FOR THE RECORD

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Y-STR Haplotypes in Autochthonous Tribal Population of Chotanagpur Plateau, India

POPULATION: The chosen population group for the study belongs to Austroloid community affiliated to the Austro-Asiatic linguistic family (1). The population is primitive nomads, inhabiting remote terrains. They are highly endogamous and carry distinct genetic signatures.

KEYWORDS: forensic science, Y-STR haplotypes, Austro-Asiatic Tribe, Chotanagpur Plateau, DNA typing, population genetics, DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385I/II, YCAII, DYS426, DYS388, DYS439, DYS437, DYSH4, DYS460, DYS447, DYS438 and DYS448

The analysis of genetic variation, in the short tandem repeats of Y-Chromosomal DNA, provides unique information on the genetic diversity of the population. The 20 typed Y-STRs are highly polymorphic and aid in human identification. An extremely informative Y-STR core set (minimal and extended haplotype), approved for court use by the forensic and scientific community (7) as well as validated by DAB/TWAGDAM (8) was chosen for typing-DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385I/II and YCAII. Along with these STRs, an additional set of 9 highly polymorphic loci were chosen for typing namely DYS426, DYS388, DYS439, DYS437, DYSH4, DYS460, DYS447, DYS438 and DYS448 by an in-house developed novel Twentyplex PCR reaction. This study characterizes the Y-STR haplotypes in 136 tribal individuals, belonging to the Austro-Asiatic linguistic family of Chotanagpur Plateau, India.

Blood samples were collected from 136 unrelated, consenting individuals. Morphometric indices and disease status were recorded at the time of sample collection. DNA was isolated from blood samples by standard phenol/chloroform procedure (2). PCR was performed with an in-house developed multiplex having primers labeled with 5′FAM, VIC, NED and PET fluorescent dyes, for all the microsatellite markers in a 10 μL final reaction volume containing 10 ng of genomic DNA. The chosen Y-STRs were amplified using the primers from Y-STR Database and the reaction conditions were validated in the laboratory (unpublished). PCR products were run on ABI Prism 3100 Genetic Analyzer and LIZ™-500 was used as the internal lane standard.

Alleles were designated according to the number of repeats. The allele frequencies were calculated by simple gene count method. Haplotype diversity for the 20 Y-Chromosomal STRs was calculated according to Nei's formula (3).

$$H = n\left(1 - \Sigma x_i^2\right)/(n - 1)$$

where n represents the number of chromosomes sampled, and x_i is the frequency of the ith allele or haplotype, using the software ARLEQUIN ver 2.0 (4).

The haplotype data is presented in Table 1. Result of allele frequency is represented in Table 2. In this study 132 unique haplotypes were observed. Haplotype sharing was observed at intra-population level. Consequentially haplotype diversity exhibited a lower value at 0.9995 ± 0.0010 for the tribe. The analyzed tribe exhibits significant allele frequency variation. The least polymorphic loci were DYS438 and DYS426 with allele 10 in the highest frequency in both. Locus DYS447 exhibited highest polymorphism having 12 alleles. This data further augments the available Y-STR information for Indian populations (5). The haplotype data were compared with three predominant world populations' namely Asian, American and European populations (6–8), however no match was found with any of the compared groups.

The complete dataset is available through electronic mail from communicating author: dtubprd@giascl01.vsnl.net.in, vkk2k@hotmail.com

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TABLE 1—*Haplotype Frequency of Autochthonous Tribal Population of Chotanagpur Plateau, India.*

