

FOR THE RECORD

Kumarasamy Thangaraj,¹ Ph.D.; Gyaneshwer Chaubey,^{1,2} M.Sc.; Vijay Kumar Singh,¹ M.Sc.; Alla G. Reddy,¹ M.Sc.; Pallavi Chauhan,³ M.Sc.; Rashmi Malvee,³ M.Sc.; P. P. Pavate,⁴ Ph.D.; and Lalji Singh,¹ Ph.D.

Y-Chromosomal STR Haplotypes in Two Endogamous Tribal Populations of Karnataka, India

POPULATION: Approximately 5.0 mL of blood sample was collected from a total of 150 men belonging to two tribal populations of coastal Uttar Kannada district of Karnataka, with their informed written consent. Both the populations are endogamous and they belong to the Dravidian linguistic family. Halakki is a tribal group having a population size of *c.* 3383. They claim that they originally belong to Gujarat and Rajasthan, and migrated through Andhra Pradesh to Karnataka. Kunabhi is also a tribal population, *c.* 35,214 in number. They were hunters and gatherers but presently they practice agriculture.

KEYWORDS: forensic science, Y-STR haplotypes, Dravidian tribe, Kunabhi, Halakki, Karnataka, DNA typing, population genetics, DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385a,b

DNA was isolated from the above samples using protocols described elsewhere (1). About 1–2 ng of DNA samples were used to amplify 9 Y-STR loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385a,b) in a multiplex reaction, following the amplification condition described by Redd et al. (2).

Amplicons were analyzed in a capillary-based ABI 3700 automated DNA Analyzer (Perkin Elmer, Foster City, CA) using GS ROX 500 as a size standard.

A total of 101 haplotypes were observed among 150 samples (Table 1). There were no haplotypes sharing between the Halakki

TABLE 1—Y chromosomal minimal haplotype (minHt.) observed in Halakki and Kunabhi populations of Karnataka, India.

Ht.	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	Halakki	Kunabhi
1	10	13	29	22	10	11	14	15	18	2	
2	12	13	28	23	10	11	15	13	16	1	
3	12	14	29	24	10	10	15	13	16	1	
4	12	14	30	22	10	11	13	12	15	1	
5	12	14	30	22	10	10	13	13	16	7	
6	12	14	29	23	10	10	13	13	16	1	
7	12	14	29	23	10	10	13	13	16	1	
8	12	14	29	23	10	11	13	13	18	5	
9	12	14	29	22	10	10	13	13	17	1	
10	12	13	28	22	10	12	15	13	15	1	
11	10	13	28	22	10	11	14	13	16	1	
12	12	13	31	22	11	11	13	13	17	1	
13	12	14	29	22	10	11	13	13	15	1	
14	12	14	29	23	10	10	13	13	16	2	
15	12	14	30	22	12	10	13	13	17	1	
16	13	14	29	23	10	11	15	12	17	1	
17	11	14	29	23	9	11	13	13	15	6	
18	11	14	30	22	10	12	14	14	17	1	

¹Centre for Cellular and Molecular Biology, Hyderabad 500 007, India.

²Department of Evolutionary Biology, Institute of Molecular and Cell Biology, University of Tartu and Estonian Biocentre, Tartu, Estonia.

³Barkatullah University, Bhopal, India.

⁴Department of Anthropology, Karnataka University, Dharwad 580 003, India.

TABLE 1—Continued.

