

GENETIC PROXIMITY OF SARASWAT BRAHMIN COMMUNITY OF NORTHERN INDIA BASED ON AUTOSOMAL STR MARKERS

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ABSTRACT

Genetic diversity and forensic parameters based on 15 AmpFISTR Identifiler STR loci were evaluated in 229 unrelated, autochthonous adults from Saraswat Brahmins of North India. Maximum genetic distance was observed between Jammu and Rajasthan Saraswat Brahmins and least was observed between Kashmiri and Punjab Saraswat Brahmins. In inter population analysis; genetic proximity was observed among studied group and other Brahmin communities of India. In the global scenario, the population was clustered with Croatian population. The results suggested that the populations were in Hardy-Weinberg equilibrium. According to measures of within-population genetic diversity, D2S1338, D18S51 and FGA may be considered as the most variable and most informative markers for forensic testing and population genetic analyses out of the 15 analyzed loci in a population of Saraswat Brahmin. D5S818 and TPOX showed to be the least variable and hence, the least informative markers. The combined power of discrimination (PD) and the combined power of exclusion (PE) for the 15 studied loci were pretty high. The data thereof is of immense significance for forensic result interpretation and is an addition to the existing autosomal STR database on Indian population.

Key Words: AmpFISTR Identifiler/ Genetic Diversity/ Population Genetics/ Saraswat Brahmin/ STRs.

No: of Figures: 2

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No: of References: 28

INTRODUCTION

Understanding the genetic origin and demographic history of Indian population is important, both for questions concerning early settlement of Eurasia and the more recent events, including the appearance of Indo-Aryan languages and agriculture in the subcontinent¹. India has served as a major corridor for dispersal of modern humans and managed to cultivate vast population diversity, despite the fact, that it is relatively isolated from the rest of Eurasia by the Himalayas to the North, and the Bay of Bengal to the East, Arabian Sea to the West and Indian Ocean to the South. It is difficult to interpret the genetic data for Indian population, as the Indian region happens to be one of the most diverse and complex the world. This large diversity in the Indian communities can be attributed to different cultural, religious and lingual practices in by the people of Indian subcontinent². In addition to the fact that Indian culture and society continues to show the impact of multiple waves of immigration and the gene flow that took place in historic and prehistoric times^{3,4}, there are elaborate social regulations of preventing marriages within the same gotras (sub-castes), and thus there is genomic sub-structuring even within a caste. These social regulations governing the institution of marriage have resulted in a sub-structuring of the Indian gene pool. Ethnic groups in India often form genetic subgroups, usually on account of geographical isolation and/or social regulations governing mating. In the Indian caste system, Brahmins occupy high

position in the hierarchical Hindu caste-based society. According to the historians, Saraswat Brahmins have an interesting migration history⁵. This population study was carried out to establish a forensic database for the population based on 15 STR loci as well as to evaluate genetic diversity and genetic differentiation among the sub-populations of the North Indian Saraswat Brahmins. We report allele frequency distribution and forensic parameters for 15 highly polymorphic STR loci included in the AmpFISTR Identifiler PCR amplification kit (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA). Population comparisons were carried out among Saraswat Brahmin population of North India and other populations from previously reported similar studies.

MATERIALS AND METHODOLOGY

Sample

The blood samples were collected from 229 unrelated and random healthy individuals of Saraswat Brahmins from five Northern regions of India [Jammu (58) and Kashmir (44), Punjab (45), Himachal Pradesh (45) and Rajasthan (37)] with their consent.

Methods

Genomic DNA was extracted using the standard Phenol-Chloroform method⁶ followed by purification by ethanol precipitation. Multiplex PCR for 15 STR loci was performed using AmpFISTR Identifiler

TM kit (Applied Biosystems, Foster City, USA). The amplification reactions were performed in Gene Amp PCR system 9700, as per manufacturer's guidelines⁷. Genotyping of all PCR products was accomplished using ABI 3130 Genetic Analyzer (Applied Biosystems, Foster City, USA). All genotypes were analyzed using the GeneMapper1 ID 3.2 software.

Data analysis

Allele frequencies, observed and expected heterozygosities, and forensic parameters were calculated using the software package PowerStats⁸. The agreement of genotype frequencies with Hardy-Weinberg equilibrium (HWE) was determined using the χ^2 -test based on the number of observed and expected. The genetic distance was calculated by Arlenquin software⁹ and the Neighbor-Joining tree was constructed by Mega6 Software¹⁰.

RESULTS

Genetic variation

The observed allele frequency distributions, summarized in Table 1, indicate that each STR locus is moderate to highly polymorphic in North Indian Saraswat Brahmin populations. This is confirmed by summary measures of within population genetic variation, namely the number of alleles, allele size variance and heterozygosity, which are presented in Table 2, together with statistical parameters for forensic testing, based on 15 AmpFISTR Identifiler loci. The allelic frequency ranged from 0.009 to the

highest 0.47 across all the North Indian Saraswat Brahmins. The agreement with Hardy-Weinberg equilibrium, based on the Chi square test, was confirmed for all the studied loci in the five groups except TH01 (0.045) for the Himachal Saraswat population. The average heterozygosity (0.812) was comparable to other Indian populations and Hispanic¹¹ and Egyptian¹² populations, whereas it was much higher than Tunisian¹³, Taiwanese¹⁴ and Indonesian¹⁵ populations.

