FOR THE RECORD

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Indian Population Data for Two Tetrameric Short Tandem Repeat Loci—vWA and D3S1359

POPULATION: Five anthropologically distinct population groups from two broad geographical areas of India were analyzed: Konkanasthas and Marathas from Western India (state of Maharashtra), and Nairs, Ezhavas, and Muslims from Southern India (state of Kerala). A total of 241 healthy adult volunteers for vWA and 194 individuals for D3S1359 were studied.

KEYWORDS: forensic science, Indian population, short tandem repeat, vWA, D3S1359

DNA Extraction—Rapid non-enzymatic salt precipitation method (1).

PCR—Amplification was achieved using locus specific primers (2,3). Forward primers were flourescently labeled with Cy5 dye amidite. Amplimers were typed using 6% denaturing gels containing 7M urea on ALF Express DNA Sequencer (Amersham Pharmacia Biotech). Internal standards in each lane and allelic ladders developed in the laboratory were used.

Access to Complete Dataset—Via electronic mail from corresponding author, M. Seshadri at *msesh@apsara.barc.ernet.in*

Analysis of Data—Arlequin ver 1.1 (4). The Polymorphic Information Content was determined according to Botstein et al. (5) and the Power of Discrimination was calculated as by Fisher (6).

vWA and D3S1359 exhibited 8 and 17 alleles respectively, which are in agreement with the other published reports on Indian and

world populations (7,8). Using Exact test (<0.05), Ezhavas and Nairs deviated from Hardy Weinberg equilibrium at locus vWA.

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TABLE 1—Allele frequency distribution at vWA locus among five Indian population groups.

Allele	Konkanasthas $(n = 122)$	Marathas $(n = 86)$	Nairs $(n = 68)$	Ezhavas $(n = 108)$	Muslims $(n = 98)$
	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.
13	0.03 ± 0.016	0.06 ± 0.025	0.03 ± 0.021	0.10 ± 0.029	0.04 ± 0.020
14	0.06 ± 0.022	0.07 ± 0.028	0.22 ± 0.051	0.10 ± 0.029	0.10 ± 0.031
15	0.09 ± 0.026	0.06 ± 0.025	0.03 ± 0.020	0.03 ± 0.016	0.06 ± 0.024
16	0.13 ± 0.031	0.22 ± 0.045	0.19 ± 0.048	0.20 ± 0.039	0.22 ± 0.042
17	0.37 ± 0.044	0.31 ± 0.050	0.34 ± 0.058	0.32 ± 0.045	0.25 ± 0.044
18	0.22 ± 0.038	0.05 ± 0.023	0.12 ± 0.039	0.08 ± 0.026	0.21 ± 0.042
19	0.09 ± 0.026	0.16 ± 0.040	0.06 ± 0.028	0.14 ± 0.033	0.09 ± 0.029
20		0.07 ± 0.027	0.01 ± 0.015	0.02 ± 0.013	0.01 ± 0.010
H	0.77	0.72	0.76	0.66	0.71
h	0.78 ± 0.023	0.82 ± 0.023	0.79 ± 0.026	0.81 ± 0.020	0.82 ± 0.016
Exact test	0.582 ± 0.0012	0.196 ± 0.0010	0.940 ± 0.0008	0.012 ± 0.0002	0.046 ± 0.0005
PIC	0.81	0.83	0.81	0.83	0.84
PD	0.92	0.93	0.92	0.92	0.92

n = number of chromosomes; H = Observed heterozygosity; h = Expected heterozygosity; PIC = Polymorphic Information Content; PD = Power of discrimination.

TABLE 2—Allele frequency distribution at D3S1359 among five Indian population groups.

Allele	Konkanasthas $(n = 94)$	Marathas $(n = 88)$	Nairs (n = 56)	Ezhavas $(n = 76)$	Muslims $(n = 74)$
	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.
10			0.02 ± 0.018		
11	0.01 ± 0.010	0.01 ± 0.011	0.04 ± 0.025	•••	•••
12	0.07 ± 0.027	0.08 ± 0.029		0.11 ± 0.035	0.07 ± 0.029
13	0.15 ± 0.037	0.15 ± 0.038	0.23 ± 0.057	0.26 ± 0.051	0.14 ± 0.040
14	0.36 ± 0.050	0.31 ± 0.049	0.23 ± 0.057	0.29 ± 0.052	0.24 ± 0.050
15	0.24 ± 0.044	0.22 ± 0.045	0.12 ± 0.044	0.20 ± 0.046	0.24 ± 0.050
16	0.02 ± 0.015	0.07 ± 0.027	0.14 ± 0.047	0.08 ± 0.031	0.14 ± 0.040
17	•••	0.01 ± 0.011	0.05 ± 0.030	0.01 ± 0.013	0.03 ± 0.019
18	•••				0.01 ± 0.013
19	•••			•••	0.03 ± 0.019
20	0.02 ± 0.015	0.02 ± 0.016		0.01 ± 0.013	0.01 ± 0.013
21	•••		0.02 ± 0.017	•••	
22	0.05 ± 0.023	0.02 ± 0.016	0.05 ± 0.030	0.03 ± 0.018	0.03 ± 0.019
23	0.01 ± 0.010	0.03 ± 0.016	0.07 ± 0.034	•••	0.05 ± 0.026
24	0.01 ± 0.010	0.03 ± 0.020	•••	•••	0.01 ± 0.013
25	0.04 ± 0.021	0.01 ± 0.011	0.02 ± 0.018	•••	
26	•••	0.03 ± 0.020	•••	0.01 ± 0.013	0.01 ± 0.013
Н	0.68	0.68	0.71	0.68	0.78
h	0.79 ± 0.025	0.83 ± 0.023	0.86 ± 0.0022	0.80 ± 0.021	0.84 ± 0.021
Exact test	0.054 ± 0.0005	0.109 ± 0.0005	0.123 ± 0.0005	0.361 ± 0.0008	0.228 ± 0.0008
PIC	0.81	0.84	0.84	0.82	0.85
PD	0.93	0.93	0.93	0.92	0.94

n = number of chromosomes; H = Observed heterozygosity; h = Expected heterozygosity; PIC = Polymorphic Information Content; PD = Power of discrimination.