℓ STR Profiler Plus loci in Kuki population of India.

| Allele | D3S1358 N: 105 | vWA N: 105 | FGA N: 105 | D8S1179 N: 105 | D21S11 N: 105 | D18S51 N: 105 | D5S818 N: 106 | D13S317 N: 105 | D7S820 N: 105 |
|--------|-------------------|---------------|---------------|-------------------|------------------|------------------|------------------|-------------------|------------------|
| 6 | ... | ... | ... | ... | ... | ... | ... | ... | 0.050 |
| 7 | ... | ... | ... | ... | ... | ... | ... | ... | 0.281 |
| 8 | ... | ... | ... | ... | ... | ... | ... | 0.291 | 0.052 |
| 9 | ... | ... | ... | ... | ... | ... | 0.020 | 0.208 | 0.135 |
| 10 | ... | ... | ... | 0.041 | ... | 0.020 | 0.145 | 0.104 | 0.187 |
| 11 | ... | ... | ... | 0.187 | ... | 0.041 | 0.270 | 0.145 | 0.114 |
| 12 | 0.103 | ... | ... | 0.062 | ... | 0.041 | 0.270 | 0.104 | 0.031 |
| 13 | ... | 0.020 | ... | 0.062 | ... | 0.104 | 0.145 | 0.125 | 0.020 |
| 13.2 | ... | ... | ... | ... | ... | 0.141 | ... | ... | ... |
| 14 | 0.104 | 0.062 | ... | 0.166 | ... | 0.270 | 0.083 | ... | 0.062 |
| 15 | 0.208 | 0.020 | ... | 0.312 | ... | 0.229 | 0.020 | 0.020 | 0.061 |
| 15.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 16 | 0.020 | 0.229 | ... | 0.145 | ... | 0.166 | 0.040 | ... | ... |
| 17 | 0.270 | 0.250 | ... | 0.020 | ... | 0.041 | ... | ... | ... |
| 18 | 0.208 | 0.250 | ... | ... | ... | 0.020 | ... | ... | ... |
| 19 | 0.083 | 0.104 | 0.021 | ... | ... | ... | ... | ... | ... |
| 20 | ... | 0.041 | 0.083 | ... | ... | 0.041 | ... | ... | ... |
| 21 | ... | ... | 0.145 | ... | ... | 0.022 | ... | ... | ... |
| 21.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 22 | ... | ... | 0.165 | ... | ... | ... | ... | ... | ... |
| 22.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 23 | ... | ... | 0.145 | ... | ... | 0.020 | ... | ... | ... |
| 23.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 24 | ... | ... | 0.166 | ... | 0.020 | ... | ... | ... | ... |
| 25 | ... | ... | 0.145 | ... | ... | ... | ... | ... | ... |
| 26 | ... | ... | 0.083 | ... | ... | ... | ... | ... | ... |
| 26.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 27 | ... | ... | 0.041 | ... | ... | ... | ... | ... | ... |
| 27.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 28 | ... | ... | ... | ... | 0.062 | ... | ... | ... | ... |
| 28.2 | ... | ... | ... | ... | 0.083 | ... | ... | ... | ... |
| 29 | ... | ... | ... | ... | 0.104 | ... | ... | ... | ... |
| 29.2 | ... | ... | ... | ... | 0.020 | ... | ... | ... | ... |
| 30 | ... | ... | ... | ... | 0.312 | ... | ... | ... | ... |
| 30.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 31 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31.2 | ... | ... | ... | ... | 0.061 | ... | ... | ... | ... |
| 32 | ... | ... | ... | ... | 0.083 | ... | ... | ... | ... |
| 32.2 | ... | ... | ... | ... | 0.125 | ... | ... | ... | ... |
| 33 | ... | ... | ... | ... | 0.020 | ... | ... | ... | ... |
| 33.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 36 | ... | ... | ... | ... | 0.020 | ... | ... | ... | ... |
| H | 0.875 | 0.834 | 0.542 | 0.792 | 0.775 | 0.895 | 0.834 | 0.821 | 0.709 |
| PD | 0.960 | 0.915 | 0.694 | 0.869 | 0.850 | 0.976 | 0.915 | 0.901 | 0.878 |
| PE | 0.744 | 0.227 | 0.668 | 0.584 | 0.553 | 0.786 | 0.663 | 0.639 | 0.441 |
| P | 0.612 | 0.042 | 0.054 | 0.663 | 0.208 | 0.250 | 0.856 | 0.291 | 0.171 |

H: observed heterozogosity; PD: power of discrimination; PE: probability of exclusion; P: Hardy-Weinberg equilibrium, exact test based on 2000 shufflings.

