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Genetic Studies in Five Population Samples of Himachal Pradesh and Punjab, North-West India

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ABSTRACT Five caste populations (Brahmins, Rajputs, Khatris, Mahajans, Kambohs) from Chamba (Himachal Pradesh) and Sanaur village near Patiala (Punjab) were typed for HP polymorphism and TF, GC and PI subtype polymorphisms. Including already published data on the distribution of red cell enzyme polymorphisms the genetic heterogeneity among these five caste populations was analyzed, which proved to be considerable concerning the polymorphic systems GC, PI, ACP 1 and GPI. Genetic distance analysis showed the existence of a clear distance pattern: Brahmins and Rajputs as well as Khatris and Mahajans are found in different subclusters forming one coherent cluster, whereas Kambohs are deviating obviously from this cluster. These analyses reflect the regional and social differentiation of the five caste groups and substantiates the importance of endogamy for emergence and maintenance of genetic diversity in man.

INTRODUCTION

In the last three decades many investigations on the regional and ethnic distribution of serum protein and red cell enzyme polymorphisms were performed on Indian populations, which revealed a remarkable genetic variability within and among them. These data were recently complied and critically discussed by Walter, Danker-Hopfe and Bhasin (1991). A comprehensive survey on the distribution of the polymorphic blood group, serum protein, red cell enzyme polymorphisms etc. in India was presented by Bhasin, Walter and Danker-Hopfe (1992). The variation of ACP 1, GLO, ESD and AK polymorphisms in India was studied in detail by Chahal et al. (1985, 1986a, 1986b, 1986c). However, from all these publications it emerges that our knowledge concerning the regional and ethnic distribution of genetic markers in India is far from being complete, and even the North-West Indian region shows still many gaps in this respect.

In order to contribute to our knowledge on the distribution of genetic markers in this part of India we are presenting here the results of HP, TF, GC and PI typings in five endogamous caste populations from Chamba (Himachal Pradesh) - Brahmins, Rajputs, Khatris, Mahajans - and Sanaur village near Patiala (Punjab) - Kambohs. Figure 1 shows the location of these places. For analyses of genetic heterogeneity and genetic distance we incorporated the data of enzyme group typings on these five populations, which have been published already elsewhere (Chahal et al., 1989, 1991).

MATERIALS AND METHODS

Serum samples of the Brahmins (n =63), Rajputs (n = 106), Khatris (n = 69), Mahajans (n = 40) and Kambohs (n = 152) were collected by one of us (S.M.S. Ch.) and air-mailed to Bremen (Germany), where the typings and statistical analyses were done in the Deptt. of Human Biology, University of Bremen. With slight modifications we used the typing methods as described by Spielmann and Kühnl (1982) and Prokop and Göhler (1986).

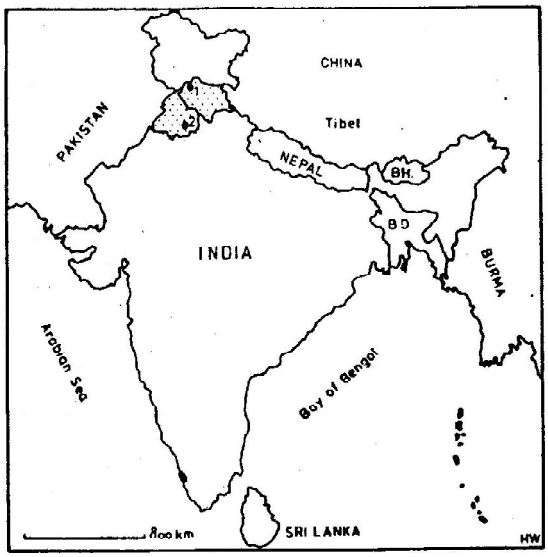

Fig. 1. Location of the population samples under study 1 = Chamba (Himachal Pradesh), 2 = Patiala (Punjab) BH = Bhutan, B.D. = Bangla Desh

RESULTS

Table 1 shows the distribution of HP phenotype numbers and allele frequencies in the five populations under study. Genetic equilibrium can be assumed for Brahmins, Rajputs, Khatris and Kambohs. The Mahajans show some deviation from Hardy-Weinberg equilibrium, which, however, seems to be caused by the small sample size (n = 38).

