

FOR THE RECORD

R. Trivedi,¹ Ph.D.; Prabal Chattopadhyay,¹ Ph.D.; R. Dutta,¹ Ph.D.; N. Sarkar;¹ A.K. Sharma,¹ Ph.D.; and V.K. Kashayp,¹ Ph.D.

D1S80 Population Data in Eight Predominant Populations of India*

POPULATION: Studied populations are Indo-Caucasian represented by Baniya (Bihar), Deshast Brahmin (Maharashtra), Bengalee Kayastha (W.Bengal), Mixed Punjabi (Punjab), Indo Mongoloids represented by Kuki and Hmar (Manipur), Indo Proto-Australoid Ekere and a mixture of Proto-Australoid and Indo-Caucasian Reddy (Andhra Pradesh).

KEYWORDS: forensic science, Indo-Caucasian, Indo-Mongoloid, Proto-Australoid, D1S80, HWE, genetic database

DNA Extraction: From blood by phenol chloroform method (1), from buccal swab by chelex method (Bio-rad chelex 100 resin).

PCR: 2.5 ng target DNA following manufacturer's instructions (2).

Typing: By silver staining based allele detection on p. 3.

Result: See Table 1.

Quality Control: Laboratory Internal Control Standards and Kit controls.

Access of data: Via electronic mail from communicating author.

Analysis of data: DNA TYPE (Windows 98/NT version Y.Zhong, CHG, University of Texas). PE & PD (4).

Other remarks: D1S80 Alleles 14 and 15 are absent in most of the important world populations (U.S., Caucasian, and African-American), but were observed in Dehshast Brahmin among studied Indian populations. The allele 14 is the most rare allele among all alleles for Indian population groups. The maximum allele occur-

rence among the Indian populations was slightly different compared to published data of other world populations. Tests for independence for the alleles within a locus revealed no deviation from expected values for the eight populations of this study. The product of allele frequencies derived from the data can be used in forensic analysis and paternity tests to estimate the frequency of a D1S80 genotype.

References:

1. Sambrook J, Fritsch EF, Maniatis T. Molecular cloning: a laboratory manual. 2nd edition. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 1989.
2. Perkin Elmer/AmpliFLP™ D1S80 PCR Amplification Kit-User Manual. 2000.
3. Budowle B, Baechtel FS, Smerick JB, Presley KW, Giusti AM, Parsons G, et al. D1S80 Population Data in African Americans, Caucasians, Southeastern Hispanics, Southwestern Hispanics, and Orientals. *J Forensic Sci* 1995;40:38-44.
4. 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. Arlington VA: American Association of Blood Banks, 1983:277-88.

Additional information and reprint requests:

Dr. V. K. Kashayp
DNA Typing Unit
Central Forensic Science Laboratory
30 Gorachand Rd.
Calcutta 700014
West Bengal, India
Phone: +91-033-284-1753
Fax: +91-033-284-1753

¹ DNA Typing Unit, Central Forensic Science Laboratory, 30 Gorachand Road, Calcutta 700014, West Bengal, India.

* This study was supported by grants from BPR&D, India.

TABLE 1—*D1S80* allele frequencies in eight sub-populations of India.

Allele	Punjabi (<i>N</i> = 25)	Kuki (<i>N</i> = 48)	Hmar (<i>N</i> = 72)	Ekere (<i>N</i> = 83)	Reddy (<i>N</i> = 72)	Baniya (<i>N</i> = 87)	Deshast Brahmin (<i>N</i> = 105)	Bengali Kayastha (<i>N</i> = 103)
14	0	0	0	0	0	0	0.024	0
15	0	0	0	0	0	0	0.014	0
16	0.071	0	0.048	0.024	0.056	0.046	0.138	0.024
17	0	0	0	0.006	0.007	0.006	0.014	0.004
18	0.214	0.208	0.152	0.331	0.347	0.379	0.276	0.349
19	0.024	0.063	0.027	0.042	0.007	0.011	0	0
20	0	0	0	0.006	0	0.046	0.029	0.004
21	0.048	0	0.02	0.018	0.021	0.017	0	0.004
22	0.024	0.021	0.062	0.078	0.056	0.023	0.057	0.033
23	0	0	0	0.018	0.035	0.006	0.033	0
24	0.019	0.146	0.118	0.223	0.306	0.241	0.152	0.291
25	0.047	0	0.042	0.09	0.021	0.034	0.028	0.043
26	0.024	0.021	0.048	0.012	0.014	0.063	0.043	0.019
27	0.072	0	0.014	0	0	0.017	0	0
28	0.048	0.208	0.069	0.048	0.042	0.011	0.052	0.043
29	0.048	0.021	0.014	0.012	0.028	0.011	0	0.024
30	0.072	0.021	0.035	0.042	0.014	0.006	0.029	0.009
31	0.095	0.125	0.111	0.048	0.021	0	0.052	0.067
32	0.024	0.125	0.188	0	0.029	0.063	0.057	0
33	0	0	0	0	0	0.011	0	0.004
34	0	0.042	0.035	0	0	0	0	0
36	0.048	0	0	0	0	0	0	0
37	0	0	0.139	0	0	0.006	0	0
39	0.024	0	0	0	0	0	0	0
41	0	0	0	0	0.029	0	0	0.024
H	0.857	0.875	0.902	0.750	0.750	0.781	0.809	0.747
PD	0.915	0.934	0.887	0.817	0.817	0.850	0.864	0.782
PE	0.709	0.745	0.799	0.510	0.510	0.565	0.616	0.505
P	0.23	0.063	0.13	0.67	0.55	0.085	0.0	0.235

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