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Distribution of Human-specific *Alu* InDel Polymorphisms in the Brahmin and Rajput Populations of Kangra District of Himachal Pradesh, North India

Dheeraj Jamwal, S.M.S. Chahal*, Manju Bala, Anu Raina and Vasundhara Raina

Department of Human Genetics, Punjabi University, Patiala 147 002, Punjab, India

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ABSTRACT The genetic constitution of two endogamous caste populations viz., the Brahmin (n=250) and Rajput (n=250) of Kangra district of the North Indian state of Himachal Pradesh was studied using six autosomal *Alu* InDel (insertion/deletion) markers viz., ACE, APO, PV92, CD4, PLAT, and TPA25. All markers were found to be polymorphic. Except for *Alu* APO and PV92 in the Rajput, genotype frequencies of other markers were in the Hardy-Weinberg equilibrium in both the populations. The average heterozygosity (*H*) was observed higher in the Brahmin (0.4134) compared to the Rajput (0.3809) and the degree of genic differentiation was low between them (G_{ST} =0.00898). The genetic distance analysis revealed close genetic affinities of the present Rajput population with the Gaddi Rajput and Gaddi Brahmin populations reported earlier from the district but the present Brahmin population was found distant from them.

INTRODUCTION

DNA polymorphisms provide a rich source of information on the human population genetic structure and evolutionary history (Perna et al. 1992). The vast majority of such polymorphisms can be split into two groups - those based on nucleotide substitutions commonly called single nucleotide polymorphisms (SNPs), and those based on the insertion or deletion of one or more nucleotides (InDels) (Weber et al. 2002). Human-specific *Alu* InDel (insertion/deletion) polymorphisms are selectively neutral, rare, irreversible, and extensively dispersed (Batzer et al. 1994) and for these reasons they are widely used in population studies.

India comprises of many ethnic, caste, religious and linguistic groups (Bhasin 2006) and the country presents a great diversity of cultural, morphological, linguistic, and genetic traits (Majumder 1998). Several *Alu* InDel marker variation studies have been reported from India, including Kshatriya et al. (2011) from West India, Majumdar et al. (1999), Chakrabarti et al. (2002), Meitei et al. (2010), Panmei et al. (2016), Kshatriya et al. (2019) and Kameih et al. (2020) from East India, Mukherjee et al. (2000) from Central India, and Veerraju et al. (2001), Vishwanathan et al. (2004), Ravindranath et al. (2005), Saraswathy et al. (2008), Gauniyal et al. (2011), Krishnaveni and Prabhakaran (2015) and Deva et al. (2016) from South India. As for North India, such investigations are mostly available on the populations of Jammu and Kashmir (Panjaliya et al. 2012, 2013), Punjab (Kaur et al. 2002, Saini et al. 2012, Singh et al. 2016 a,b), Uttar Pradesh (Chakrabarti et al. 2002; Tripathi et al. 2008) and Rajasthan (Dada et al. 2011) while from the State of Himachal Pradesh only a single study (Bala et al. 2019) has been reported. Therefore, the present study was planned to fill the void on the genomic map of the State.

*Address for correspondence:
E-mail: smschahal@rediffmail.com

Objectives

The objectives of the present study were, first to establish the genetic profiles of two main endogamous caste populations of Kangra district of Himachal Pradesh viz., the Brahmin, and Rajput using six diallelic *Alu* InDel polymorphisms viz., ACE, APO, PV92, CD4, PLAT, and TPA25. Secondly, to assess the average heterozygosity, genic differentiation, and genetic similarities and differences among the present and other populations reported from North India.

MATERIAL AND METHODS

Blood sampling was done from various villages of Dharamshala, Fatehpur, Nurpur, Baijnath, Nagrota Bagwan and Paragpur tehsils of Kangra

district of Himachal Pradesh, and the Govt. Degree Colleges at Dharamshala and Baijnath. After the informed consent, intravenous blood samples (about 5 ml each) were collected in sterile EDTA.Na_2 vials from a total of 500 random not closely related healthy subjects of the Brahmin (n=250) and Rajput (n=250) populations in 6 different field works from February 2018 to November 2019. The ethical clearance for this study was obtained from the Institutional Ethical Committee of the Punjabi University, Patiala (Punjab).

