

FOR THE RECORD

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Genetic Polymorphism at 15 Tetrameric Short Tandem Repeat Loci in Four Aboriginal Tribal Populations of Bengal

POPULATIONS: This study reports the genetic polymorphism observed at 15 short tandem repeat loci D3S1358, TH01, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, CSF1PO, vWA, D8S1179, TPOX, D2S1338, D19S433, and FGA in four aboriginal populations of Bengal. The analysis was performed to decipher the suitability of CODIS as well as six other highly polymorphic and unlinked markers in Forensic Testing. Studied populations include four tribes: Karmali, Kora, Maheli, and Lodha.

KEYWORDS: forensic science, DNA typing, population genetics, D3S1358, TH01, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, CSF1PO, vWA, D8S1179, TPOX, D2S1338, D19S433, FGA, polymorphism, short tandem repeat, Australoid, tribe, Bengal, allele frequency, power of discrimination, power of exclusion

All the four studied tribal groups are Australoids. *Karmali* belong to the traditional blacksmith community. *Kora* is another tribal community from eastern India that comprises earth-workers and well-diggers. Although the Kora as well as Karmali belong to the Australoid Racial family, they use an Indo-Aryan language “Khotta” for communication (1). *Maheli* were mainly associated with Indigo cultivation, and their name means bamboo, which signifies their involvement with the bamboo work. They speak the Indoaryan language, Sadri (1). *Lodha* derive its name from the word “Lubdhak” meaning “Forest robbers” (1). They use the Austro-Asiatic language called “Lodha” for communication. They are mainly concentrated in the west Midnapore district of Chhotanagpur area and were considered a criminal tribe until the revocation of the Criminal Tribe Act. Among the varied occupations, hunting and food-gathering are still their principal sources of livelihood. This study carries great significance, as they are unique due to their association with crime in the past. Besides, no microsatellite study has ever been performed on these populations.

Blood samples were collected randomly from different rural areas of Bankura, Midnapur (east and west), and Burdwan districts of Bengal. Genomic DNA was isolated through the organic method of extraction (2). The quantitation of DNA was carried out using the Quantiblot kit (PE Applied Biosystems, Foster City, CA), and PCR amplification of the mentioned short tandem repeat (STR) loci was performed using the AmpF ℓ STR[®]

Identifiler[™] Multiplex system (PE Applied Biosystems) following the manufacturer’s manual (3). Analysis was carried out on a 4% polyacrylamide gel using an ABI Prism 377 Automated DNA Sequencer machine (PE Applied Biosystems), and genotype classification was carried out by comparison with allelic ladders provided with the Identifiler kit (3).

The forensic utility of these markers was evaluated by calculating the allele frequency, likelihood ratio test (LR), exact test (ET), observed heterozygosity (h), and probability of homozygosity (HP) using DNA Type software (4,5) (Tables 1–4). Keeping in view the criteria mentioned in NRC (National Research Council) Report II (6), the power of discrimination (PD) and the power of exclusion (PE) were also computed for those microsatellite markers in these populations (Tables 5 and 6).

In the studied populations, the average PD computed is 0.766, whereas the average PE is 0.545. Among the 15 STR studied, loci the highest PD was observed at the D2S1338 locus in Karmali (0.877) population. These 15 STR markers are found to be highly polymorphic in the populations, and they meet Hardy–Weinberg expectations except D19S433 in Karmali and TPOX in Lodha. This work is intended to supplement the ever-increasing information on the Indian population database (7–11) throughout the world.

The complete dataset is available at the institute’s website (<http://humstr.ndacdb.org>) and can also be obtained from the authors upon request.

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TABLE 1—Genetic polymorphism at fifteen STR loci in Lodha (N = 198) of Bengal.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.076							
7					0.126			0.146							
8	0.005		0.005		0.313			0.066	0.091	0.136				0.339	
9	0.046		0.005		0.030			0.667	0.081	0.086				0.333	
9.3								0.045							
10	0.126		0.192		0.162	0.177			0.167	0.091		0.005		0.04	
11	0.394		0.035		0.268	0.222			0.434	0.328				0.288	
11.2												0.005			
12	0.303		0.147		0.101	0.465			0.202	0.273		0.199			0.030
12.2												0.026			
13	0.106		0.091			0.131			0.025	0.076		0.174			0.126
13.2												0.01			
14	0.020		0.217			0.005	0.052			0.01		0.245	0.100		0.435
14.2												0.077			0.010
15			0.202				0.304					0.107	0.040		0.232
15.2												0.112			0.005
16			0.081				0.098					0.026	0.330		0.086
16.2												0.015			
17			0.025				0.438				0.020		0.310		0.071
18		0.010					0.108				0.314		0.200		
19		0.020									0.081		0.030		0.005
20		0.120									0.020				
21		0.170									0.005				
21.2		0.010													
22		0.180									0.086				
22.2		0.010													
23		0.090									0.222				
24		0.210									0.131				
25		0.150									0.121				
26		0.040													
27				0.121											
28				0.051											
29				0.207											
30				0.136											
30.2				0.081											
31				0.096											
31.2				0.162											
32.2				0.121											
33.2				0.015											
35.2				0.010											
ET	0.355	0.030	0.432	0.109	0.341	0.378	0.948	0.431	0.113	0.578	0.148	0.566	0.700	0.002	0.318
LR	0.322	0.020	0.435	0.057	0.293	0.459	0.95	0.243	0.316	0.403	0.073	0.587	0.770	0.002	0.364
h	0.748	0.850	0.818	0.909	0.768	0.636	0.68	0.556	0.626	0.788	0.859	0.857	0.820	0.596	0.717
HP	0.748	1.00	0.612	0.194	0.821	0.285	0.812	0.504	0.024	0.809	0.185	0.62	0.090	0.043	0.809