Haplotype	n	DYS438	DYS389II	DYS439	DYS437	DYS389I	DYS391	DYS385a	DYS385b	DYS390	YCAIIa	YCAIIb	DYS393	DYS426	DYS392	DYS19	DYS388	DYSH4	DYS460	DYS448	DYS447
JH1	1	9	28	16	15	12	10	11	15	25	18	20	12	11	10	16	16	11	11	22	24
JH2	1	9	28	17	13	12	9	13	15	22	15	18	11	10	10	15	10	11	9	21	23
JH3	1	9	28	18	13	11	11	11	16	23	16	17	11	10	0	0	11	9	10	22	24
JH4	1	9	28	18	13	12	9	12	15	25	15	19	14	10	11	16	11	10	9	21	22
JH5	1	9	29	16	13	12	9	13	15	23	15	18	14	10	13	15	11	10	9	21	31
JH6	1	9	29	16	13	12	9	13	16	21	15	17	11	10	9	15	11	11	9	23	23
JH7	1	9	29	17	13	12	9	13	15	28	15	19	11	10	0	0	0	0	0	21	30
JH8	1	9	29	17	13	13	9	13	15	21	15	18	11	10	9	15	11	11	10	22	23
JH9	1	9	29	17	13	13	9	13	15	21	15	18	11	10	10	0	0	10	9	21	23
JH10	1	9	30	16	13	12	10	12	16	21	16	17	11	10	0	15	11	10	9	22	23
JH11	1	9	30	16	13	11	9	12	15	22	15	18	11	12	10	14	11	13	9	23	22
JH12	1	9	30	16	13	13	9	13	14	21	15	18	11	10	10	16	10	13	9	22	23
JH13	1	9	30	16	13	13	9	13	14	21	15	18	11	10	10	16	11	13	9	26	22
JH14	1	9	30	16	13	13	9	13	16	22	15	17	11	10	9	15	11	11	9	22	22
JH15	1	9	30	16	14	13	10	13	14	23	18	18	12	11	0	15	12	13	10	23	23
JH16	1	9	30	16	14	13	10	13	14	24	18	19	12	11	10	15	12	13	10	23	23
JH17	1	9	30	17	13	13	9	13	15	17	15	18	11	10	0	15	10	11	9	21	23
JH18	1	9	30	17	13	13	9	13	15	17	15	18	11	10	0	15	11	11	9	21	23
JH19	1	9	30	17	13	13	9	13	15	22	15	19	11	10	0	0	0	0	0	21	23
JH20	1	9	30	17	13	13	9	13	17	22	15	18	11	10	0	0	0	0	0	21	23
JH21	1	9	30	18	14	12	9	11	15	23	15	17	11	10	9	15	11	10	9	22	30
JH22	1	10	26	14	13	11	11	10	16	25	18	19	13	11	10	14	12	13	11	20	26
JH23	1	10	27	17	14	13	11	13	20	26	18	20	14	11	10	15	12	11	10	21	0
JH24	1	10	28	16	13	12	9	13	16	22	15	16	11	10	9	15	11	11	10	22	22
JH25	1	10	28	17	13	11	9	13	14	23	15	17	13	10	11	14	11	12	10	22	21
JH26	1	10	28	17	13	12	9	13	15	24	15	19	14	11	12	15	11	10	8	21	28
JH27	1	10	28	17	13	12	9	13	18	17	15	19	15	10	0	15	11	10	9	21	25
JH28	1	10	28	17	13	12	9	13	20	24	15	18	14	10	13	15	11	10	9	21	24
JH29	1	10	28	17	13	13	11	13	19	26	18	20	14	11	12	15	12	11	10	21	28
JH30	1	10	28	17	13	13	11	14	19	25	18	20	14	11	10	15	12	11	10	21	25
JH31	1	10	28	17	14	13	10	11	19	26	18	21	14	11	12	15	13	11	10	21	25
JH32	1	10	28	17	14	13	11	13	19	26	18	20	14	11	10	17	12	11	10	21	28
JH33	1	10	28	18	13	12	9	13	17	25	15	18	14	10	13	15	11	10	9	21	30
JH34	1	10	28	18	13	12	9	13	19	23	15	18	14	10	12	15	11	10	9	21	25
JH35	1	10	28	18	13	12	9	13	19	25	15	18	14	10	13	15	11	10	9	21	25
JH36	1	10	28	18	14	13	10	13	18	26	18	21	15	11	13	15	12	11	10	21	25
JH37	1	10	29	16	13	12	8	12	15	23	15	19	12	10	10	15	11	12	10	22	23
JH38	1	10	29	16	13	12	9	13	18	25	15	18	13	10	13	15	11	10	9	21	30
JH39	1	10	29	16	13	12	10	13	17	25	15	18	13	10	13	15	11	10	9	21	30
JH40	1	10	29	16	14	14	10	13	14	23	18	19	12	11	11	15	13	13	10	22	23
JH41	1	10	29	17	13	11	9	13	14	22	15	17	13	10	13	16	10	11	10	22	24
JH42	1	10	29	17	13	11	10	13	14	22	15	17	13	10	9	14	11	12	10	22	22
JH43	1	10	29	17	13	11	10	13	14	23	15	17	12	10	13	14	11	12	10	22	27
JH44	1	10	29	17	13	11	10	13	16	25	15	18	13	10	13	16	11	10	9	21	29
JH45	1	10	29	17	13	12	9	10	16	23	15	16	13	10	9	14	11	10	9	22	24
JH46	1	10	29	17	13	12	9	11	19	25	15	18	14	10	13	15	11	10	9	20	30
JH47	1	10	29	17	13	12	9	12	15	24	15	17	14	10	0	0	0	0	0	21	25
JH48	1	10	29	17	13	12	9	12	17	24	15	20	14	10	12	15	11	10	9	21	28
JH49	1	10	29	17	13	12	9	12	18	24	15	18	13	10	13	15	11	10	9	21	30
JH50	1	10	29	17	13	12	9	12	19	24	15	18	14	10	13	15	11	10	9	20	30
JH51	1	10	29	17	13	12	9	13	15	23	15	19	14	10	12	15	11	10	9	21	28
JH52	1	10	29	17	13	12	9	13	15	23	15	19	14	11	12	15	11	10	9	21	28
JH53	1	10	29	17	13	12	9	13	16	24	15	18	13	10	13	15	11	10	9	21	29
JH54	1	10	29	17	13	12	9	13	17	24	15	18	13	10	13	15	11	10	9	21	31
JH55	1	10	29	17	13	12	9	13	18	24	15	18	13	10	12	15	11	10	9	22	27
JH56	1	10	29	17	13	12	9	13	19	25	15	18	14	10	13	15	11	10	9	21	25