According to measures of within-population genetic diversity, D21S11, D2S1338, and FGA were the most variable loci for Rajasthan Saraswats (0.8815 - 0.9322), TH01, FGA and D2S1338 for Kashmir Saraswats (0.8746 - 0.8911), FGA, D8S1179 and D2S1338 for Punjab Saraswat (0.8504 - 0.8647), TH01, D2S1338 and FGA for Himachal Saraswats (0.8864 - 0.8951) and FGA, D2S1338 and D21S11 for Jammu Saraswats (0.8663 - 0.8726), showing the highest level of observed and expected heterozygosity. Least variable locus was TPOX, where the lowest observed heterozygosity in Rajasthan (0.6246), Kashmir (0.7069) and Punjab (0.7044) Saraswat Brahmins. Locus CSF1PO was least variable for Himachal Pradesh (0.7194) and Jammu Saraswat Brahmins (0.7067).

Forensic parameters

Out of the 15 analyzed loci in the population of polymorphism information content (Table 1) as measures of informativeness, D2S1338 and FGA may be considered the most informative markers for population genetic analyses and

forensic testing. The least informative markers according to heterozygosity, power of exclusion (PE) and polymorphism information content (PIC) are D5S818 and TPOX. These loci have the lowest observed (0.545 and 0.624, respectively) and expected (0.616 and 0.694, respectively) heterozygosities, the lowest PE (0.230 and 0.320, respectively) and also the lowest PIC (0.644 and 0.573, respectively). Regardless the measures of heterozygosity, forensic parameters such as power of discrimination (PD) and PIC (with the exception of the above mentioned decreased value in TPOX and D5S818) are high for all loci.

Inter-population comparisons

In intra population comparisons, maximum genetic distance was observed between Jammu and Rajasthan Saraswat Brahmins (0.1211), followed by the distance between Jammu and Punjab Saraswat Brahmins (0.1145). The least genetic distance was observed between Kashmir and Punjab Saraswat Brahmins (0.069),

followed by Kashmir and Himachal Saraswat Brahmins (0.0766). The North Indian Saraswat Brahmins were compared with other Indian populations to find out the genetic relatedness of this population with others. It was observed that the Brahmin communities of Bihar (0.011), Madhya Pradesh Brahmins (0.0270) and Maharashtra (Desasht) (0.0297) were genetically closer group to the Saraswats as compared to the other populations, indicating the genetic proximity of these populations. The Patels of Gujarat (0.3826), Oraon (0.1596), Chhatisgarh Brahmins (0.1444) and Vaish (0.1361) of Uttar Pradesh had the maximum DA distance from Saraswat.

In comparative analysis to the world populations, least genetic distance was observed with Brazil (0.0438), Croatian (0.0496), Cyprus (0.0493) and Hispanic (0.052) populations, whereas the maximum DA distance was observed from that of Tunisian (0.1638), Taiwanese (0.1302) and Indonesian (0.1017) populations.

Figure1. Phylogenetic relationships of Saraswat Brahmins with Indian populations conducted with MEGA6.

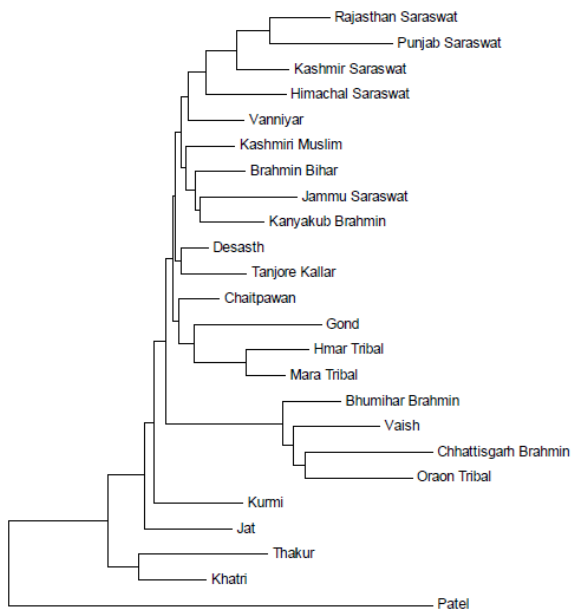
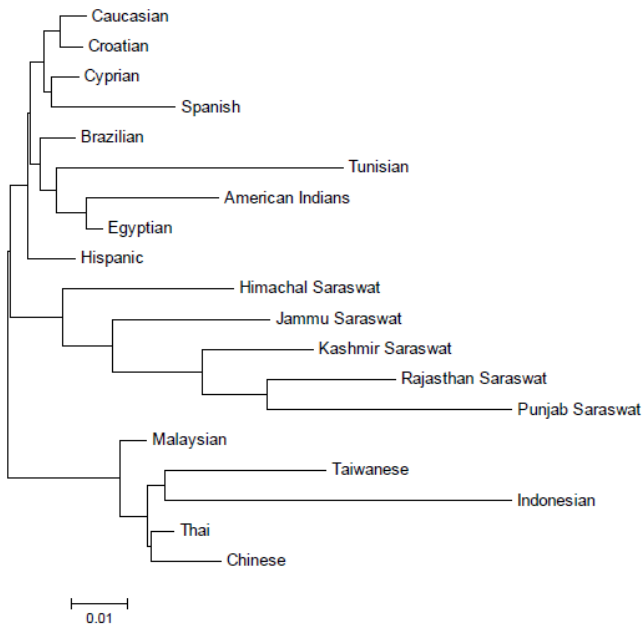