STR, short tandem repeat; N, number of chromosomes; h, observed heterozygosity; ET, exact test; LR, likelihood ratio test; HP, probability of homozygosity.

TABLE 2—Genetic polymorphism at fifteen STR loci in Kora (N = 118) of Bengal.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.093							
7								0.102							
8					0.246			0.093	0.339	0.042				0.271	
9	0.025				0.068	0.034		0.551	0.068	0.085				0.305	
9.3								0.161							
10	0.161		0.127		0.195	0.203			0.110	0.068		0.008		0.110	0.025
11	0.390		0.136		0.280	0.500			0.203	0.398				0.297	
12	0.297		0.102		0.212	0.263			0.246	0.195		0.051		0.017	0.051
13	0.127		0.034						0.017	0.144		0.407			0.076
13.2												0.009			
14			0.254				0.076		0.017	0.068		0.178	0.238		0.263
14.2												0.025			
15			0.263				0.280					0.136	0.059		0.381
15.2												0.127	0.127		
16			0.076				0.356					0.017			0.127
16.2			0.008									0.042	0.314		
17							0.203				0.051		0.203		0.051
18		0.025					0.085				0.102		0.059		0.017
19		0.034									0.28				0.009

TABLE 2—*Continued.*

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
20		0.136									0.093				
21		0.102									0.059				
21.2		0.043													
22		0.203									0.059				
22.2		0.008													
23		0.178									0.093				
24		0.136									0.068				
24.2		0.008													
25		0.110									0.025				
26		0.017									0.170				
28				0.127											
29				0.178											
30				0.144											
31				0.042											
31.2				0.280											
32				0.025											
32.2				0.153											
33.2				0.051											
ET	0.454	0.204	0.120	0.693	0.195	0.946	0.643	0.352	0.584	0.141	0.001	0.522	0.025	0.872	0.338
LR	0.243	0.125	0.160	0.509	0.292	0.947	0.473	0.474	0.497	0.048	0.002	0.396	0.020	0.804	0.372
h	0.763	0.932	0.898	0.899	0.661	0.678	0.814	0.610	0.797	0.848	0.780	0.814	0.780	0.780	0.763
HP	0.439	0.125	0.097	0.138	0.038	0.528	0.202	0.600	0.579	0.133	0.127	0.359	0.983	0.418	0.924

STR, short tandem repeat; *N*, number of chromosomes; h, observed heterozygosity; ET, exact test; LR, likelihood ratio test; HP, probability of homozygosity.

TABLE 3—*Genetic polymorphism at fifteen STR loci in Karmali (N = 102) of Bengal.*

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.216							
7			0.098		0.010	0.039		0.049	0.010						
8	0.029		0.019		0.422			0.108	0.186	0.020				0.167	
9	0.029				0.049			0.529	0.078	0.186		0.010		0.147	
9.3								0.098							
10	0.206		0.118		0.098	0.127			0.108	0.127				0.137	
11	0.353		0.088		0.225	0.216			0.314	0.333		0.049		0.520	
11.2															
12	0.324		0.039		0.167	0.490			0.265	0.186		0.078		0.029	0.176
12.2											0.029				
13	0.039		0.137		0.029	0.088			0.020	0.069		0.187			0.167
13.2											0.069				
14			0.275			0.020	0.176		0.019	0.079		0.088	0.186		0.324
14.2											0.049				
15	0.020		0.225			0.020	0.284					0.157	0.078		0.225
15.2							0.059					0.186	0.010		
16			0.049				0.176					0.029	0.216		0.078
16.2							0.088					0.020			0.010
17			0.039				0.137				0.088	0.049	0.147		0.020
18							0.049				0.059		0.226		
19		0.078					0.029				0.186		0.127		
20		0.265									0.157		0.010		
21		0.118									0.039				
22		0.255									0.059				
23		0.118									0.079				
24		0.108									0.137				
25		0.039									0.137				
26		0.019		0.010							0.059				
27				0.010											
28				0.039											
29				0.304											
30				0.265											
30.2				0.02											
31				0.098											
32.2				0.245											
33.2				0.009											
ET	0.910	0.275	0.366	0.344	0.544	0.310	0.006	0.357	0.588	0.834	0.104	0.002	0.184	0.869	0.873
LR	0.897	0.232	0.183	0.253	0.717	0.189	0.008	0.708	0.581	0.850	0.064	0.0045	0.178	0.833	0.770
h	0.823	0.784	0.882	0.784	0.823	0.745	0.764	0.588	0.765	0.902	0.902	0.784	0.902	0.647	0.882
HP	0.114	0.539	0.298	0.753	0.135	0.369	0.270	0.359	0.817	0.053	0.589	0.041	0.143	0.835	0.075