JH57	1	10	29	17	13	13	9	13	14	24	15	18	13	10	13	15	11	10	9	21	32
JH58	1	10	29	17	13	13	10	14	15	23	15	17	12	10	9	15	11	10	9	22	22
JH59	1	10	29	17	14	12	9	11	17	18	14	16	13	10	10	16	12	11	10	21	24
JH60	1	10	29	17	14	12	9	12	15	21	13	17	13	11	10	16	11	11	9	21	24
JH61	1	10	29	17	14	12	9	13	17	21	14	16	13	11	9	16	12	11	9	21	24
JH62	1	10	29	17	14	13	10	12	17	26	18	21	15	11	12	15	12	11	10	21	25
JH63	1	10	29	17	14	13	10	12	17	26	20	21	15	11	12	15	12	11	10	21	27
JH64	1	10	29	17	14	13	10	13	19	26	18	18	14	11	12	15	12	11	10	21	27
JH65	1	10	29	17	15	11	10	12	13	22	15	17	12	10	10	15	11	12	9	21	22
JH66	1	10	29	17	16	12	9	12	17	24	15	19	14	10	12	15	11	10	9	22	27
JH67	1	10	29	18	13	11	10	13	14	22	15	17	13	10	12	14	11	12	10	22	22
JH68	1	10	29	18	13	12	9	10	16	24	15	18	14	10	12	15	11	10	9	22	27
JH69	1	10	29	18	13	12	9	11	17	24	15	18	13	10	13	14	11	10	9	21	31
JH70	1	10	29	18	13	12	9	13	17	23	15	19	13	10	0	15	11	10	9	22	28
JH71	1	10	29	18	13	12	9	13	17	24	15	19	13	10	12	15	11	10	9	21	27
JH72	1	10	29	18	13	12	9	13	17	24	15	19	13	10	0	15	11	10	9	21	28
JH73	3	10	29	18	13	12	9	13	17	24	15	19	13	10	12	15	11	10	9	21	28
JH74	1	10	29	18	13	12	9	13	17	25	15	17	13	10	13	15	11	10	9	21	31
JH75	2	10	29	18	13	12	9	13	17	25	15	19	13	10	12	15	11	10	9	21	28
JH76	1	10	29	18	13	12	9	12	17	25	15	18	12	10	13	15	11	10	9	21	30
JH77	1	10	29	18	13	12	9	13	19	24	15	18	12	10	13	15	11	10	9	21	30
JH78	1	10	29	18	13	12	10	13	17	25	15	18	13	10	13	15	11	11	9	21	31
JH79	1	10	29	18	13	12	10	13	18	17	15	19	12	10	12	15	11	10	9	21	27
JH80	1	10	29	18	13	13	10	10	15	23	18	19	14	11	8	14	12	11	11	22	23
JH81	1	10	29	18	13	13	10	10	15	23	18	19	14	11	11	14	12	11	11	22	23
JH82	2	10	29	18	13	13	10	13	17	25	18	21	14	11	13	15	12	11	10	21	31
JH83	1	10	29	18	13	13	11	10	17	26	18	20	14	11	9	0	0	11	10	21	0
JH84	1	10	29	18	14	13	10	13	15	25	18	20	15	11	10	15	12	11	10	21	28
JH85	1	10	29	18	14	13	10	13	17	25	18	21	13	11	12	15	12	11	10	21	27
JH86	1	10	29	18	14	13	10	13	18	25	18	21	16	11	12	15	12	11	10	21	27
