

FOR THE RECORD

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Molecular Genetic Analysis of TPO and CD4 Loci Among Two Endogamous Ethnic Groups of Maharashtra in Western India

POPULATION: Molecular genetic polymorphism study was undertaken in two endogamous ethnic groups of Maharashtra in Western India at two microsatellites i.e., TPO, a tetranucleotide repeat locus and CD4, a pentanucleotide repeat locus. The two ethnic groups studied were Konkanastha Brahmins and Marathas belonging to Indo-European language family. Eighty-two random, unrelated individuals were genotyped for the locus TPO, whereas for CD4 locus, 79 individuals were genotyped.

KEYWORDS: forensic science, TPO, CD4, Western Indian population

TABLE 1—Allele frequencies at TPO locus.

Allele (repeats)	Konkanastha Brahmins (n = 104)		Marathas (n = 60)	
	No. observed	Frequency ± SD	No. observed	Frequency ± SD
5	1	0.017 ± 0.017
6	1	0.017 ± 0.017
7	7	0.067 ± 0.025	5	0.083 ± 0.036
8	21	0.202 ± 0.040	17	0.283 ± 0.059
9	10	0.096 ± 0.029	11	0.183 ± 0.050
10	31	0.298 ± 0.045	19	0.317 ± 0.061
11	21	0.202 ± 0.040	4	0.067 ± 0.031
12	12	0.115 ± 0.032	2	0.033 ± 0.023
13	2	0.019 ± 0.014
H		0.88		0.70
h		0.81 ± 0.017		0.79 ± 0.027
PD		0.90		0.86
PIC		0.83		0.81
Exact test (P value)		0.024 ± 0.0006		0.004 ± 0.0001

SD: Standard deviation, No.: Number, H: Observed heterozygosity, h: Expected heterozygosity, PD: Power of discrimination, PIC: Polymorphic information content, n: Number of chromosomes.

Genomic DNA was extracted using a rapid non-enzymatic method (1) and PCR amplification of TPO and CD4 loci were performed using locus specific primers flanking the repeat region (2,3). Amplimers were electrophoresed on 6% denaturing urea gel (7M) and analyzed in ALF Express DNA Sequencer (Amersham Pharmacia Biotech, Uppasala, Sweden) using the software Fragment manager. Internal ladders and allelic ladders were used for both the loci for correct assignment of the allele sizes.

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TABLE 2—Allele frequencies at CD4 locus.

Allele	Konkanastha Brahmins (n = 102)		Marathas (n = 56)	
	No. observed	Frequency ± SD	No. observed	Frequency ± SD
2	1	0.018 ± 0.018
3	2	0.020 ± 0.014	2	0.036 ± 0.025
4	51	0.500 ± 0.050	19	0.339 ± 0.064
5	13	0.127 ± 0.033	5	0.089 ± 0.039
7	2	0.036 ± 0.025
8	12	0.118 ± 0.032	15	0.268 ± 0.060
9	19	0.186 ± 0.039	12	0.214 ± 0.055
10	5	0.049 ± 0.022
H		0.59		0.68
h		0.69 ± 0.037		0.77 ± 0.028
PD		0.85		0.88
PIC		0.70		0.80
Exact test (P value)		0.052 ± 0.0008		0.015 ± 0.0003

SD: Standard deviation, No.: Number, H: Observed heterozygosity, h: Expected heterozygosity, PD: Power of discrimination, PIC: Polymorphic information content, n: Number of chromosomes.

Nomenclature of alleles for both the loci (TPO and CD4) was based on the number of repeat units.

Allele and genotype frequencies, gene diversities and exact tests were performed using the program ARLEQUIN Ver. 1.1 (4). The polymorphic information content (PIC) was determined according to Botstein et al. (5) and the power of discrimination (PD) was calculated as described by Fisher (6).

A total number of 9 alleles (5–13 repeats) were observed at TPO (Table 1), whereas 8 alleles (2–10 repeats) were observed at CD4 locus (Tables 2). At TPO locus, allele 10 was observed to be the predominant for both ethnic groups. Similarly, allele 4 was the predominant allele among both the ethnic groups. Because of high PIC

and PD values, these two loci would be very useful and informative for forensic investigations in India.

Access to the complete dataset is available via electronic mail from communicating authors: msesh@apsara.barc.ernet.in and birajalaxmi@yahoo.co.in

References

1. Lahiri D, Nurnberger J. A rapid non-enzymatic method for the preparation of HMW DNA from blood for RELP studies. *Nucleic Acids Res* 1991;19:5444. [\[PubMed\]](#)
2. Anker R, Steinbreuk T, Donnis-Keller H. Tetranucleotide polymorphisms at the human thyroid peroxidase (hTPO) locus. *Hum Mol Genet* 1992;1:137. [\[PubMed\]](#)
3. Edwards MC, Clemens PR, Tristan M, Pizzuti A, Gibbs RA. Pentanucleotide repeat length polymorphism at the human CD4 locus. *Nucleic Acids Res* 1991;19:4791. [\[PubMed\]](#)

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. Botstein D, White RL, Skolnick M, Davis RW. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *Am J Hum Genet* 1980;32:314–31. [\[PubMed\]](#)
6. Fisher R. Standard calculations for evaluating a blood group system. *Heredity* 1951;5:95–102. [\[PubMed\]](#)

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