

FOR THE RECORD

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Allele Frequency Distribution of D8S592 (STR) and PDGFA (VNTR) Among Five Endogamous Population Groups of India

POPULATION: Allele frequency distribution have been analyzed at D8S592 (short tandem repeat) and PDGFA (variable number of tandem repeat) among five distinct endogamous groups of India namely Ezhavas, Nayars, Arayas, Vishwakarma and Muslims. Muslims are religio-ethnic group while other populations mentioned above belong to distinct section of Hindu religion. All these populations are from Kollam district of Kerala in Southern India and speak Malayalam, an Indo-Dravidian language. A total of 228 for D8S592 and 212 for PDGFA loci, random, healthy individuals were analyzed.

KEYWORDS: forensic science, DNA typing, Indian population, short tandem repeat, variable number of tandem repeat, D8S592 and PDGFA

DNA Extraction: DNA was extracted using rapid, non-enzymatic salt precipitation method (1).

Amplification and Genotyping: PCR amplification of D8S592 and PDGFA loci was carried out using locus specific primers (2,3), in EppendorfTM Gradient Master Cycler. The forward primer of D8S592 was fluorescently labeled using Cy5 dye amidite. Amplification was carried out in 25 μ L PCR reaction mixture containing 25 ng of genomic DNA. The amplified product of D8S592 locus was analyzed on 6% denaturing polyacrylamide gel containing 7 M urea using Alf Express DNA Sequencer (Amersham Pharmacia Biotech). In addition to external standard (107, 228 and 395 bps), internal standards were also used in each lane of the gel to overcome lane to lane variation.

PDGFA (49 bp VNTR present on IVS3 of PDGFA gene) amplicon were electrophoresced on 4% native polyacrylamide and visualized by silver staining method (4). Alleles were assigned using allelic ladder prepared in the lab and sizes were confirmed using Marker VI (Roche Biochemical) and Sequaid 2 ver 3.5 (5).

Analysis of Data: Allele frequencies and heterozygosity were calculated using software Popgene ver 1.31 (6). Binomial standard errors were calculated separately for each allele frequency estimates as $\{\pi(1 - \pi)/n\}^{1/2}$ Chang et al. (7). The polymorphism information content (PIC) was calculated as per Bolstein et al. (8) and power of discrimination (PD) as mentioned by Fisher (9).

Allele frequencies for D8S592 and PDGFA are presented in Tables 1 and 2, respectively. At D8S592 locus 7 alleles were observed. Alleles were classified as per their number of repeats. Fourteen repeat was predominant in Ezhvas, Nayars, Arayas and Muslim population, while in Vishwakarma 15 repeat was predominant. In case of PDGFA locus 8 alleles were observed. Repeat 8 was

TABLE 1—Allele frequency distribution at D8S592 in five Indian population groups.

Allele (Repeats)	Ezhavas (n = 160)	Nayars (n = 72)	Arayas (n = 72)	Vishwakarma (n = 34)	Muslims (n = 118)
	Freq. S.E	Freq. S.E	Freq. S.E	Freq. S.E	Freq. S.E
11	0.01 \pm 0.008	...	0.01 \pm 0.011
12	0.03 \pm 0.013	0.08 \pm 0.032	0.01 \pm 0.011	...	0.03 \pm 0.016
13	0.29 \pm 0.036	0.33 \pm 0.055	0.33 \pm 0.055	0.29 \pm 0.078	0.33 \pm 0.043
14	0.36 \pm 0.038	0.34 \pm 0.056	0.38 \pm 0.057	0.29 \pm 0.078	0.42 \pm 0.018
15	0.27 \pm 0.035	0.18 \pm 0.045	0.21 \pm 0.048	0.35 \pm 0.082	0.18 \pm 0.035
16	0.03 \pm 0.013	0.06 \pm 0.028	0.06 \pm 0.028	0.07 \pm 0.043	0.03 \pm 0.016
17	0.01 \pm 0.008	0.01 \pm 0.011	0.01 \pm 0.009
H	0.688	0.722	0.750	0.824	0.780
h	0.713	0.745	0.711	0.720	0.678
PIC	0.764	0.779	0.739	0.759	0.733
PD	0.859	0.884	0.972	0.846	0.831

n = No of chromosomes; H = Observed heterozygosity; h = Expected heterozygosity; PIC = Polymorphism information content; PD = Power of discrimination.

TABLE 2—PDGFA allele frequencies in five Indian population groups.

Allele (Repeats)	Ezhavas (n = 140)	Nayers (n = 68)	Arayas (n = 62)	Vishwakarma (n = 34)	Muslims (n = 110)
	Freq. S.E	Freq. S.E	Freq. S.E	Freq. S.E	Freq. S.E
4	0.03 ± 0.014	0.02 ± 0.017	0.01 ± 0.009
5	0.01 ± 0.009
6	0.07 ± 0.021	0.03 ± 0.021	0.19 ± 0.049	0.15 ± 0.061	0.08 ± 0.026
7	0.36 ± 0.041	0.07 ± 0.031	0.36 ± 0.061	0.32 ± 0.080	0.44 ± 0.047
8	0.40 ± 0.041	0.29 ± 0.055	0.26 ± 0.056	0.47 ± 0.086	0.35 ± 0.045
9	0.14 ± 0.029	0.47 ± 0.061	0.15 ± 0.045	0.03 ± 0.029	0.10 ± 0.029
10	...	0.10 ± 0.036	0.02 ± 0.017	0.03 ± 0.029	0.01 ± 0.009
11	...	0.02 ± 0.017	0.02 ± 0.017
H	0.757	0.941	0.677	0.588	0.746
h	0.688	0.685	0.752	0.670	0.671
PIC	0.739	0.724	0.805	0.712	0.724
PD	0.842	0.844	0.888	0.813	0.829

n = No of chromosomes; H = Observed heterozygosity; h = Expected heterozygosity; PIC = Polymorphism information content; PD = Power of discrimination.

predominant among Ezhavas and Vishwakarma. In Nayers repeat 9 and for Arayas and Muslims repeat 7 was predominant. The expected and observed heterozygosity did not show any significant difference at all the three loci. Alleles at both the loci for all five populations were in Hardy Weinberg Equilibrium. High PIC and PD value of these STR and VNTR showed these markers were informative and can be used for forensic DNA typing and paternity testing.

The complete dataset is available to any researcher via electronic mail from corresponding author at msesh@apsara.barc.ernet.in.

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