JH87	1	10	29	18	14	14	10	12	16	26	17	21	12	11	12	15	12	11	10	21	27
JH88	1	10	29	18	15	13	10	11	16	26	18	18	13	11	10	15	14	11	10	23	24
JH89	1	10	30	16	13	12	9	13	15	24	15	18	13	10	13	15	11	10	9	22	24
JH90	1	10	30	16	13	13	9	13	16	22	14	17	12	10	9	15	15	11	9	22	23
JH91	1	10	30	17	13	11	10	12	14	22	15	17	13	10	10	14	11	12	10	23	22
JH92	1	10	30	17	13	11	10	13	14	23	15	17	13	10	11	14	11	11	9	22	21
JH93	1	10	30	17	13	12	10	13	18	24	15	18	13	10	13	16	11	10	9	21	29
JH94	1	10	30	17	13	12	10	13	18	25	15	18	13	10	13	15	11	10	9	21	29
JH95	1	10	30	17	14	14	10	12	17	26	18	21	14	11	12	15	12	12	10	21	27
JH96	1	10	30	17	14	14	10	12	18	25	18	21	15	11	12	15	12	11	10	21	28
JH97	1	10	30	18	13	13	9	13	20	17	15	17	13	10	0	15	10	10	9	21	26
JH98	1	10	30	18	13	13	11	13	16	26	18	20	14	11	12	15	12	11	10	21	25
JH99	1	10	0	18	14	13	11	11	15	26	18	20	14	11	12	15	13	11	10	21	0
JH100	1	10	30	18	14	13	11	13	16	26	17	19	14	11	13	17	12	11	10	21	25
JH101	1	10	30	18	14	13	11	13	16	26	18	20	14	11	12	15	12	11	10	21	25
JH102	1	10	30	18	14	14	10	12	17	26	18	21	14	11	12	15	12	11	10	21	27
JH103	1	10	30	19	13	13	9	11	17	28	15	19	13	10	0	0	0	0	0	21	23
JH104	1	10	30	19	13	13	9	12	18	0	15	19	13	10	0	0	0	0	0	21	26
JH105	1	10	30	19	14	14	10	12	16	26	18	21	14	11	12	15	12	11	10	21	28
JH106	1	10	31	17	13	12	9	14	18	17	15	19	13	10	11	15	11	10	10	21	27
JH107	1	10	31	18	13	13	9	13	18	25	15	18	13	10	13	15	11	10	9	21	31
JH108	1	10	31	18	13	14	10	13	17	25	18	21	14	11	13	15	12	11	10	21	30
JH109	1	10	31	19	13	12	10	13	17	17	15	17	13	10	12	16	11	10	10	21	27
JH110	1	11	27	16	13	11	9	10	14	23	16	18	12	10	9	15	11	10	9	24	22
JH111	1	11	27	17	13	11	9	10	16	22	16	18	12	10	9	15	11	10	8	23	23
JH112	1	11	27	17	13	12	10	12	15	24	18	19	13	11	12	14	10	12	11	23	24
JH113	1	11	27	17	14	12	10	12	15	24	18	19	13	11	11	15	10	12	11	23	24
JH114	1	11	27	17	14	12	10	12	15	24	18	19	13	11	12	15	11	12	11	23	24
JH115	1	11	28	17	14	12	10	12	15	24	19	23	13	11	14	14	11	12	11	23	0
JH116	1	11	29	15	15	13	9	11	18	23	15	17	12	11	9	14	11	10	9	22	30