Figure 2. Evolutionary relationships of Saraswat with world populations



The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.46994229 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Phylogenetic analyses were conducted in MEGA6.

Table 1: The Allelic Frequency and Forensic Parameters for the Saraswat Brahmins of North India

KASHMIR SARASWAT BRAHMINs															
Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5															
5.3						0.125									
6						0.114									
6.3						0.068									
7			0.011			0.091						0.011		0.011	
7.3						0.102									
8			0.228			0.034	0.102	0.045				0.398			
8.3						0.102									
9			0.068	0.034		0.171	0.114	0.124				0.102		0.068	
9.3						0.159									
10	0.182		0.114	0.261		0.034	0.091	0.148				0.136		0.057	
11	0.045		0.295	0.228			0.341	0.33		0.011		0.33	0.023	0.318	
12	0.068		0.193	0.352			0.239	0.182		0.057		0.023	0.125	0.296	
12.2															
13	0.216		0.068	0.091	0.011		0.102	0.148		0.307	0.011		0.182	0.25	
13.2										0.023					
14	0.307		0.023	0.023	0.068		0.011	0.023		0.251	0.193		0.261		
14.2										0.068					
15	0.102			0.011	0.342					0.159	0.045		0.148		
15.2										0.045					
16	0.080				0.261					0.023	0.182		0.057		
16.2										0.045					
17					0.182				0.045	0.011	0.318		0.136		
17.2															
18					0.136				0.148		0.114		0.068		0.011
18.2															
19									0.136		0.114				0.068
19.2															
20									0.148		0.023				0.057

20.2															
21									0.023						0.17
21.2															
22									0.193						0.148
22.2															
23									0.136						0.137
23.2															
24									0.08						0.17
24.2															
25									0.091						0.148
26															0.08
27															
27.2															
28		0.068													0.011
28.2		0.023													
29		0.239													
29.2		0.023													
30		0.193													
30.2		0.011													
31		0.034													
31.2		0.125													
32															
32.2		0.227													
33															
33.2		0.057													
34	1.000	1.000	1.000	1.000	1.000	1	1.000	1	1	1	1	1	1	1	1
Forensic															
RMP	0.070	0.068	0.075	0.119	0.113	0.046	0.097	0.077	0.048	0.071	0.071	0.135	0.066	0.117	0.048
1 in.....	14.2	14.7	13.3	8.4	8.9	21.5	10.3	12.9	21	14	14	7.4	15.1	8.6	21
PD	0.930	0.932	0.925	0.881	0.887	0.954	0.903	0.923	0.952	0.929	0.929	0.865	0.934	0.883	0.952
PIC	0.78	0.81	0.77	0.7	0.72	0.87	0.76	0.77	0.85	0.78	0.77	0.65	0.81	0.7	0.85
PE	0.591	0.51	0.51	0.51	0.633	0.677	0.722	0.401	0.633	0.677	0.51	0.254	0.633	0.401	0.51

TPI	2.44	2	2	2	2.75	3.14	3.67	1.57	2.75	3.14	2	1.16	2.75	1.57	2
Ho	0.7955	0.75	0.75	0.75	0.8182	0.8409	0.8636	0.6818	0.8182	0.8409	0.75	0.5455	0.8182	0.6818	0.75
HE	0.8119	0.838	0.8101	0.7544	0.7678	0.8911	0.7936	0.8056	0.8746	0.814	0.809	0.7069	0.8438	0.7495	0.875
HWE	0.87873	0.067	0.6061	0.61305	0.73388	0.239	0.4268	0.516447	0.40376	0.89369	0.98	0.4121	0.0614	0.1237	0.417

RAJASTHAN SARASWAT BRAHMINS															
Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5															
5.3						0.068									
6						0.149									
6.3						0.149									
7			0.095			0.122		0.014				0.108			
7.3						0.041									
8			0.149			0.041	0.122	0.095				0.581			
8.3						0.081									
9	0.068		0.095	0.027		0.2	0.054	0.108				0.054		0.054	
9.3						0.149									
10	0.122		0.27	0.176			0.041	0.189				0.068		0.108	
11	0.095		0.256	0.378			0.202	0.338				0.162	0.041	0.257	
12	0.135		0.108	0.324			0.351	0.202		0.081		0.027	0.027	0.351	
12.2										0.014					
13	0.176		0.027	0.054			0.189	0.054		0.216	0.014		0.068	0.203	
13.2										0.054					
14	0.230			0.041	0.108		0.041			0.255	0.162		0.47	0.027	
14.2										0.054					
15	0.162				0.418					0.176	0.108		0.23		
15.2										0.041			0.014		
16	0.014				0.176				0.014	0.014	0.255		0.041		
16.2										0.027					
17					0.216				0.054		0.284		0.068		
17.2										0.068					
18					0.068				0.176		0.149		0.041		
18.2															
19					0.014				0.106		0.014				0.027