Ht.	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	Halakki	Kunabhi
19	11	14	30	23	10	13	13	12	17	1	
20	13	15	31	24	10	14	13	14	17	5	
21	12	15	30	22	11	11	13	13	17	1	
22	13	13	29	22	10	10	13	13	16	1	
23	13	14	28	25	10	12	13	13	18	2	
24	11	13	31	22	10	12	13	13	19	1	
25	12	15	31	23	10	11	13	13	17	1	
26	13	14	29	22	10	10	14	13	17	1	
27	12	12	29	23	10	12	15	13	16	1	
28	11	15	29	22	10	10	13	12	19	2	
29	12	13	30	22	10	10	13	11	15	1	
30	10	13	31	23	11	12	13	12	17	1	
31	12	13	30	22	10	10	13	12	19	1	
32	12	12	29	22	11	13	13	12	16	2	
33	11	12	30	23	10	10	13	9	11	1	
34	12	13	29	23	11	10	13	13	18	2	
35	11	12	31	22	10	14	13	11	15	1	
36	10	13	30	21	11	10	13	14	18	2	
37	12	12	31	22	10	11	13	13	18	1	
38	11	14	30	22	11	10	13	10	14	2	
39	12	12	29	23	11	12	13	11	15	1	
40	10	14	30	21	10	10	13	11	15	1	
41	12	12	29	21	10	10	13	15	19	1	
42	10	13	30	23	10	12	13	11	15	1	
43	12	13	29	22	11	12	13	13	19	2	
44	12	12	30	21	10	10	13	14	17	1	
45	10	14	28	22	11	12	13	17	18	1	
46	12	12	30	23	10	10	13	13	18	1	
47	10	15	31	22	11	12	13	12	21	1	
48	12	12	30	23	9	11	13	13	21	1	
49	13	15	29	22	11	13	11	14	17		1
50	15	15	30	24	11	12	13	9	11		1
51	15	15	30	24	12	13	12	10	18		1
52	15	15	22	25	12	13	13	10	16		1
53	16	14	26	22	12	14	13	11	14		2
54	15	13	29	22	11	12	13	12	17		1
55	16	15	23	24	12	12	13	11	18		1
56	13	15	31	24	12	13	13	11	19		1
57	14	15	28	24	13	12	13	12	16		1
58	15	15	29	24	11	13	11	13	15		1
59	15	15	30	24	12	13	12	13	16		1
60	15	14	21	23	10	12	13	13	16		1
61	15	14	27	22	11	13	12	13	16		1
62	14	13	30	23	11	13	13	8	21		1
63	15	15	22	24	12	12	12	14	15		1
64	14	15	30	25	11	13	13	14	15		1
65	14	15	28	24	13	13	13	8	19		1
66	14	15	30	24	11	13	13	13	17		1
67	16	15	30	25	11	13	12	13	16		1
68	16	14	24	23	10	13	13	12	17		1
69	15	14	27	22	12	13	12	9	11		1
70	14	15	29	23	12	13	13	14	16		1
71	15	14	25	22	12	13	11	12	16		2
72	15	16	31	25	11	13	13	12	12		1
73	15	15	28	24	12	13	13	12	16		2
74	14	14	31	25	11	13	13	14	15		1
75	15	15	29	22	11	13	13	13	16		6
76	16	14	24	24	11	13	12	12	16		3
77	15	13	30	23	12	14	12	13	17		3
78	15	14	30	25	11	13	13	13	16		3
79	15	15	29	23	11	13	12	13	13		1
80	16	14	28	22	12	13	13	13	16		1
81	15	15	29	23	11	13	13	14	15		1
82	14	16	30	22	11	14	13	13	17		2
83	15	15	31	24	11	13	11	13	17		1
84	16	15	29	24	12	13	13	12	16		1
85	14	15	27	23	11	13	13	9	14		1
86	15	15	29	25	11	14	13	8	16		1
87	13	16	25	22	12	13	12	12	20		3
88	15	16	26	25	11	13	13	10	20		2
89	15	16	29	22	12	12	13	10	16		1
90	14	16	26	25	11	13	12	10	19		2
91	15	16	28	22	11	14	13	11	13		1

TABLE 1—Continued.

Ht.	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	Halakki	Kunabhi
92	13	15	29	22	11	13	13	12	15		1
93	14	15	31	25	12	13	11	10	16		2
94	14	15	30	22	12	12	13	11	18		1
95	15	14	29	22	11	13	12	8	19		2
96	13	14	31	25	12	13	13	9	22		1
97	15	15	29	22	11	13	13	16	16		1
98	16	14	30	24	12	12	12	12	19		1
99	16	12	29	22	11	14	13	11	14		1
100	13	15	27	23	11	13	13	13	15		1
101	15	13	28	22	11	12	11	10	20		1

and Kunabhi populations, suggesting these two populations maintain strict endogamy, despite both being tribes and residing in the same geographical region. Alleles were designated according to the number of repeats. The allele frequencies were calculated by a simple gene control method. AMOVA analysis was carried out by Arlequin ver.2.00 software (3).

AMOVA analysis of these two studied populations with other Indian populations ((4), our unpublished data) suggest the variation among the populations within groups (1.67%), which although small but is statistically significant. Most of the variation (98.2%) is, however, found between individuals within the populations. Interestingly, locus *DYS389II* is highly polymorphic in Kunabhi.

The complete dataset is available through electronic mail from the corresponding author at lalji@ccmb.res.in

Acknowledgments

We thank anonymous subjects from the Halakki and Kunabhi tribes of Karnataka, India, who volunteered to give blood samples.

References

1. Thangaraj K, Joshi MB, Reddy AG, Gupta NJ, Chakravarty BN, Singh L. CAG repeat expansion in the androgen receptor gene is not associated with male infertility in Indian populations. *J Androl* 2002;23:815–8.
2. Redd AJ, Agellon AB, Kearney VA, Contreras VA, Karafet T, Park H, et al. Forensic value of 14 novel STRs on the human Y chromosome. *Forensic Sci Int* 2002;130:97–111.
3. Schneider S, Rosslie D, Excoffier L. Arlequin ver 2.000, a software for population genetics data analysis. Geneva: Genetics and Biometry Laboratory, University of Geneva, 1997, <http://anthropologie.unige.ch/arlequin>
4. Banerjee J, Trivedi R, Kashyap VK. Y-STR haplotypes in autochthonous tribal population of Chotanagpur Plateau, India. *J Forensic Sci* 2005;50:1–5.

Additional information and reprint requests:

Lalji Singh, Ph.D.

Center for Cellular and Molecular Biology

Uppal Road

Hyderabad 500 007

India

E-mail: lalji@ccmb.res.in