Laboratory Analysis

The DNA was isolated by the method of Miller et al. (1988). The quality and quantity of the DNA samples were assessed using the spectrophotometer and agarose gel electrophoresis. The studied *Alu* InDel markers were genotyped by the standard PCR protocols following Stoneking et al. (1997), Majumder et al. (1999) and Edwards and Gibbs (1992). The DNA samples were amplified by the polymerase chain reaction (PCR) technique in 0.5 ml Eppendorf vials containing 1µl template DNA, 5µl Mastermix, 0.5µl each of the forward and reverse primers, and 3µl nuclease-free water using a Thermal Cycler (Applied Biosystems 2720). The primer sequences and annealing temperatures used for various *Alu* InDels are listed in Table 1. The amplified PCR products were separated by 2.0-2.5 percent agarose gel electrophoresis at 100 V for 1h and thereafter the genotypes were visualized under a UVP GelDoc-It Imaging System and recorded.

Statistical Analysis

The allele frequencies were calculated by the gene counting method (Mourant et al. 1976), and genotype counts were examined for the Hardy-Weinberg equilibrium by the Goodness of fit chi-square (χ^2_{HW}) test. The Contingency χ^2 test was used to study the inter-population differences. Heterozygosity and genic differentiation were estimated following Nei (1973). The genetic relationships among the present and other populations reported from different North Indian States were assessed using the UPGMA dendrograms (Felsenstein 2005) based on genetic distance measure *D* values (Nei 1972).

RESULTS

The distribution of genotypes, allele frequencies, and the goodness of fit chi-square (χ^2_{HW}) test values of the studied *Alu* InDel markers in the Brahmin and Rajput populations of Kangra district of Himachal Pradesh is presented in Table 2. Barring *Alu* APO (χ^2_{HW}=7.44, d.f.=1, p<0.006) and *Alu* PV92 (χ^2_{HW}=4.94, d.f.=1, p<0.026) in the Rajput, the goodness of fit chi-square test revealed statistically non-significant differences between the observed and expected genotype counts demonstrating that on the whole the investigated markers were in genetic equilibrium in the present caste populations. The frequency of the + (*I*) allele of *Alu* ACE was observed 0.4740 in the Brahmin and much higher in the Rajput (0.6260). Similarly, for *Alu* APO, the + (*I*) allele

Table 1: Primer sequences and annealing temperatures used for genotyping of various studied *Alu* InDel markers

Alu marker	*Primer sequence*	*Annealing temperature*	*Reference*
ACE	Forward Primer: 5'– CTG GAG ACC ACT CCC ATC CTT TCT – 3' Reverse Primer: 5'– GAT GTG GCC ATC ACA TTC GTC AGA T – 3'	58°C	Stoneking et al. (1997)
APO	Forward Primer: 5'– AAG TGC TGT AGG CCA TTT AGA TTA G – 3' Reverse Primer: 5'– AGT CTT CGATGACAGCGTATACAGA – 3'	54.2°C	Stoneking et al. (1997)
PV92	Forward Primer: 5'– AAC TGG GAA AAT TTG AAG AGA AAG T – 3' Reverse Primer: 5'– TGA GTT CTC AAC TCC TGT GTG TTA G – 3'	54°C	Majumder et al. (1999)
CD4	Forward Primer: 5'– AGG CCT TGT AGG GTT GGT CTG ATA – 3' Reverse Primer: 5'– TGC AGC TGC TGA GTG AAA GAA CTG – 3'	58°C	Edwards and Gibbs (1992)
PLAT	Forward Primer: 5'-GTG AAA AGC AAG GTC TAC CAG-3' Reverse Primer: 5'-GAC ACC GAG TTC ATC TTG AC-3'	60°C	Stoneking et al. (1997)
TPA25	Forward Primer: 5'– GTA AGA GTT CCG TAA CAG GAC AGC T – 3' Reverse Primer: 5'– CCC CAC CCT AGG AGA ACT TCT CTT T – 3'	58°C	Majumder et al. (1999)

