

FOR THE RECORD

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Distribution of Allele Frequencies for Two Short Tandem Repeats (HUMTH01 and F13A01) Among Five Indian Population Groups

POPULATION: Populations studied include two groups from the state of Maharashtra, namely Konkanasthas and Marathas, and three groups from the state of Kerala, namely Nairs, Ezhavas, and Muslims. All the five groups are endogamous ethnic groups representing two geographically, linguistically, and culturally distinct Western and Southern regions of India. A total of 205 unrelated healthy donors for HUMTH01 and 227 individuals for F13A01 were analyzed.

KEYWORDS: forensic science, DNA typing, Indian population, short tandem repeat, HUMTH01, F13A01, allele frequency

DNA Extraction—Using rapid non-enzymatic method as per Lahiri and Numberger (1).

PCR—Amplification was carried out in Eppendorf™ Master Cycler using locus specific primers (2,3). The forward primers were fluorescently labeled using Cy5 dye amidite. The amplified products were analyzed on 6% polyacrylamide gels containing 7M urea using ALF Express DNA Sequencer (Amersham Pharmacia Biotech). In addition to Cy5 labeled 50 to 500 bp ladder (Amersham Pharmacia Biotech), internal standards in each lane and allelic ladders developed in our laboratory were used.

Access to Data—Via email from M. Seshadri, Ph.D., at msesh@apsara.barc.ernet.in

Analysis of Data—Allele frequencies, gene diversities, and exact test were calculated using Arlequin ver. 1.1 (4), Polymorphic

Information Content as per Botstein et al. (5) and Power of Discrimination as detailed in Fisher (6).

Allele frequencies for HUMTH01 and F13A01 are presented in Tables 1 and 2, respectively. Allele 9 was predominant for HUMTH01 in four populations except Marathas and allele 5 was most common for F13A01 across all the five population groups. Nairs deviated from Hardy-Weinberg equilibrium at locus F13A01 ($p = 0.028$) (Table 3).

References

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TABLE 1—Allele frequency distribution of *HUMTH01* locus among five Indian population groups.

Allele	Konkanasthas (n = 92)	Marathas (n = 86)	Nairs (n = 68)	Ezhavas (n = 100)	Muslims (n = 64)
	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.
5	0.03 ± 0.021 (2)	0.01 ± 0.010 (1)	0.06 ± 0.030 (4)
6	0.23 ± 0.044 (21)	0.31 ± 0.050 (27)	0.21 ± 0.050 (14)	0.22 ± 0.042 (22)	0.26 ± 0.055 (17)
7	0.22 ± 0.043 (20)	0.12 ± 0.035 (10)	0.15 ± 0.043 (10)	0.20 ± 0.040 (20)	0.11 ± 0.039 (7)
8	0.09 ± 0.029 (8)	0.15 ± 0.039 (13)	0.21 ± 0.049 (14)	0.18 ± 0.039 (18)	0.12 ± 0.042 (8)
9	0.28 ± 0.047 (26)	0.30 ± 0.050 (26)	0.26 ± 0.054 (18)	0.28 ± 0.045 (28)	0.33 ± 0.059 (21)
9.3	0.16 ± 0.038 (15)	0.05 ± 0.023 (4)	0.07 ± 0.032 (5)	0.02 ± 0.014 (2)	0.06 ± 0.030 (4)
10	0.02 ± 0.015 (2)	0.07 ± 0.027 (6)	0.06 ± 0.029 (4)	0.09 ± 0.029 (9)	0.01 ± 0.015 (1)
11	0.01 ± 0.015 (1)	...	0.03 ± 0.022 (2)

n = number of chromosomes; The number in the parenthesis denotes the observed number for each allele.

TABLE 2—Allele frequency distribution of *F13A01* locus among five Indian population groups.

Allele	Konkanasthas (n = 104)	Marathas (n = 102)	Nairs (n = 78)	Ezhavas (n = 98)	Muslims (n = 72)
	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.	Freq. ± s.d.
3.2	0.12 ± 0.033 (13)	0.18 ± 0.038 (18)	0.26 ± 0.050 (20)	0.23 ± 0.043 (23)	0.10 ± 0.035 (7)
4	0.08 ± 0.026 (8)	0.04 ± 0.019 (4)	0.13 ± 0.038 (10)	0.08 ± 0.028 (8)	0.14 ± 0.041 (10)
5	0.27 ± 0.043 (28)	0.45 ± 0.049 (46)	0.35 ± 0.054 (27)	0.38 ± 0.049 (37)	0.39 ± 0.058 (28)
6	0.20 ± 0.040 (21)	0.14 ± 0.034 (14)	0.14 ± 0.040 (11)	0.17 ± 0.038 (17)	0.21 ± 0.048 (15)
7	0.20 ± 0.040 (21)	0.16 ± 0.036 (16)	0.06 ± 0.028 (5)	0.01 ± 0.010 (1)	0.08 ± 0.033 (6)
8	0.01 ± 0.013 (1)	...	0.01 ± 0.014 (1)
9	0.04 ± 0.022 (3)
10
11	...	0.01 ± 0.010 (1)
12	...	0.01 ± 0.001 (1)
13	0.05 ± 0.021 (5)	...	0.01 ± 0.013 (1)	0.07 ± 0.026 (7)	0.01 ± 0.014 (1)
14	0.03 ± 0.017 (3)	0.01 ± 0.014 (1)
15	0.03 ± 0.016 (3)	0.02 ± 0.014 (2)	...	0.02 ± 0.014 (2)	0.03 ± 0.019 (2)
16	0.05 ± 0.021 (5)	0.01 ± 0.014 (1)

n = number of chromosomes; The number in the parenthesis denotes the observed number for each allele.

TABLE 3—Statistical analysis for *HUMTH01* and *F13A01* locus among five Indian population groups.

	Konkanasthas	Marathas	Nairs	Ezhavas	Muslims
HUMTH01					
H	0.76	0.74	0.82	0.74	0.81
h	0.79 ± 0.015	0.77 ± 0.022	0.82 ± 0.019	0.80 ± 0.014	0.80 ± 0.028
Exact test	0.990 ± 0.0003	0.210 ± 0.0013	0.848 ± 0.0011	0.061 ± 0.0005	0.257 ± 0.0014
PIC	0.82	0.80	0.84	0.82	0.81
PD	0.92	0.91	0.93	0.91	0.90
F13A01					
H	0.88	0.71	0.64	0.71	0.61
h	0.83 ± 0.016	0.72 ± 0.032	0.78 ± 0.025	0.77 ± 0.026	0.78 ± 0.033
Exact test	0.145 ± 0.0009	0.221 ± 0.0008	0.028 ± 0.0004	0.052 ± 0.0006	0.094 ± 0.0004
PIC	0.87	0.75	0.80	0.79	0.80
PD	0.91	0.88	0.90	0.89	0.91

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