

FOR THE RECORD

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Allele Frequency Distribution at Five Y-Chromosomal Short Tandem Repeat Loci Among Five Distinct Ethnic Groups of India

POPULATION: We have analyzed the distribution of allele frequencies at five Y-chromosomal short tandem repeat (STR) loci (DYS19, DYS389I, DYS389II, DYS391 and DYS393) among five anthropologically distinct ethnic groups of India, namely, Konkanasthas, Marathas, Nairs, Ezhavas and Muslims. Konkanasthas and Marathas belong to the state of Maharashtra in Western India and both the population groups speak "Marathi", an Indo-European language. Nairs, Ezhavas and Muslims belong to Kollam district of Kerala state in South India and all the three population groups speak "Malayalam", an Indo-Dravidian language. About 220 random, healthy and normal male volunteers were studied at these loci.

KEYWORDS: forensic science, Y-chromosomal STRs, DYS19, DYS389I, DYS389II, DYS391, DYS393, allele frequency, Indian population

Genomic DNA was extracted using a rapid non-enzymatic method (1). The PCR primers and the parameters for PCR amplification of all the five Y-chromosomal STRs were as described by Kayser et al. (2) and de Knijff et al. (3). The forward primer of each locus was labeled with fluorescent CY5™ dye amidite (Amersham Pharmacia Biotech) and PCR was carried out in a Hybaid™ thermal cycler using Taq polymerase (Roche Molecular Biochemicals). Amplimers were electrophoresed in 6% denaturing urea gel (7M) and analyzed by fragment manager using ALF Express DNA Sequencer (Amersham Pharmacia Biotech). Internal ladders were used for the accurate size determination. Allelic ladders were prepared for each locus and used as external standards in addition to CY5™ labelled 50 to 500 bp DNA ladder (Amersham Pharmacia Biotech). At each locus, the amplimers were compared with the standards, kindly supplied by Dr. Chris Tyler-Smith from Oxford University, Oxford, UK, for confirmation.

Access to Data—Via electronic mail from communicating author, Birajalaxmi Das, M. Phil, msesh@apsara.bare.ernet.in.

Analysis of Data—Allele frequencies and gene diversities were calculated by using the software ARLEQUIN ver. 1.1 (4). The

nomenclature of the allele sizes were as described by Kayser et al. (2) except for DYS389I and DYS389 II, which was according to Cooper et al. (5).

Allele frequencies and the gene diversities observed at five Y-chromosomal STRs among Konkanasthas, Marathas, Nairs, Ezhavas, and Muslims are given in Tables 1 to 5, respectively. At DYS19 locus, the predominant allele was found to be allele 15 in all the groups except Ezhavas where allele 14 was predominant. At DYS389I and DYS391 loci, the predominant allele was allele 10 among all the five population groups. At DYS389II locus, allele 16 was observed to be predominant among Konkanasthas, allele 17 was among Marathas, Nairs, and Ezhavas and allele 18 was among Muslims. At DYS393 locus, allele 12 was predominant among Konkanasthas, Nairs, and Muslims whereas allele 11 was found to be predominant among Marathas and Ezhavas. Highest gene diversity was observed at DYS389II locus and the lowest at DYS391 across all the five Indian population groups.

References

1. Lahiri K, Nurnberger JL. A rapid non-enzymatic method for the preparation of HMW DNA from blood for RFLP studies. *Nucleic Acid Res* 1991; 19:5444.
2. Kayser M, Caglia A, Corach D, Fretwell N, Gehrig C, Graziosi G, et al. Evaluation of Y chromosomal STRs: a multicentre study. *Int J Legal Med* 1997;110:125–33 and 141–9.
3. de knijff P, Kayser M, Kaglia A, Corach D, Fretwell N, Gehrig C, et al. Chromosome Y microsatellites: Population genetic and evolutionary aspects. *Int J Legal Med* 1997;110:134–40 and 141–9.
4. Schneider S, Kueffer JM, Roessli D, Excoffier L. ARLEQUIN version 1.1: a software for population genetic data analysis. Genetics and Biometry Laboratory, University of Geneva, Switzerland. 1997.
5. Cooper G, Amos W, Hoffman D, Rubinsztein C. Network analysis of human Y icrosatellite haplotypes. *Hum Mol Genet* 1996;5(11):1759–66.