Table 2: Distribution of genotypes, allele frequencies and goodness of fit Chi-square (χ^2_{HW}) (d.f.1) test values of various studied *Alu* InDel markers in the Brahmin and Rajput populations of Kangra district of Himachal Pradesh

Alu marker	*Population*	*n*		*Genotype count*			*Allele frequencya*		χ^2_{HW}	*p*
				+ (*I*) + (*I*)	+ (*I*) - (*D*)	- (*D*) - (*D*)	+ (*I*)	- (*D*)		
ACE	Brahmin	250	Observed	51	135	64	0.4740	0.5260	1.72	0.189
			Expected	56.17	124.66	69.17				
	Rajput	250	Observed	100	113	37	0.6260	0.3740	0.30	0.583
			Expected	97.97	117.06	34.97				
APO	Brahmin	250	Observed	123	99	28	0.6900	0.3100	1.38	0.230
			Expected	119.03	106.95	24.02				
	Rajput	250	Observed	176	60	14	0.8240	0.1760	7.44	0.006*
			Expected	169.74	72.51	7.74				
PV92	Brahmin	250	Observed	16	103	131	0.2660	0.7340	0.51	0.475
			Expected	18.22	98.55	133.22				
	Rajput	250	Observed	27	87	136	0.2820	0.7180	4.94	0.026*
			Expected	19.88	101.24	128.88				
CD4	Brahmin	250	Observed	196	53	1	0.8900	0.1100	1.71	0.191
			Expected	198.02	48.95	3.02				
	Rajput	250	Observed	210	37	3	0.9140	0.0860	0.85	0.354
			Expected	208.85	39.30	1.85				
PLAT	Brahmin	250	Observed	49	107	94	0.4100	0.5900	3.33	0.068
			Expected	42.03	120.95	87.03				
	Rajput	249	Observed	55	108	86	0.4370	0.5630	3.52	0.061
			Expected	47.71	122.57	78.71				
TPA25	Brahmin	249	Observed	41	122	86	0.4096	0.5094	0.04	0.837
			Expected	41.78	120.43	86.78				
	Rajput	250	Observed	41	110	99	0.3840	0.6160	1.22	0.269
			Expected	36.86	118.27	94.86				

+ *(I)* =Insertion allele, - *(D)* =Deletion allele, d.f. =Degree of freedom *Statistically significant ($p<0.05$)

frequency was rather high in the Rajput (0.8240) compared to the Brahmin (0.6900). As for *Alu* PV92, the + (*I*) allele frequency was observed almost similar in the Brahmin (0.2660) and Rajput (0.2820). The allele frequencies in the Brahmin and Rajput populations of Kangra district were not much different for *Alu* CD4 (respectively, 0.8900 and 0.9140), *Alu* PLAT (respectively, 0.4100 and 0.4370) and *Alu* TPA25 (respectively, 0.4096 and 0.3840) markers.

The contingency Chi-square (χ^2) test values of the studied *Alu* InDel polymorphisms between the Brahmin and Rajput populations of the Kangra district of Himachal Pradesh are presented in Table 3. The table shows statistically significant differences in the genotype distribution of *Alu* markers ACE (χ^2=25.07, d.f. 2, p =0.001) and APO (χ^2=23.63, d.f. 2, p =0.001) between the present two castes populations, and for the remaining markers (*Alu* PV92, CD4, PLAT, TPA25) there were no such differences. Therefore, overall there was little evidence of genotypic heterogeneity between the Brahmin and Rajput populations of Kangra district.

Table 3: Contingency Chi-square (χ^2) (d.f. 2) test values of various studied *Alu* InDel markers in the Brahmin and Rajput populations of Kangra district of Himachal Pradesh

Alu marker	χ^2	*p*
ACE	25.07	0.001*
APO	23.63	0.001*
PV92	4.25	0.119
CD4	4.33	0.115
PLAT	0.70	0.705
TPA25	1.53	0.465

*Statistically significant ($p \leq 0.05$)

Heterozygosity

Heterozygosity (*h*) and average heterozygosity (*H*) estimates in the Brahmin and Rajput populations of the Kangra district of Himachal Pradesh are given in Table 4. It was observed that in the Brahmin barring *Alu* CD4 (*h*=0.1958), the range of heterozygosity in the remaining five markers was observed high, varying from 0.3905 for *Alu* PV92 to 0.0.4986 for *Alu* ACE. On the other hand, in the Rajput the *h* values were low for *Alu* CD4 (0.1572) and *Alu* APO (0.2900) markers compared to the values observed for the remaining four markers (range 0.4682 for *Alu* ACE to 0.4921 for *Alu* PLAT). The average heterozygosity (*H*) over the studied markers was found higher in the Brahmin (0.4134) than the Rajput (0.3809).