TABLE 4—Allele frequencies for the AmpF Φ STR Profiler Plus loci in Hmar population of India.

| Allele | D3S1358 N: 101 | vWA N: 101 | FGA N: 101 | D8S1179 N: 101 | D21S11 N: 101 | D18S51 N: 101 | D5S818 N: 101 | D13S317 N: 101 | D7S820 N: 101 |
|--------|-------------------|---------------|---------------|-------------------|------------------|------------------|------------------|-------------------|------------------|
| 6 | ... | ... | ... | ... | ... | ... | ... | ... | 0.110 |
| 7 | ... | ... | ... | ... | ... | ... | 0.010 | ... | 0.250 |
| 8 | ... | ... | ... | ... | ... | ... | 0.010 | 0.281 | ... |
| 9 | ... | ... | ... | 0.010 | ... | ... | 0.135 | 0.229 | 0.250 |
| 10 | ... | ... | ... | 0.093 | ... | 0.010 | 0.145 | 0.104 | 0.277 |
| 11 | ... | ... | ... | 0.125 | ... | 0.020 | 0.260 | 0.125 | 0.111 |
| 12 | 0.051 | ... | ... | 0.104 | ... | 0.031 | 0.208 | 0.145 | ... |
| 13 | ... | 0.010 | ... | 0.208 | ... | 0.104 | 0.156 | 0.104 | ... |
| 13.2 | ... | ... | ... | ... | ... | 0.073 | ... | ... | ... |
| 14 | 0.083 | 0.062 | ... | 0.145 | ... | 0.208 | 0.041 | ... | ... |
| 15 | 0.270 | 0.030 | ... | 0.198 | ... | 0.239 | 0.010 | 0.010 | ... |
| 15.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 16 | 0.010 | 0.260 | ... | 0.093 | ... | 0.125 | 0.020 | ... | ... |
| 17 | 0.312 | 0.281 | ... | 0.020 | ... | 0.093 | ... | ... | ... |
| 18 | 0.218 | 0.198 | 0.022 | ... | ... | 0.020 | ... | ... | ... |
| 19 | 0.052 | 0.114 | 0.031 | ... | ... | 0.010 | ... | ... | ... |
| 20 | ... | 0.031 | 0.094 | ... | ... | 0.020 | ... | ... | ... |
| 21 | ... | 0.010 | 0.145 | ... | ... | 0.020 | ... | ... | ... |
| 21.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 22 | ... | ... | 0.103 | ... | ... | ... | ... | ... | ... |
| 22.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 23 | ... | ... | 0.186 | ... | ... | 0.010 | ... | ... | ... |
| 23.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 24 | ... | ... | 0.187 | ... | 0.010 | ... | ... | ... | ... |
| 25 | ... | ... | 0.135 | ... | ... | 0.010 | ... | ... | ... |
| 26 | ... | ... | 0.062 | ... | ... | ... | ... | ... | ... |
| 26.2 | ... | ... | 0.011 | ... | ... | ... | ... | ... | ... |
| 27 | ... | ... | 0.021 | ... | ... | ... | ... | ... | ... |
| 27.2 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 28 | ... | ... | ... | ... | 0.062 | ... | ... | ... | ... |
| 28.2 | ... | ... | ... | ... | 0.052 | ... | ... | ... | ... |
| 29 | ... | ... | ... | ... | 0.166 | ... | ... | ... | ... |
| 29.2 | ... | ... | ... | ... | 0.010 | ... | ... | ... | ... |
| 30 | ... | ... | ... | ... | 0.281 | ... | ... | ... | ... |
| 30.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 31 | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 31.2 | ... | ... | ... | ... | 0.061 | ... | ... | ... | ... |
| 32 | ... | ... | ... | ... | 0.093 | ... | ... | ... | ... |
| 32.2 | ... | ... | ... | ... | 0.156 | ... | ... | ... | ... |
| 33 | ... | ... | ... | ... | 0.010 | ... | ... | ... | ... |
| 33.2 | ... | ... | ... | ... | 0.041 | ... | ... | ... | ... |
| 36 | ... | ... | ... | ... | 0.010 | ... | ... | ... | ... |
| H | 0.730 | 0.750 | 0.667 | 0.792 | 0.580 | 0.700 | 0.813 | 0.781 | 0.688 |
| PD | 0.823 | 0.827 | 0.732 | 0.869 | 0.636 | 0.768 | 0.892 | 0.857 | 0.765 |
| PE | 0.476 | 0.379 | 0.509 | 0.584 | 0.267 | 0.428 | 0.623 | 0.564 | 0.410 |
| P | 0.386 | 0.127 | 0.049 | 0.168 | 0.187 | 0.250 | 0.730 | 0.166 | 0.129 |

H: observed heterozygosity; PD: power of discrimination; PE: probability of exclusion; P: Hardy-Weinberg equilibrium; exact test based on 2000 shufflings.