19.2															
20									0.176		0.014				0.108
20.2															
21									0.108						0.187
21.2															0.014
22									0.122						0.161
22.2															0.014
23									0.149						0.122
23.2															0.014
24									0.027						0.108
24.2															0.014
25									0.068						0.122
26															0.095
27		0.081													0.014
27.2		0.027													
28		0.121													
28.2		0.054													
29		0.081													
29.2		0.054													
30		0.068													
30.2		0.068													
31		0.121													
31.2		0.094													
32		0.068													
32.2		0.068													
33		0.014													
33.2		0.054													
34		0.027													
	1.000	1.000	1.000	1.000	1.000	1	1.000	1	1	1	1	1	1	1	1
RMP	0.058	0.039	0.074	0.16	0.134	0.058	0.093	0.087	0.053	0.071	0.09	0.192	0.126	0.121	0.042
l in.....	17.3	25.8	13.6	6.3	7.5	17.3	10.8	11.5	18.8	14.1	11.1	5.2	7.9	8.3	24
PD	0.942	0.961	0.926	0.84	0.866	0.942	0.907	0.913	0.947	0.929	0.91	0.808	0.874	0.879	0.958
PIC	0.82	0.91	0.78	0.67	0.69	0.85	0.75	0.76	0.86	0.82	0.76	0.58	0.68	0.72	0.86
PE	0.521	0.834	0.569	0.619	0.619	0.779	0.619	0.569	0.619	0.521	0.432	0.284	0.476	0.671	0.569
TPI	2.06	6.17	2.31	2.64	2.64	4.63	2.64	2.31	2.64	2.06	1.68	1.23	1.85	3.08	2.31

Ho	0.7568	0.9189	0.7838	0.8108	0.8108	0.8919	0.8108	0.7838	0.8108	0.7568	0.7027	0.5946	0.7297	0.8378	0.7838
HE	0.8549	0.9322	0.8197	0.7253	0.7405	0.8752	0.7893	0.796	0.8815	0.8482	0.8038	0.6246	0.7183	0.7645	0.8863
HWE	0.489651	0.296939	0.517506	0.919123	0.705097	0.3879	0.840523	0.67687	0.233781	0.058838	0.3731	0.4000	0.936622	0.732895	0.2881

PUNJAB SARASWAT BRAHMINS															
Allele	D8S1179	D21S11	D7S820	CSFIPO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5															
5.3						0.078									
6						0.111									
6.3						0.111									
7			0.067			0.122		0.011				0.056			
7.3						0.067									
8	0.011		0.211			0.111	0.144	0.144				0.389			
8.3						0.089									
9	0.078		0.1	0.022		0.178	0.078	0.156				0.144		0.078	
9.3						0.111									
10	0.167		0.277	0.245		0.022	0.078	0.122				0.1		0.089	
11	0.100		0.2	0.222			0.267	0.312				0.289		0.356	
12	0.144		0.078	0.411	0.011		0.333	0.167		0.135	0.011	0.022	0.122	0.356	
12.2										0.022					
13	0.222		0.056	0.1	0.011		0.067	0.033					0.222	0.11	
13.2										0.011					
14	0.133		0.011			0.122		0.033	0.044		0.311	0.144		0.189	0.011
14.2											0.033				
15	0.078					0.267		0.011		0.1	0.122		0.145		
15.2											0.044				
16	0.044					0.245				0.011	0.211		0.133		
16.2										0.022					
17	0.022					0.2				0.067		0.246		0.111	
17.2															
18					0.133					0.056		0.111		0.067	

18.2															
19									0.134		0.089				0.078
19.2															
20					0.011				0.122		0.022				0.089
20.2															
21									0.044						0.178
21.2															
22									0.122		0.011				0.187
22.2															
23									0.189				0.011		0.156
23.2															
24									0.133						0.156
24.2															0.011
25									0.111						0.067
26									0.022						0.078
27															
27.2															
28		0.156													
28.2															
29		0.189													
29.2															
30		0.133													
30.2		0.056													
31		0.178													
31.2															
32		0.232													
32.2		0.056													
33															
33.2	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
34															
Forensic															
RMP	0.052	0.07	0.076	0.139	0.08	0.044	0.081	0.074	0.047	0.092	0.066	0.122	0.055	0.145	0.051
1 in....	19.3	14.4	13.2	7.2	12.6	22.8	12.3	13.6	21.3	10.8	15.2	8.2	18.2	6.9	19.7
PD	0.948	0.93	0.924	0.861	0.92	0.956	0.919	0.926	0.953	0.908	0.934	0.878	0.945	0.855	0.949