Table 4: Distribution of heterozygosity (*h*) and average heterozygosity (*H*) of various studied *Alu* InDel markers in the Brahmin and Rajput populations of Kangra district of Himachal Pradesh

Alu marker	*Heterozygosity (h)*	
	Brahmin	*Rajput*
ACE	0.4986	0.4682
APO	0.4278	0.2900
PV92	0.3905	0.4050
CD4	0.1958	0.1572
PLAT	0.4838	0.4921
TPA25	0.4837	0.4731
Average heterozygosity (*H*)	0.4134	0.3809

Gene Diversity and Differentiation

The results of the gene diversity measures (H_T, H_S, D_{ST}) and the coefficient of gene differentiation (G_{ST}) estimates of the studied 6 *Alu* InDel loci in the Brahmin and Rajput populations of the Kangra district of Himachal Pradesh are given in Table 5. The intra-subpopulational gene diversity (H_S) varied widely from 0.17650 at *Alu* CD4 locus to 0.48829 at *Alu* PLAT locus with an average of 0.39719. The total genomic diversity (H_T) ranged from a minimum of 0.17679 at *Alu* CD4 locus to a maximum of 0.49500 at *Alu* ACE locus with an average of 0.40076. In contrast, inter-subpopulational gene diversity (D_{ST}) estimates were found very low (range 0.00013-0.01155) with an average of 0.00360 over the six loci. Thus H_S contributed most to the H_T and only a minor fraction was contributed by $D_{ST.}$

The coefficient of gene differentiation (G_{ST}) value ranged from as low as 0.00032 at *Alu PV92* locus to as high as 0.02440 at *Alu APO* locus, suggesting that the former locus was the least differentiated and the latter locus was the most differentiated in the Brahmin and Rajput populations of the Kangra district of Himachal Pradesh. The average G_{ST} value over the six studied loci was recorded 0.00898 which demonstrated little genetic differentiation between the present two caste populations of Kangra district.

Table 5: Measures of gene diversity (H_T, H_S, D_{ST}) and coefficient of gene differentiation (G_{ST}) estimates of various studied *Alu* InDel loci in the Brahmin and Rajput populations of Kangra district of Himachal Pradesh

Alu InDel locus	*Total gene diversity of the population (H_T)*	*Intra- subpopulational gene diversity (H_S)*	*Inter-subpopulational gene diversity (D_{ST})*	*Coefficient of gene differentiation (G_{ST})*
ACE	0.49500	0.48334	0.01155	0.02334
APO	0.36790	0.35892	0.00898	0.02440
PV92	0.39785	0.39772	0.00013	0.00032
CD4	0.17679	0.17650	0.00029	0.00163
PLAT	0.48830	0.48829	0.00031	0.00074
TPA25	0.47870	0.47837	0.00033	0.00065
Average	0.40076	0.39719	0.00360	0.00898

Genetic Distance

An UPGMA (unweighted pair group method with arithmetic mean) dendrogram based on genetic distances was constructed **(**Fig.1) to comprehend the overall genomic relationships among the present Brahmin and Rajput populations of the Kangra district of Himachal Pradesh along with the previously reported Gaddi Brahmin and Gaddi Rajput populations of the district (Bala et al. 2019). The figure showed that the present Brahmin population separated earlier in a single line cluster from the present Rajput and two Gaddi populations of the Kangra district which were placed together in a cluster.

