

## FOR THE RECORD

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# Distribution of Allele Frequencies of One VNTR and Two STR Loci in Five Population Groups of South India

**POPULATIONS:** Ezhavas, Muslims, Arayas, Nairs, and Vishwakarmas of the Kerala state in South India for one VNTR (DRD4) and two STR markers (D7S820 and D9S926).

**KEYWORDS:** forensic science, South Indian populations, short tandem repeats, variable number of tandem repeats

DNA was extracted by using a non-enzymatic method (1) from blood of normal, healthy, and random individuals. Amplification of each of the three loci was performed using locus specific primers and PCR conditions were as described by Lichter et al. (2) for DRD4 and Perez-lezaun et al. (3) for STR markers. Forward primer of both the STR markets was labeled with fluorescent Cy5<sup>TM</sup>dye amidite (Amersham Pharmacia Biotech Pvt.Ltd, Sweden). Amplification was carried out in 25  $\mu$ L PCR reaction mixture containing 25 ng of genomic DNA in Eppendorf Gradient Master Cycler for all three of the loci.

For DRD4, PCR amplicons were electrophoresed in 4% native polyacrylamide gels and visualized by silver staining method. Alleles were assigned by allelic ladder and sizes were confirmed by marker VIII (Roche Biochemicals). PCR amplicons for STR markers were electrophoresed in 6% (w/v acrylamide/bisacrylamide) denaturing gels using ALF Express DNA sequencer (Amersham Pharmacia Biotech). External size standards (107, 228, 395 bps) were used in every 10<sup>th</sup> lane and internal standards (107 and 395 bps) in each lane of the gel.

The allele frequency estimates of these markers reveal that alleles are not equally distributed in all of the five populations included

in the study. Alleles at most of the loci were in Hardy Weinberg equilibrium. Markers are informative and can be used for forensic DNA analysis and paternity testing.

Analysis of data: Popgene (4)

The complete dataset is available to any unlisted parties via electronic mail from the corresponding author at mesh@apsara.bare.ernet.in

## Reference

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TABLE 1—*DRD4 allele frequencies in five population groups of South India.*

Repeats	Ezhavas N = 104	Muslims N = 60	Nairs N = 40	Arayas N = 33	Vishwakarmas N = 20
2	0.101	0.175	0.088	0.046	0.125
3	0.005	0.025	0.013	0.030	0.100
4	0.784	0.750	0.712	0.788	0.725
5	0.024	0.008	0.013	0.030	0.025
6	0.024	...	0.013	...	...
7	0.043	0.042	0.150	0.046	0.025
8	0.019	...	0.013	0.060	...
H	0.40	0.50	0.57	0.42	0.55
h ± SE	0.37 ± 0.04	0.40 ± 0.06	0.47 ± 0.07	0.38 ± 0.08	0.45 ± 0.10
PD	0.61	0.62	0.70	0.55	0.69
PIC	0.36	0.37	0.44	0.36	0.42
P	0.89	0.45	0.98	0.99	0.95

N: Number of individuals sampled; H: Observed heterozygosity; h: Expected heterozygosity; PD: Power of discrimination; PIC: Polymorphic information content; P: Probability value of maximum likelihood ratio test for Hardy Weinberg equilibrium.

TABLE 2—*D7S820 allele frequencies in five population groups of South India.*

Repeats	Ezhavas N = 75	Muslims N = 56	Nairs N = 30	Arayas N = 29	Vishwakarmas N = 17
6	0.013	0.009	...	0.017	...
7	0.060	0.027	0.017	0.189	...
8	0.207	0.161	0.117	0.069	0.029
9	0.087	0.080	0.033	0.207	0.118
10	0.167	0.196	0.267	0.397	0.471
11	0.273	0.339	0.433	0.069	0.294
12	0.147	0.179	0.133	...	0.088
13	0.020	0.009	...	0.052	...
14	0.027	...	...	...	...
H	0.74	0.75	0.70	0.66	0.76
h ± SE	0.82 ± 0.04	0.78 ± 0.05	0.72 ± 0.08	0.76 ± 0.07	0.69 ± 0.1
PD	0.92	0.90	0.85	0.89	0.76
PIC	0.80	0.750	0.66	0.72	0.62
P	0.09	0.45	0.48	0.28	0.19

N: Number of individuals sampled; H: Observed heterozygosity; h: Expected heterozygosity; PD: Power of discrimination; PIC: Polymorphic information content; P: Probability value of maximum likelihood ratio test for Hardy Weinberg equilibrium.

TABLE 3—*D9S926 allele frequencies in five population groups of South India.*

Repeats	Ezhavas N = 87	Muslims N = 62	Nairs N = 34	Arayas N = 27	Vishwakarmas N = 21
7	0.115	0.113	0.088	0.110	0.167
8	0.006	...	...	0.019	0.024
9	0.012	0.024	...	0.019	0.024
10	0.023	0.032	0.029	0.056	...
11	0.259	0.242	0.221	0.278	0.143
12	0.369	0.274	0.397	0.259	0.333
13	0.161	0.226	0.176	0.222	0.214
14	0.052	0.089	0.089	0.037	0.071
15	0.006	...	...	...	0.024
H	0.75	0.77	0.73	0.81	0.80
h ± SE	0.76 ± 0.04	0.80 ± 0.05	0.76 ± 0.07	0.80 ± 0.07	0.81 ± 0.08
PD	0.88	0.91	0.88	0.89	0.83
PIC	0.72	0.68	0.71	0.76	0.76
P	0.35	0.02	0.24	0.91	0.76

N: Number of individuals sampled; H: Observed heterozygosity; h: Expected heterozygosity; PD: Power of discrimination; PIC: Polymorphic information content; P: Probability value of maximum likelihood ratio test for Hardy Weinberg equilibrium.