PIC	0.84	0.81	0.79	0.66	0.77	0.87	0.75	0.79	0.86	0.74	0.82	0.69	0.83	0.67	0.84
PE	0.728	0.684	0.684	0.519	0.519	0.519	0.558	0.599	0.641	0.411	0.684	0.519	0.558	0.599	0.864
TPI	3.75	3.21	3.21	2.05	2.05	2.05	2.25	2.5	2.81	1.61	3.21	2.05	2.25	2.5	7.5
Ho	0.8	0.867	0.6889	0.7556	0.8222	0.8	0.7778	0.7333	0.8222	0.8222	0.9111	0.7111	0.7333	0.7556	0.9556
He	0.8512	0.844	0.811	0.7366	0.7483	0.8312	0.829	0.7725	0.8504	0.8297	0.8242	0.7044	0.8382	0.7413	0.8647
HWE	0.530282	0.226	0.108667	0.854462	0.831837	0.062169	0.645783	0.122135	0.901659	0.504429	0.983144	0.711865	0.677966	0.173074	0.927735

HIMACHAL SARASWAT BRAHMINS															
Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5															
5.3															
6															
6.3						0.133									
7			0.033			0.144	0.022								
7.3															
8	0.011		0.178			0.222	0.144	0.089				0.401			
8.3															
9	0.011		0.122	0.022		0.133	0.1	0.167				0.122		0.044	
9.3						0.235									
10	0.189		0.278	0.222		0.133	0.089	0.078				0.089	0.033	0.1	
11	0.067		0.245	0.367			0.233	0.4				0.344	0.022	0.322	
12	0.089		0.111	0.278			0.268	0.155		0.056		0.044	0.056	0.356	
12.2										0.056					
13	0.167		0.033	0.1			0.122	0.1		0.289			0.168	0.156	
13.2										0.011					
14	0.233			0.011	0.044		0.022	0.011		0.245	0.156		0.322	0.022	
14.2										0.056					
15	0.156				0.289					0.144	0.067		0.1		
15.2										0.044					
16	0.056				0.356					0.044	0.2		0.133		

16.2										0.011					
17	0.022				0.189				0.044	0.044	0.222		0.033		
17.2															
18					0.111				0.2		0.233		0.067		0.011
18.2															
19					0.011				0.222		0.111		0.033		0.044
19.2															
20									0.111		0.011		0.011		0.1
20.2															
21									0.011						0.2
21.2															
22									0.1				0.011		0.1
22.2															0.022
23									0.201						0.144
23.2															
24									0.044				0.011		0.235
24.2															0.011
25									0.056						0.044
26									0.011						0.067
27		0.044													0.022
27.2															
28		0.133													
28.2															
29		0.144													
29.2															
30		0.257													
30.2		0.022													
31		0.022													
31.2		0.2													
32															
32.2		0.122													
33															
33.2		0.056													
34	1.000	1.000	1.000	1.000	1.000	1	1.000	1	1	1	1	1	1	1	1
Forensic															

RMP	0.057	0.068	0.079	0.131	0.136	0.08	0.066	0.104	0.056	0.074	0.076	0.16	0.07	0.128	0.057
l in.....	17.6	14.8	12.7	7.6	7.4	12.6	15.2	9.6	17.9	13.6	13.2	6.2	14.4	7.8	17.6
PD	0.943	0.932	0.921	0.869	0.864	0.92	0.934	0.896	0.944	0.926	0.924	0.84	0.93	0.872	0.943
PIC	0.82	0.81	0.77	0.68	0.7	0.8	0.8	0.74	0.82	0.8	0.79	0.64	0.81	0.69	0.84
PE	0.599	0.728	0.411	0.519	0.641	0.599	0.558	0.482	0.641	0.641	0.818	0.446	0.482	0.519	0.91
TPI	2.50	3.75	1.61	2.05	2.81	2.5	2.25	1.88	2.81	2.81	5.63	1.73	1.88	2.05	11.25
Ho	0.8667	0.8444	0.8444	0.7556	0.7556	0.7556	0.7778	0.8	0.8222	0.6889	0.8444	0.7556	0.7778	0.8	0.9333
HE	0.8662	0.8352	0.8237	0.7194	0.805	0.8951	0.788	0.8212	0.8864	0.783	0.8472	0.7391	0.8564	0.7288	0.8694
HWE	0.27114	0.381704	0.142886	0.936259	0.919357	0.045681	0.98992	0.762315	0.35971	0.775534	0.082415	0.428908	0.270272	0.758276	0.900456