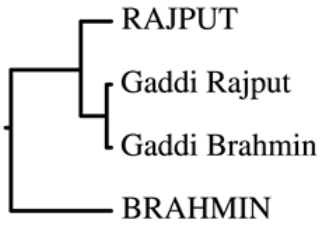

Fig. 1. UPGMA dendrogram based on the 6 studied *Alu* InDel markers showing genetic relationships among the present Brahmin and Rajput populations, and the Gaddi Brahmin and Gaddi Rajput populations reported from Himachal Pradesh

DISCUSSION

The present results were compared with previously published data available in the literature on other North Indian populations. Due to the paucity of studies from Himachal Pradesh on all six *Alu* InDel markers included in this study, the comparison was limited to five common markers viz., *Alu* ACE, APO, PV92, CD4, and PLAT reported in the Gaddi population of Himachal Pradesh (Bala et al. 2019), the Brahmin, Rajput, Gujjar and Jat Sikh of Jammu and Kashmir (Panjaliya et al. 2012, 2013), the Brahmin, Khatri, Scheduled Castes and Jat Sikh of Punjab (Kaur et al. 2002), and the Katharia Tharu and Rana Tharu of Uttar Pradesh (Chakrabarti et al. 2002).

Table 6 lists the distribution of the Insertion + (*I*) allele frequencies of various *Alu* markers in different populations of North India, including the present two populations of Himachal Pradesh. The *Alu* ACE insertion + (*I*) allele frequency varied from a low of 0.3800 in the Gujjar to a high of 0.7200 in the Brahmin, both of Jammu and Kashmir State (Panjaliya et al. 2012, 2013). For *Alu* APO, the + (*I*) allele frequency ranged from a low of 0.4400 in the Gujjar of Jammu and Kashmir to a high of 0.9270 in the Jat Sikh of Punjab (Kaur et al. 2002). Similarly there was great variation in *Alu* PV92 insertion + (*I*) allele frequency values in the populations of North India, ranging from 0.2660 in the Brahmin of Himachal Pradesh (present study) to as high as 0.8210 in the Rana Tharu of Uttar Pradesh (Chakrabarti et al. 2002). The range of *Alu* CD4 insertion + (*I*) allele frequency was also observed high, varying from 0.0140 in the Katharia Tharu of Uttar Pradesh (Chakrabarti et al. 2002) to 0.9479 in the Scheduled Castes of Punjab (Kaur et al. 2002). As for the *Alu* PLAT marker, the range of the insertion + (*I*) allele frequency was found varying from 0.4100 in the Brahmin of Himachal Pradesh (present study) to as high as 0.8190 in the Katharia Tharu of Uttar Pradesh (Chakrabarti et al. 2002).

Table 6: Distribution of Insertion + (*I*) allele frequency of 5 *Alu* InDel markers common among the present study populations of Himachal Pradesh and different other populations reported from different North Indian states

State	*Population*	*+ (I) Allele frequency*					*Reference*
		ACE	*APO*	*PV92*	*CD4*	*PLAT*	
Himachal Pradesh	Brahmin	0.4720	0.6900	0.2660	0.8900	0.4100	Present study
	Rajput	0.6260	0.8240	0.2820	0.9140	0.4370	
Himachal Pradesh	Gaddi Brahmin	0.5532	0.9184	0.4138	0.8908	0.5719	Bala et al. (2019)
	Gaddi Rajput	0.6029	0.8829	0.4114	0.9029	0.5603	
Jammu and Kashmir	Brahmin	0.7200	0.6150	0.5500	0.8900	0.5500	Panjaliya et al. (2012, 2013)
	Rajput	0.5750	0.7400	0.4750	0.8600	0.6000	
	Gujjar	0.3800	0.4400	0.3600	0.8700	0.5700	
	Jat Sikh	0.6200	0.8100	0.3000	0.8400	0.5600	
Punjab	Brahmin	0.4895	0.9062	0.3541	0.9166	0.4468	Kaur et al. (2002)
	Khatri	0.6250	0.8750	0.4062	0.9375	0.5119	
	Scheduled Castes	0.4791	0.9062	0.5000	0.9479	0.4896	
	Jat Sikh	0.6979	0.9270	0.3958	0.8437	0.4559	
Uttar Pradesh	Katharia Tharu	0.5690	0.8470	0.6940	0.0140	0.8190	Chakrabarti et al. (2002)
	Rana Tharu	0.6230	0.7260	0.8210	0.0190	0.7920	