TABLE 1—*Continued.*

Haplotype	n	DYS438	DYS389II	DYS439	DYS437	DYS389I	DYS391	DYS385a	DYS385b	DYS390	YCAIIa	YCAIIb	DYS393	DYS426	DYS392	DYS19	DYS388	DYSH4	DYS460	DYS448	DYS447
JH117	1	11	29	16	13	11	9	9	12	24	15	20	12	11	9	15	12	12	9	21	24
JH118	1	11	29	17	13	12	9	12	17	24	14	18	12	11	13	16	11	10	9	21	31
JH119	1	11	29	17	13	12	9	13	17	24	15	18	13	10	13	15	11	10	9	21	30
JH120	1	11	29	20	13	13	10	13	17	25	18	20	15	11	12	15	12	11	10	21	26
JH121	1	11	30	15	13	13	9	9	12	17	15	20	12	11	10	15	11	12	10	23	24
JH122	1	11	30	15	15	13	10	10	16	26	18	21	13	11	12	14	12	11	10	21	25
JH123	1	11	30	16	15	14	10	10	15	24	18	19	13	12	12	15	12	11	10	22	22
JH124	1	11	30	17	15	14	10	12	17	25	17	20	15	12	9	14	12	12	10	22	27
JH125	1	11	31	15	13	13	10	9	17	23	14	20	12	11	11	16	11	11	11	23	24
JH126	1	11	31	18	13	13	9	13	17	25	15	18	13	10	13	15	11	10	9	21	31
JH127	1	11	32	17	13	13	9	13	15	22	15	18	13	10	12	16	11	9	9	21	23
JH128	1	11	32	17	13	13	9	13	15	23	15	18	13	10	12	16	11	9	9	21	22
JH129	1	11	32	18	14	14	10	13	18	26	18	21	14	11	12	15	12	11	10	21	28
JH130	1	0	0	18	13	12	9	13	15	0	15	0	14	10	0	0	0	0	0	20	30
JH131	1	0	0	19	13	13	9	12	12	23	15	0	0	0	10	0	11	10	9	21	27
JH132	1	0	0	0	0	0	0	0	0	26	0	0	12	10	0	15	0	0	0	0	0

n: frequency of the haplotype.

TABLE 2—*Allele Frequency Data of Autochthonous Tribal Population of Chotanagpur Plateau, India.*

Allele	DYS438	DYS389II	DYS439	DYS437	DYS389I	DYS391	DYS385a	DYS385b	DYS390	YCAIIa	YCAIIb	DYS393	DYS426	DYS392	DYS19	DYS388	DYSH4	DYS460	DYS448	DYS447
8						0.008								0.009				0.016		
9	0.163					0.557	0.023							0.139			0.024	0.532		
10	0.682					0.361	0.076						0.611	0.174		0.087	0.428	0.371		
11	0.155				0.115	0.084	0.084					0.130	0.366	0.061		0.615	0.371	0.081		
12					0.443		0.214	0.008				0.160	0.023	0.322		0.279	0.121			
13				0.718	0.366		0.580	0.008		0.008		0.367		0.278		0.025	0.056			
14				0.222	0.076		0.023	0.099		0.031		0.275			0.140	0.008				
15			0.031	0.053				0.221		0.611		0.061			0.719	0.008				
16			0.152	0.008				0.145		0.031	0.023	0.008			0.124					
17			0.458					0.252	0.062	0.023	0.162				0.017					
18			0.305					0.115	0.008	0.280	0.338									
19			0.038					0.069		0.008	0.208									
20			0.008					0.023		0.008	0.123								0.023	
21									0.062		0.115								0.649	0.016
22									0.100										0.221	0.094
23									0.169		0.008								0.092	0.157
24									0.215										0.008	0.126
25									0.185										0.008	0.094
26		0.008							0.162											0.024
27		0.047																		0.126
28		0.141							0.008											0.110
29		0.483																		0.031
30		0.250																		0.110
31		0.047																		0.071
32		0.023																		0.008

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