JAMMU SARASWAT BRAHMIN															
Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5															
5.3															
6						0.337						0.017			
6.3						0.009									
7						0.103						0.155			
7.3						0.009									
8			0.198			0.129	0.086	0.026				0.216			
8.3						0.034									
9			0.19	0.026		0.207	0.095	0.164				0.129		0.034	
9.3						0.155									
10	0.043		0.198	0.19		0.017	0.034	0.103				0.285		0.216	
11	0.043		0.138	0.318			0.233	0.345				0.138	0.009	0.241	
12	0.121		0.198	0.397			0.293	0.25		0.06	0.009	0.06	0.095	0.328	
12.2															
13	0.388		0.078	0.06			0.172	0.103		0.415	0.026		0.155	0.181	
13.2															
14	0.190			0.009	0.06		0.078	0.009		0.293	0.095		0.257		
14.2															
15	0.155				0.397		0.009			0.172	0.216		0.164		
15.2											0.017				

16	0.060				0.267				0.009	0.06	0.266		0.095		
16.2													0.009		
17					0.216				0.086		0.259		0.095		
17.2															
18					0.043				0.216		0.095		0.026		0.009
18.2															0.009
19					0.017				0.164		0.017		0.052		0.034
19.2															0.009
20									0.103				0.026		0.06
20.2															0.017
21									0.017				0.017		0.095
21.2															0.026
22									0.052						0.164
22.2															
23									0.155						0.206
23.2															0.017
24									0.112						0.181
24.2															
25									0.069						0.121
26									0.017						0.052
27															
27.2															
28		0.147													
28.2															
29		0.19													
29.2		0.009													
30		0.19													
30.2															
31		0.034													
31.2		0.121													
32		0.043													
32.2		0.146													
33		0.086													
33.2		0.034													
34	1.000	1.000	1.000	1.000	1.000	1	1.000	1	1	1	1	1	1	1	1

Forensic															
RMP	0.098	0.047	0.071	0.14	0.128	0.086	0.071	0.087	0.04	0.136	0.087	0.074	0.045	0.107	0.051
l in.....	10.3	21.3	14	7.1	7.8	11.6	14	11.4	24.7	7.4	11.4	13.5	22.4	9.3	19.8
PD	0.902	0.953	0.929	0.86	0.872	0.914	0.929	0.913	0.96	0.864	0.913	0.926	0.955	0.893	0.949
PIC	0.74	0.84	0.8	0.65	0.67	0.76	0.78	0.74	0.85	0.66	0.77	0.78	0.83	0.71	0.85
PE	0.495	0.651	0.586	0.387	0.439	0.618	0.495	0.495	0.618	0.362	0.618	0.387	0.685	0.439	0.618
TPI	1.93	2.9	2.42	1.53	1.71	2.64	1.93	1.93	2.64	1.45	2.64	1.53	3.22	1.71	2.64
Ho	0.741	0.8276	0.7931	0.6724	0.7069	0.8103	0.7414	0.7414	0.8103	0.6552	0.8103	0.6724	0.8448	0.7069	0.8103
HE	0.774	0.8663	0.8282	0.7067	0.7253	0.7979	0.8135	0.7763	0.8714	0.712	0.8028	0.7991	0.8582	0.7606	0.8726
HWE	0.245	0.0516	0.1479	0.0663	0.1769	0.1222	0.3684	0.849365	0.956044	0.192174	0.451668	0.132896	0.957605	0.705524	0.20908



Table 2: Allelic Variation and Heterozygosity of the Saraswat Brahmin Populations