TF phenotype numbers and allele frequencies are demonstrated in table 2. Genetic equi-

Table 1 : HP phenotype numbers and allele frequencies in five North-West Indian population samples

	Brahmins		*Rajputs*		*Khatris*		*Mahajans*		*Kambohs*	
Phenotypes	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*
1	1	2.56	5	4.61	5	6.37	1	3.79	8	7.61
2-1	23	19.88	34	34.78	31	28.26	22	16.42	52	52.79
2	37	38.56	66	65.61	30	31.37	15	17.79	92	91.60
Total	61	61.00	105	105.00	66	66.00	38	38.00	152	152.00
χ^2	1.503		0.053		0.620		4.388		0.034	
df	1		1		1		1		1	
p	ns		ns		ns		0.05>p>0.02		ns	
Alleles										
*HP*1*	0.2049		0.2095		0.3106		0.3158		0.2237	
*HP*2*	0.7951		0.7905		0.6894		0.6842		0.7763	
Total	1.0000		1.0000		1.0000		1.0000		1.0000	

librium can be assumed for all the samples except Rajputs and Khatris. Both populations show lower numbers of the observed homozygous phenotypes TF C1 and TF C2 as compared to the expected ones, and higher numbers of the heterozygous phenotype TF C2-1 in comparison with the expected ones. This tendency can also be observed in the other three population samples. One cannot exclude, however, that this is due to the sample sizes. It is interesting to note that in the Brahmins, Rajputs and Khatris only two TF alleles - *TF*C1* and *TF*C2* - were found, whereas in the Mahajans and Kambohs in addition to these alleles a third one was also recorded: *TF*C3*. Rare TF alleles were observed in none of the five populations.

Table 3 shows the phenotype numbers and allele frequencies of the GC polymorphism. With the only exception of the Brahmins genetic equilibrium can be assumed for all the other population samples. A convincing explanation for this deviation cannot be given, and one can take into consideration that it might also be due to the relatively small sample size (n = 63). In none of the five populations rare GC alleles were found.

The PI phenotype numbers and allele frequencies in the populations under study are shown in table 4. Genetic equilibrium is present in all of them except the Rajputs. The reasons for the differences between observed and expected phenotype numbers in them are unclear, and since these concern both homozygous as well as heterozygous phenotypes one cannot exclude that these deviations may be also due to chance. Rare PI alleles were not found in any of the five populations.

DISCUSSION

From the allele frequencies presented in tables 1-4 one can recognize a more or less marked genetic variability among these five population samples for the distribution of the four serum protein systems under study. In order to check the statistical significance of the distribution of HP, TF, GC and PI polymorphisms we analyzed their locus and allele specific heterogeneity according to Rao (1952). The result of these tests are shown in table 5, which contains also the corresponding results for the red cell enzyme polymorphisms (GLO, ESD, AK, ACP1 and GPI analyzed previously by Chahal et al. (1989, 1991).

According to table 5 significant locus specific heterogeneities are to be seen only concerning the polymorphic serum protein and red cell enzyme systems GC, PI, ACP 1 and GPI; the others (HP, TF, GLO, ESD and AK) do not show any appreciable variations of the allele frequencies. Regarding the GC, PI and ACP1 polymorphisms it is noteworthy to ascertain that the locus specific heterogeneities are caused by particular alleles, namely: *GC*2; PI*M1, PI*M3; ACP1*A, ACP1*B*. These observations are corroborated by the F_{ST} values.

Altogether one can conclude from table 5 a considerable genetic heterogeneity among the five population groups of Himachal Pradesh and Punjab, respectively, which is moreover statistically significant at four loci. One can assume that this heterogeneity is caused by different microevolutive processes in these populations, in which factors like genetic drift might have played an important role. These genetic population differences could be preserved because of the endogamous marriage patterns of all the five caste groups under study, and by which gene flow among them could not take place, at least to any considerable extent.