STR, short tandem repeat; *N*, number of chromosomes; h, observed heterozygosity; ET, exact test; LR, likelihood ratio test; HP, probability of homozygosity.

TABLE 4—Genetic polymorphism at fifteen STR loci in Maheli (N = 98) of Bengal.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.133							
7						0.010		0.255							
8					0.214			0.214	0.306	0.061				0.306	
9	0.061				0.041	0.020		0.286	0.061	0.082				0.123	
9.3								0.112							
10	0.245		0.092		0.214	0.194			0.143	0.092		0.010		0.204	
11	0.235		0.143		0.276	0.286			0.214	0.408		0.010		0.347	
11.2												0.010			
12	0.347		0.020		0.224	0.398	0.010		0.174	0.173		0.164		0.020	0.153
12.2												0.010			
13	0.112		0.102		0.031	0.072	0.020		0.061	0.143		0.204			0.194
13.2												0.031			
14			0.224			0.020	0.153		0.041	0.010		0.082	0.082		0.357
14.2												0.082			
15			0.337				0.245			0.031		0.306	0.051		0.061
15.2							0.082					0.061			
16			0.082				0.296					0.020	0.357		0.122
16.2							0.031								
17							0.122				0.051	0.010	0.255		0.051
18							0.041				0.082		0.194		
19		0.020									0.265		0.061		
20		0.184									0.112				0.031
21		0.276									0.143				0.031
22		0.092									0.051				
22.2		0.020													
23		0.225									0.163				
24		0.102		0.010							0.051				
25		0.061									0.072				
26		0.020		0.010							0.010				
28				0.071											
29				0.398											
30				0.184											
31				0.061											
31.2				0.041											
32.2				0.225											
ET	0.943	0.146	0.630	0.544	0.061	0.301	0.210	0.673	0.022	0.848	0.041	0.385	0.716	0.93	0.484
LR	0.828	0.074	0.554	0.570	0.126	0.369	0.062	0.478	0.030	0.914	0.027	0.366	0.572	0.889	0.554
h	0.837	0.878	0.867	0.816	0.674	0.755	0.816	0.898	0.796	0.755	0.918	0.878	0.796	0.714	0.735
HP	0.153	0.267	0.421	0.263	0.074	0.547	0.831	0.042	0.933	0.896	0.182	0.287	0.523	0.818	0.359

STR, short tandem repeat; N, number of chromosomes; h, observed heterozygosity; ET, exact test; LR, likelihood ratio test; HP, probability of homozygosity.

TABLE 5—Power of discrimination and power of exclusion values at fifteen STR loci in Lodha, Kora, Karmali, and Maheli tribes of Bengal.

Allele	Lodha		Kora		Karmali	
	PD	PE	PD	PE	PD	PE
D5S818	0.723	0.506	0.717	0.455	0.724	0.506
FGA	0.847	0.689	0.864	0.722	0.817	0.629
D8S1179	0.836	0.633	0.814	0.626	0.818	0.580
D21S11	0.864	0.814	0.824	0.646	0.765	0.504
D7S820	0.777	0.541	0.773	0.551	0.73	0.561
CSF1PO	0.686	0.336	0.638	0.34	0.687	0.454
D3S1358	0.691	0.398	0.74	0.494	0.824	0.606
TH01	0.522	0.241	0.643	0.345	0.65	0.557
D13S317	0.727	0.323	0.766	0.538	0.778	0.600
D16S539	0.777	0.577	0.764	0.535	0.792	0.533
D2S1338	0.805	0.713	0.85	0.695	0.877	0.695
D19S433	0.838	0.709	0.762	0.532	0.877	0.635
vWA	0.744	0.633	0.780	0.563	0.824	0.522
TPOX	0.690	0.286	0.733	0.481	0.660	0.475
D18S51	0.727	0.455	0.757	0.523	0.779	0.578

STR, short tandem repeat; PD, power of discrimination; PE, power of exclusion.

TABLE 6—Average power of exclusion and discrimination at 15 STR loci in Lodha, Kora, Karmali, and Maheli of Bengal.

	Average PD	Average PE
Lodha	0.750	0.523
Kora	0.761	0.536
Karmali	0.773	0.558
Maheli	0.779	0.562

STR, short tandem repeat; PD, power of discrimination; PE, power of exclusion.

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