Pop		D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
Jammu	N	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58
	Na	7	6	6	6	6	5	8	7	11	5	8	7	11	5	9
	Ne	4.302	5.835	5.588	3.341	3.560	3.452	5.167	4.341	7.345	3.400	4.728	5.232	6.629	4.065	6.675
	I	1.667	1.777	1.749	1.352	1.425	1.347	1.792	1.615	2.126	1.367	1.694	1.755	2.070	1.465	2.008
	Ho	0.741	0.828	0.793	0.672	0.707	0.810	0.741	0.741	0.810	0.655	0.810	0.672	0.845	0.707	0.810
	He	0.768	0.829	0.821	0.701	0.719	0.710	0.806	0.770	0.864	0.706	0.788	0.809	0.849	0.754	0.850
	UHe	0.774	0.836	0.828	0.707	0.725	0.716	0.813	0.776	0.871	0.712	0.795	0.816	0.857	0.761	0.858
	F	0.034	0.001	0.034	0.040	0.017	-0.141	0.081	0.037	0.062	0.072	-0.028	0.169	0.005	0.062	0.047
Kashmir	N	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44
	Na	7	6	8	7	6	6	7	7	9	7	8	6	8	6	10
	Ne	5.068	5.035	5.022	3.935	4.150	4.665	4.643	4.914	7.389	3.849	4.996	3.373	6.031	3.860	7.418
	I	1.762	1.685	1.765	1.525	1.533	1.640	1.691	1.727	2.072	1.503	1.764	1.374	1.907	1.468	2.089
	Ho	0.795	0.750	0.750	0.750	0.818	0.841	0.864	0.682	0.818	0.841	0.750	0.568	0.818	0.682	0.750
	He	0.803	0.801	0.801	0.746	0.759	0.786	0.785	0.796	0.865	0.740	0.800	0.704	0.834	0.741	0.865
	UHe	0.812	0.811	0.810	0.754	0.768	0.795	0.794	0.806	0.875	0.749	0.809	0.712	0.844	0.749	0.875
	F	0.009	0.064	0.064	-0.006	-0.078	-0.070	-0.101	0.144	0.054	-0.136	0.062	0.192	0.019	0.080	0.133
Punjab	N	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45
	Na	10	7	7	6	6	5	8	7	10	6	7	5	13	6	10
	Ne	6.318	5.400	5.050	3.682	3.846	4.162	5.548	4.236	6.289	4.290	5.407	3.295	5.844	3.747	6.470
	I	1.983	1.794	1.735	1.423	1.474	1.519	1.843	1.649	1.990	1.580	1.760	1.344	2.078	1.475	2.025
	Ho	0.800	0.867	0.689	0.756	0.822	0.800	0.778	0.733	0.822	0.822	0.911	0.711	0.733	0.756	0.956
	He	0.842	0.815	0.802	0.728	0.740	0.760	0.820	0.764	0.841	0.767	0.815	0.697	0.829	0.733	0.845
	UHe	0.851	0.824	0.811	0.737	0.748	0.768	0.829	0.773	0.850	0.776	0.824	0.704	0.838	0.741	0.855
	F	0.050	-0.064	0.141	-0.037	-0.111	-0.053	0.051	0.040	0.022	-0.072	-0.118	-0.021	0.115	-0.031	-0.130
Himachal	N	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45
	Na	10	5	8	5	8	6	7	9	10	5	10	6	8	6	8
	Ne	7.118	4.748	5.393	3.464	4.903	4.650	4.530	5.322	8.100	3.722	6.164	3.716	6.429	3.581	6.959
	I	2.082	1.585	1.826	1.359	1.694	1.613	1.689	1.839	2.174	1.414	1.966	1.481	1.929	1.443	2.003
	Ho	0.867	0.844	0.844	0.756	0.756	0.756	0.778	0.800	0.822	0.689	0.844	0.756	0.778	0.800	0.933
	He	0.860	0.789	0.815	0.711	0.796	0.785	0.779	0.812	0.877	0.731	0.838	0.731	0.844	0.721	0.856

	UHe	0.869	0.798	0.824	0.719	0.805	0.794	0.788	0.821	0.886	0.740	0.847	0.739	0.854	0.729	0.866
	F	-0.008	-0.070	-0.037	-0.062	0.051	0.037	0.002	0.015	0.062	0.058	-0.008	-0.034	0.079	-0.110	-0.090
Rajasthan	N	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
	Na	8	8	7	6	6	5	7	7	10	6	8	6	8	6	9
	Ne	6.382	6.694	5.225	3.515	3.710	3.884	4.518	4.656	7.669	4.319	4.829	2.605	3.360	4.068	7.075
	I	1.928	1.968	1.770	1.424	1.482	1.461	1.680	1.685	2.127	1.583	1.700	1.288	1.550	1.536	2.031
	Ho	0.757	0.919	0.784	0.811	0.811	0.892	0.811	0.784	0.811	0.757	0.703	0.595	0.730	0.838	0.784
	He	0.843	0.851	0.809	0.715	0.730	0.743	0.779	0.785	0.870	0.768	0.793	0.616	0.702	0.754	0.859
	UHe	0.855	0.862	0.820	0.725	0.740	0.753	0.789	0.796	0.882	0.779	0.804	0.625	0.712	0.765	0.870
	F	0.103	-0.080	0.031	-0.133	-0.110	-0.201	-0.041	0.002	0.068	0.015	0.114	0.035	-0.039	-0.111	0.087
Mean and SE over Populations for each Locus																
		D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
N	Mean	45.800	45.800	45.800	45.800	45.800	45.8	45.800	45.800	45.800	45.800	45.8	45.800	45.800	45.800	45.800
	SE	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397	3.397
Na	Mean	8.400	6.400	7.200	6.000	6.400	5.400	7.400	7.400	10.000	5.800	8.200	6.000	9.600	5.800	9.200
	SE	0.678	0.510	0.374	0.316	0.400	0.245	0.245	0.400	0.316	0.374	0.490	0.316	1.030	0.200	0.374
Ne	Mean	5.838	5.543	5.256	3.587	4.034	4.163	4.881	4.694	7.359	3.916	5.225	3.644	5.658	3.864	6.919
	SE	0.506	0.341	0.107	0.103	0.238	0.232	0.205	0.197	0.299	0.175	0.262	0.436	0.591	0.094	0.164
I	Mean	1.884	1.762	1.769	1.416	1.522	1.516	1.739	1.703	2.098	1.489	1.777	1.448	1.907	1.478	2.031
	SE	0.075	0.064	0.016	0.031	0.046	0.053	0.033	0.039	0.031	0.044	0.050	0.083	0.096	0.016	0.015
Ho	Mean	0.792	0.842	0.772	0.749	0.783	0.820	0.794	0.748	0.817	0.753	0.804	0.660	0.781	0.756	0.847
	SE	0.022	0.028	0.026	0.022	0.022	0.023	0.021	0.021	0.003	0.036	0.036	0.035	0.023	0.029	0.041
He	Mean	0.823	0.817	0.809	0.720	0.749	0.757	0.794	0.785	0.863	0.743	0.807	0.711	0.812	0.741	0.855
	SE	0.017	0.011	0.004	0.008	0.013	0.014	0.008	0.009	0.006	0.012	0.009	0.031	0.028	0.006	0.003
UHe	Mean	0.832	0.826	0.819	0.728	0.757	0.765	0.803	0.794	0.873	0.751	0.816	0.719	0.821	0.749	0.865
	SE	0.017	0.011	0.004	0.008	0.014	0.015	0.008	0.009	0.006	0.012	0.009	0.031	0.027	0.006	0.004
F	Mean	0.037	-0.030	0.047	-0.040	-0.046	-0.086	-0.002	0.047	0.054	-0.013	0.005	0.068	0.036	-0.022	0.009
	SE	0.019	0.027	0.029	0.029	0.034	0.041	0.032	0.025	0.008	0.040	0.040	0.047	0.027	0.041	0.051
Sample Size, No. Alleles, No. Effective Alleles, Information Index, Observed Heterozygosity, Expected and Unbiased Expected Heterozygosity, and Fixation Index																