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TABLE 1—Allele frequency distribution at five Y-chromosomal STRs among Konkanasthas.

Allele (repeats)	DYS19 (N = 52)		DYS389I (N = 41)		DYS389II (N = 41)		DYS391 (N = 40)		DYS393 (N = 42)	
	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq
8	4	0.098
9	9	0.220
10	23	0.561	28	0.700	9	0.214
11	5	0.122	12	0.300	8	0.190
12	20	0.476
13	5	0.119
14	11	0.212
15	22	0.423	5	0.122
16	17	0.327	17	0.415
17	2	0.038	9	0.220
18	7	0.171
19	3	0.073
Gene diversity	0.66		0.65		0.73		0.42		0.68	

No. Obs. = Number of alleles observed, Freq = frequency.

TABLE 2—Allele frequency distribution at five Y-chromosomal STRs among Marathas.

Allele (repeats)	DYS19 (N = 83)		DYS389I (N = 61)		DYS389II (N = 57)		DYS391 (N = 52)		DYS393 (N = 60)	
	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq
8
9	17	0.279
10	36	0.590	46	0.885	3	0.050
11	8	0.131	6	0.115	24	0.400
12	19	0.317
13	1	0.012	14	0.233
14	16	0.193	1	0.018
15	39	0.470	4	0.070
16	19	0.229	17	0.298
17	8	0.096	18	0.316
18	9	0.158
19	8	0.140
Gene diversity	0.68		0.56		0.76		0.20		0.68	

No. Obs. = Number of alleles observed, Freq = frequency.

TABLE 3—Allele frequency distribution at five Y-chromosomal STRs among Nairs.

Allele (repeats)	DYS19 (N = 22)		DYS389I (N = 24)		DYS389II (N = 22)		DYS391 (N = 22)		DYS393 (N = 22)	
	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq
9	4	0.167
10	16	0.667	17	0.772	2	0.091
11	4	0.167	5	0.228	6	0.273
12	11	0.500
13	1	0.045	3	0.136
14	3	0.136
15	14	0.636	1	0.045
16	2	0.091	5	0.227
17	2	0.091	8	0.364
18	7	0.318
19	1	0.045
Gene diversity	0.56		0.52		0.71		0.35		0.65	

No. Obs. = Number of alleles observed, Freq = frequency.

TABLE 4—Allele frequency distribution at five Y-chromosomal STRs among Ezhavas.

Allele (repeats)	DYS19 (N = 37)		DYS389I (N = 40)		DYS389II (N = 37)		DYS391 (N = 37)		DYS393 (N = 37)	
	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq
9	5	0.125
10	29	0.725	30	0.811	6	0.162
11	6	0.150	7	0.189	14	0.378
12	13	0.351
13	0	0.0	4	0.108
14	15	0.406	3	0.081
15	10	0.270	3	0.081
16	11	0.297	8	0.216
17	1	0.027	9	0.243
18	8	0.216
19	6	0.162
Gene diversity	0.67		0.44		0.81		0.31		0.70	

No. Obs. = Number of alleles observed, Freq = frequency.

TABLE 5—Allele frequency distribution at five Y-chromosomal STRs among Muslims.

Allele (repeats)	DYS19 (N = 27)		DYS389I (N = 28)		DYS389II (N = 27)		DYS391 (N = 27)		DYS393 (N = 27)	
	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq	No. Obs.	Freq
9	5	0.179
10	18	0.643	23	0.852
11	5	0.179	4	0.148	8	0.296
12	13	0.481
13	0	0.0	6	0.222
14	8	0.296	1	0.037
15	12	0.444	2	0.074
16	5	0.185	5	0.185
17	2	0.074	7	0.259
18	9	0.333
19	3	0.111
Gene diversity	0.68		0.48		0.77		0.25		0.63	

Obs. No. = Observed number of alleles, Freq = frequency.