We finally analyzed the genetic relationships of the five population groups applying the method proposed by Nei (1972). Nine polymorphic loci could be considered therefore, namely: HP, TF, GC, PI, GLO, ESD, AK, ACP1 and GPI. The allele frequency data for the enzyme polymorphisms were taken from Chahal et al. (1989, 1991). Figure 2 shows the genetic distance pattern, which is characterized

Table 2 : TF phenotype numbers and allele frequencies in five North-West Indian population samples

	Brahmins		*Rajputs*		*Khatris*		*Mahajans*		*Kambohs*	
Phenotypes	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*
C 1	25	26.74	47	51.84	28	31.43	19	20.31	68	72.10
2-1	26	22.52	50	40.32	33	26.14	18	15.68	71	62.40
2	3	4.74	3	7.84	2	5.43	2	3.02	9	13.50
3-1	—	—	—	—	—	—	1	0.71	1	1.39
3-2	—	—	—	—	—	—	—	0.27	1	0.60
3	—	—	—	—	—	—	—	0.01	—	0.01
Total	54	54.00	100	100.00	63	63.00	40	40.00	150	150.00
χ^2	1.290		5.764		4.341		1.172		3.301	
df	1		1		1		3		3	
P	ns		0.02>p>0.01		0.05>p>0.02		ns		ns	
Alleles										
*TF*C1*	0.7037		0.7200		0.7063		0.7125		0.6933	
*TF*C2*	0.2963		0.2800		0.2937		0.2750		0.3000	
*TF*C3*	—		—		—		0.0125		0.0067	
Total	1.0000		1.0000		1.0000		1.0000		1.0000	

by one cluster containing the Brahmins, Rajputs, Khatris and Mahajans. The first two caste groups are found in a clear-cut subcluster, the other two in another one. The Kambohs are striking by an obviously deviating position in the dendrogram. This indicates that their genetic constitution is quite different from that of the other four population groups, which

Table 3 : GC phenotype numbers and allele frequencies in five North-West Indian population samples

	Brahmins		*Rajputs*		*Khatris*		*Mahajans*		*Kambohs*	
Phenotypes	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*
1F	1	2.68	7	4.57	6	3.48	2	1.60	3	4.65
1F-1S	18	12.79	20	22.21	11	15.05	8	9.40	23	22.46
1S	16	15.26	26	27.00	15	16.26	13	13.81	28	27.12
2-1F	6	7.84	10	12.66	8	8.99	4	3.40	24	21.24
2-1S	12	18.70	35	30.78	26	19.42	13	9.99	49	51.28
2	10	5.73	8	8.77	3	5.80	—	1.81	24	24.25
Total	63	63.00	106	105.99	69	69.00	40	40.01	151	151.00
χ^2	9.226		2.754		6.702		3.175		1.090	
df	3		3		3		3		3	
P	0.05>p>0.02		ns		ns		ns		ns	
Alleles										
*GC*1F*	0.2063		0.2075		0.2246		0.2000		0.1755	
*GC*1S*	0.4921		0.5048		0.4855		0.5875		0.4238	
*GC*2*	0.3016		0.2877		0.2899		0.2125		0.4007	
Total	1.0000		1.0000		1.0000		1.0000		1.0000	

Table 4 : PI phenotype numbers and allele frequencies in five North-West Indian population samples

	Brahmins		*Rajputs*		*Khatris*		*Mahajans*		*Kambohs*	
Phenotypes	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*
M 1	16	17.32	40	36.50	25	24.71	19	16.94	53	56.56
2-1	23	19.18	28	26.99	14	13.92	5	8.47	44	37.00
2	3	5.31	3	4.99	2	1.96	2	1.06	2	6.05
3-1	10	11.19	11	19.02	7	7.65	5	5.65	12	11.88
3-2	7	6.20	10	7.03	2	2.16	3	1.41	5	3.88
3	2	1.81	5	2.48	1	0.59	—	0.47	—	0.62
Total	61	61.01	97	97.01	51	50.99	34	34.00	116	115.99
χ^2	2.116		8.364		0.357		4.844		5.207	
df	3		3		3		3		3	
p	ns		0.05>p>0.02		ns		ns		ns	
Alleles										
*PI*M1*	0.5328		0.6134		0.6961		0.7059		0.6983	
*PI*M2*	0.2951		0.2268		0.1961		0.1765		0.2284	
*PI*M3*	0.1721		0.1598		0.1078		0.1176		0.0733	
Total	1.0000		1.0000		1.0000		1.0000		1.0000	