DISCUSSION

This observation corroborates prevalent historical accounts, which suggested that the Brahmin populations of different parts of the subcontinent were natives of upper Gangetic region, who later dispersed to different parts of the country, to propagate their cultural and religious ideologies, as also to explore better economic opportunities¹⁶. Since the natives were assimilated into the caste system, they adopted the language and culture of the expanding and dominant upper caste population, as a consequence of elite-dominance. Their gene pool, however, still remained closer to the aboriginals of the region. Therefore, except Brahmins, other groups were probably pooled from the local people to serve the needs of upper castes in the brahminical society. The level of population structuring triggered by the caste system further gets accentuated due to an additional level of endogamy practiced mainly by the most stringent higher caste group¹⁷. Amongst the studied populations, the North Indian Saraswat Brahmins were clustered along with South Indian Dravidian populations Vanniyar Brahmins, Kanyakubj Brahmins, Bihar Brahmin and Kashmiri Muslims. The Gujarat Patel caste¹⁸ formed a different clade on the NJ tree. The Bhumihar Brahmins of Bihar¹⁹, Chhattisgarh²⁰, Chitpavan and Desasht Brahmins²¹ (Saraswat Brahmins from the southwest India) were clustered on the different branch, indicating genetic differentiation from North Indian Saraswat Brahmins. The other North Indian

communities²² e.g. Jat, Kurmi, Vaish and tribal populations were also found on different branches. Other non-Brahmin castes from North India (Khatri, Thakur) were organized with each other on different clade. The Kashmiri Muslims were found to be clustered with the Kashmiri Saraswat Brahmins. These results are in congruence with the observations of Majumder *et al.*²³, wherein populations studied from widely separated geographic areas were found to exhibit closer genomic affinities with their geographic neighbors, than with those sharing similar social ranks. The autosomal genetic similarity of Saraswat Brahmins to Brahmins from Bihar and Kanyakunj Brahmins of Madhya Pradesh²⁴ indicated that, these gene pools probably consisted of genetic inputs from both the Brahmin groups. Amongst the caste groups, Kanyakubj Brahmin expressed closer affinity to the other upper caste populations of North India, rather than with its geographic neighbors.

Kashmiri Muslim group was thought to be genetically similar to local populations. Generally identical genetic relationship between Muslims and other studied groups was expected due to regional conversions from diverse castes that occurred during the period of Islamic dominance. But microsatellite study emphasized on no genetic similarity among the Kashmir Saraswat Brahmin and Kashmiri Muslim populations.

The Indo-European Saraswat population was expected to be clustered with other Asian populations i.e. Taiwan, Thai, Malaysia and China. But autosomal STR

data rendered the clustering of Saraswat Brahmins with American-Africans and Egyptian¹² populations. The populations from European (Caucasian¹¹, Hispanic¹¹, Tunisian¹³, Brazil²⁵, Croatia²⁶ and Spain²⁷) and African origins (Cyprus²⁸) were claded on the other branches of the tree. The North Indian Brahmins belong to a cluster together with geographically diverse European and African populations, showing their affinity with the Caucasian gene pool. These results were expected in the same way as the Asian populations, selected for comparison belonged to the Australoids group and genetic differentiation between Indo-European and Australoids groups had been well established. Intriguingly, in the present study, Saraswat community belonging to the upper strata of the Hindu caste hierarchy displayed almost identical genetic affinity with American Indians as compared to the other Mongoloid Asian populations. The NJ tree confirmed the distinction between the Saraswat Brahmin sub-clade and European (US Caucasians, US Hispanics, and African Americans). Indian Saraswat Brahmins displayed a branch nearer to Caucasians and to some extent closer to Egypt, suggesting a strong Caucasian element along with African admixtures. The data generated from the present study has shown that these five North Indian populations are genetically closer to the Caucasian than to the Asian populations.

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