Table 7 shows the comparison of the + (*I*) allele frequency ranges of 5 *Alu* InDel markers (ACE, APO, PV92, CD4, PLAT) common among the present study populations of the Kangra district of Himachal Pradesh and various other populations reported from different North Indian States. The ranges observed for *Alu* ACE (0.4720-0.6260), *Alu* APO (0.6900-0.8240), and *Alu* CD4 (0.8900-0.9140) markers in the present Brahmin and Rajput populations of Himachal Pradesh were found to fit in the respective ranges of the populations of North India (0.3800-0.7200, 0.4400-0.9270, and 0.0140-0.9479). The + (*I*) allele frequency ranges of the remaining two markers, *Alu* PV92 (0.2660-0.2820) and PLAT (0.4100-0.4370), were observed below the lower limits of the ranges of the populations of North India (respectively, 0.3000-0.8210 and 0.4468-0.8190).

Table 7: Range of Insertion (*I*) + allele frequency of *Alu* InDel markers common among the present study populations of Himachal Pradesh and various other populations reported from different North Indian states

Alu Marker	*Insertion +(I) Allele frequency range*	
	Present populations	*North Indian Populations*
ACE	0.4720-0.6260	0.3800-0.7200
APO	0.6900-0.8240	0.4400-0.9270
PV92	0.2660-0.2820	0.3000-0.8210
CD4	0.8900-0.9140	0.0140-0.9479
PLAT	0.4100-0.4370	0.4468-0.8190

The average heterozygosity (*H*) estimates based on the five *Alu* InDel markers common among the Brahmin and Rajput populations of Kangra district of Himachal Pradesh and 12 other populations reported from different North Indian States are presented in Table 8. It was observed that the *H* estimates in the present Brahmin and Rajput populations (range 0.3625-0.3993) were similar to the values of the measure reported in the Gaddi Brahmin and Gaddi Rajput populations of Himachal Pradesh (range 0.3627-0.3676, Bala et al. 2019). Outside Himachal Pradesh, it was noted that the present estimates were much lower than those reported in 4 populations of Jammu and Kashmir (*H* range 0.3921-0.4282, Panjaliya et al. 2012, 2013) but higher than that reported in 4 populations of Punjab (*H* range 0.3535-0.3590, Kaur et al. 2002) and much higher than 2 Tharu populations of Uttar Pradesh (*H* range 0.2997-0.3057, Chakrabarti et al. 2002). Therefore, the Brahmin and Rajput populations of Himachal Pradesh showed higher genetic variation than the populations of both Punjab and Uttar Pradesh States but the extent of the variation in them was lower compared to the populations of Jammu and Kashmir State.

Table 9 shows that the G_{ST} estimate in the Brahmin and Rajput populations of the Kangra district of Himachal Pradesh (0.0090) was higher than that reported in two Gaddi populations of the district (G_{ST} =0.0019, Bala et al. 2019). On the other hand, the present G_{ST} value in general was

Table 8: Estimates of average heterozygosity (*H*) based on 5 *Alu* InDel markers (ACE, APO, PV92, CD4, PLAT) common among the present populations of Himachal Pradesh and 12 other populations reported from various North Indian states

State	*Population*	*Average Heterozygosity (H)*	*Range*	*Reference*
Himachal Pradesh	Brahmin	0.3993	0.3625-0.3993	Present study
	Rajput	0.3625		
Himachal Pradesh	Gaddi Brahmin	0.3627	0.3627-0.3676	Bala et al. (2019)
	Gaddi Rajput	0.3676		
Jammu and Kashmir	Brahmin	0.4125	0.3921-0.4282	Panjaliya et al. (2012, 2013)
	Rajput	0.4186		
	Gujjar	0.4282		
	Jat Sikh	0.3921		
Punjab	Brahmin	0.3549	0.3535-0.3590	Kaur et al. (2002)
	Khatri	0.3574		
	Scheduled Castes	0.3535		
	Jat Sikh	0.3590		
Uttar Pradesh	Katharia Tharu	0.2997	0.2997-0.3057	Chakrabarti et al. (2002)
	Rana Tharu	0.3057		