could be pointed out already by Chahal et al. (1989). Brahmins, Rajputs, Khatris and Mahajans are from the same place - Chamba town in Himachal Pradesh -, whereas the Kamboh sample comes from a small village in Punjab: Sanaur near Patiala city. This may explain the genetic distance pattern obtained in figure 2. Chahal et al. (1991), who analyzed the distribution of six red cell enzyme polymorphisms in the four Himachal Pradesh groups came to the conclusion: "The variabilities observed in the distributions of various enzyme polymorphisms in the present urban sample from the Chamba district suggest that the genetic composition of the four caste groups investigated is homogeneous. Much of this genetic similarity among the present caste primarily derives from similarities in their ethnic backgounds and environmental conditions, and particularly in this case, perhaps also from geographical isolation of this remote hill region from the plains of North India" (p. 76). Considering this one can understand that Brahmins, Rajputs, Khatris and Mahajans, all from the Chamba district of Himachal Pradesh, are found in one cluster, and that the Kamboh group is genetically quite different from them. This group - a cultivating backward caste of Punjab - has its own ethnohistory and origin, so that it cannot surprise that it is characterized by a genetic make up which is rather different from that of the other four population groups under study.

The subclustering found within the Himachal Pradesh Population group requires still some comments. Brahmins and Rajputs show the smallest genetic distance and are thus found in one subcluster. The other one is formed by Khatris and Mahajans, who are comparatively somewhat more distant from each other than Brahmins and Rajputs. This could indicate more similarities concerning ethnic backgrounds and environmental conditions between these two groups and possibly also some more gene flow between them as in comparison with the Khatris and Mahajans. It would be of considerable interest to follow up these genetic differentiation within the population groups of

Table 5 : Locus and allele specific heterogeneity and F_{ST} values in five North-West Indian population samples

Locus/Allele		χ^2	*df*	*p*	F_{ST}	χ^2	*df*	*p*
HP		8.35	4	ns	.0050	9.11	4	ns
TF		4.39	8	ns	-.0044			
	*TF*C1*	0.44	4	ns	-.0044	0.77	4	ns
	*TF*C2*	0.35	4	ns	-.0045	0.83	4	ns
	*TF*C3*	4.03	4	ns	-.0002	4.05	4	ns
GC		15.78	8	*	.0058			
	*GC*1F*	1.75	4	ns	-.0027	2.33	4	ns
	*GC*1S*	8.14	4	ns	.0048	8.09	4	ns
	*GC*2*	14.97	4	**	0131	12.23	4	*
PI		17.53	8	*	.0077			
	*PI*M1*	12.72	4	*	.0122	11.52	4	*
	*PI*M2*	4.70	4	ns	.0011	4.65	4	ns
	*PI*M3*	10.74	4	*	.0092	12.70	4	*
GLO		6.54	4	ns	.0025	6.82	4	ns
ESD		1.63	4	ns	-.0024	1.64	4	ns
AK		4.32	4	ns	.0002	4.30	4	ns
ACP1		19.17	8	*	.0081			
	*ACP1*A*	12.02	4	*	.0083	11.12	4	*
	ACP1 B*	11.72	4	*	.0080	10.93	4	*
	*ACP1*C*	7.25	4	ns	.0027	7.28	4	ns
GPI		13.39	4	**	.0106	13.99	4	**

*** : $p < 0.001$, ** : $0.01 > p > 0.001$, * : $0.05 > p > 0.01$, ns : $p > 0.05$

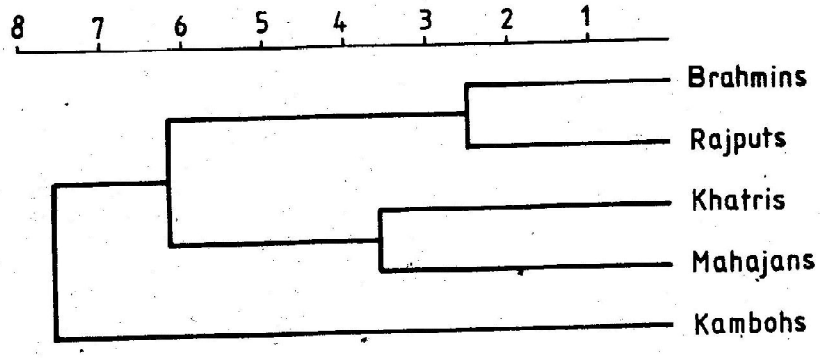

Fig. 2. Genetic distances (d x 100), based on 9 loci

the Chamba district of Himachal Pradesh in further studies, which should, however, include as many genetic markers as possible.

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