Table 9: Coefficient of gene differentiation (G_{ST}) values in the present populations of Himachal Pradesh and other populations reported from various North Indian states

State	*Number of populations*	*Number of markers*	G_{ST}	*Reference*
Himachal Pradesh	2	6	0.0090	Present study
Himachal Pradesh	2	6	0.0019	Bala et al. (2019)
Jammu and Kashmir	5	6	0.0306	Panjaliya et al. (2012)
	4	3	0.0159	Panjaliya et al. (2013)
Punjab	4	8	0.0134	Kaur et al. (2002)
	5	5	0.0133	Saini et al. (2012)
	5	7	0.0166*	Singh et al. (2016a)
	5	3	0.0053*	Singh et al. (2016b)
Uttar Pradesh	9	10	0.1498	Tripathi et al. (2008)
Rajasthan	6	12	0.0491	Dada et al. (2011)

*F_{ST}

much lower in comparison to the values reported in the populations of Jammu and Kashmir (G_{ST} =0.0306, Panjaliya et al. 2012; G_{ST} =0.0159, Panjaliya et al. 2013), Punjab (G_{ST}=0.0134, Kaur et al. 2002; G_{ST} =0.0133, Saini et al. 2012; F_{ST}=0.0166, Singh et al. 2016a; F_{ST}=0.0053, Singh et al. 2016b), Uttar Pradesh (G_{ST} =0.1498, Tripathi et al. 2008) and Rajasthan (G_{ST} =0.0491, Dada et al. 2011). This suggests that in comparison to the populations of different North Indian States, the degree of genic differentiation was least in the populations of Himachal Pradesh.

An UPGMA dendrogram was constructed to comprehend the overall genetic similarities and differences among various North Indian populations using the Nei's genetic distances (Fig. 2). The figure shows that the present Rajput population of the Kangra district of Himachal Pradesh and the Jat Sikh population of Jammu region of Jammu and Kashmir State were placed together in a sub-cluster near to a single line cluster of the Jat Sikh of Punjab. On the other hand, the present Brahmin population separated in a single line cluster at an early stage of evolution.

CONCLUSION

The present genetic study has provided baseline data on the distribution of a battery of 6 *Alu* InDel (insertion/deletion) markers in the Brahmin and Rajput endogamous populations of the Kangra district of Himachal Pradesh enabling the es-

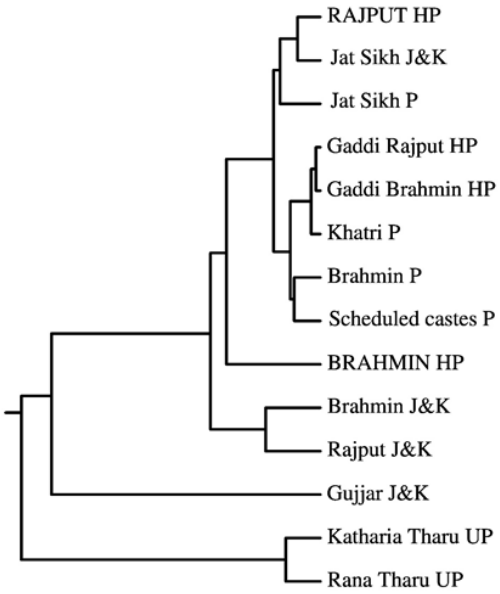

Fig. 2. UPGMA dendrogram based on 5 *Alu* InDel markers common among the present Brahmin and Rajput populations of Himachal Pradesh (HP), and various other North Indian populations reported from Himachal Pradesh (HP), Jammu and Kashmir (J&K), Punjab (P) and Uttar Pradesh (UP)

tablishment of their genomic profiles. There was little evidence of heterogeneity between the present caste populations, and the allele frequencies observed in them for most of the markers were found to be similar to various North Indian populations. The genetic distance analysis demonstrated close genetic affinities of the Rajput population with both the Gaddi Rajput and Gaddi Brahmin populations reported earlier from the district.

RECOMMENDATION

Further genetic studies on the people inhabiting different areas of Himachal Pradesh using a variety of DNA markers, including the *Alu* InDels and SNPs, are desirable to complete the genomic map of this hill state of North India.

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