SEROGENETIC INVESTIGATIONS OF TIBETANS AND HIMACHALIS FROM HIMACHAL PRADESH, INDIA: GENETIC RELATIONSHIP BETWEEN TIBETANS AND CERTAIN SELECTED MONGOLOID POPULATIONS

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Summary   Twenty two serogenetic systems were investigated in 115 Tibetans and 128 Himachalis from the state of Himachal Pradesh, northwest India.   For eight of the loci (ABO, Rh, MNSs, P, Fy, 6PGD, EsD, and AK) the two populations showed conclusive heterogeneity and their frequency distribution showed that the serogenetic differences between two populations are due to their different racial affiliations.   The Tibetans were also analysed for their genetic relationship with certain selected populations from the Cis-Himalayan, far east and south Asian regions.   The calculations of the Harpending's kinship matrix R and the genetic distances showed that the Tibetans are closer to the mongoloid populations of the Cis-Himalayan region and the differences in the present day population structure of the mongoloid groups of this region are more likely to be due to differential migration, admixture and racial affiliation although there is a slight possibility of disruptive selection for certain loci such as 6PGD and AK which showed an exceptionally high value of Canning (*6PGD*C*) and *AK*1* genes.

INTRODUCTION

The topography of the state of Himachal Pradesh (HP) is Himalayan and with its geographical position in the north-west of India it shares its eastern border with Chinese occupied Tibet.   The isolation of the populations of HP has never been complete.   In the past, several mountain passes at the height of 14,000 feet acted as a trade route and facilitated migration of populations from Tibet, who brought their cultural and religious influences to the area (Papiha *et al.*, 1984).   More recently the political unrest brought waves of Tibetan refugees who settled in several parts of HP but predominantly in Dharmsala where their political and religious

leader has taken shelter. These known historical movements and the gene flow between the Himachal and Tibetan populations provide an interesting background for the study of their genetic differences.

Genetic knowledge of the Tibetans is limited to a few genetic systems tested on refugees living in Nepal and India, although a few extensive studies on the populations of Himachal Pradesh have recently been reported (Papiha *et al.*, 1980, 1984; Chahal *et al.*, 1982). There is as yet no comprehensive attempt to analyse the affinity of Tibetans with other populations of mongoloid origin. The present investigation therefore provides information on twenty-two genetic systems on Tibetans and compares these with the local population of Himachal Pradesh. The present analysis also examines genetic relationship of Tibetans with certain selected mongoloid populations.

METHODS AND MATERIALS

Samples were collected from healthy male individuals from Dharmsala and Simla districts of Himachal Pradesh, India. 5 ml EDTA blood samples of 115 Tibetans and 128 Himachalis was transported by air at wet ice temperature to the Department of Human Genetics, University of Newcastle upon Tyne, U.K. where the blood grouping and biochemical genetic markers were typed.

On all available samples the serological systems were tested for the following antigens: A1, A2, B, M, N, S, s, C, c, D, E, e, P_1, K, k, Lu^a, Lu^b, Le^a, Fy^a, Fy^b, Jk^a, Jk^b. Red cell lysate and plasma samples were stored at $-30°C$ until analysed. Red cell enzymes, 6-phosphogluconate dehydrogenase (6PGD), acid phosphatase (AP), phosphoglucomutase locus I and II (PGM), adenosine deaminase (ADA), adenylate kinase (AK), esterase D (EsD), phosphoglucose isomerase (PGI), glucose-6-phosphate dehydrogenase (G6PD), lactate dehydrogenase (LDH), malate dehydrogenase (MDH) and superoxide dismutase (SOD) were examined according to the method listed in Harris and Hopkinson (1976). G6PD specimens which did not show staining on the gel were characterised as deficient. Haptoglobin (Hp) was tested with discontinuous buffer of Poulik (1957) using starch gel electrophoresis.

RESULTS

The observed numbers and percentage observed frequency of various blood groups, red cell enzyme and serum protein haptoglobin are given in Table 1. In no system was there any deviation from Hardy-Weinberg equilibrium except for the PGM1 in Himachalis and for Hp system in Tibetans, where respectively an excess and decrease of observed homozygous phenotypes were encountered. The phenotype frequencies between the two populations were also compared by Fisher's exact probability test or contingency chi-square test, and chi-square values or p values are given in Table 1. The allele frequencies for all these systems and for

Table 1. Phenotype numbers and percentage frequencies of various polymorphic systems in Tibetans and Himachalis.

System	Tibetans		Himachalis		χ^2 or Fisher's exact p between populations
	Number observed	(%)	Number observed	(%)	
ABO					
O	42	36.5	29	22.7	
B	43	37.4	46	35.9	
A_1	24	20.9	32	25.0	9.9*
A_2	—	—	2	1.6	
A_1B	6	5.2	17	13.6	
A_2B	—	—	2	1.6	
Total	115		128		
χ^2	0.959		0.267		
Rhesus					
CCDEE	0	0			
CcDEE	1	0.9			
ccDEE	13	11.3	6	4.7	
CCDEe	1	0.9			
CcDEe	33	28.7	21	16.4	
ccDEe	9	7.8			28.57*
CCDee	46	40.0	42	32.8	
CcDee	12	10.4	31	24.2	
ccDee	0	0	7	5.5	
ccdee	0	0	10	7.8	
Ccdee	0	0	1	0.8	
Total	115		128		
χ^2	3.0		6.5		
MNS					
MMSS	4	3.5	6	5.7	
MMSs	27	23.5	18	16.9	
MMss	32	27.8	15	14.2	
MNSS	0	0	7	6.6	
MNSs	11	9.6	21	19.8	20.85*
MNss	30	26.1	23	21.7	
NNSS	0	0	1	0.9	
NNSs	4	3.5	9	8.5	
NNss	7	6.1	6	5.7	
Total	115		106		
χ^2	5.83		1.04		
P					
p^+	49	42.6	81	76.4	24.65*
p^-	66	57.4	25	23.6	
Total	115		106		

Table 1.   Continued.

System	Tibetans		Himachalis		χ^2 or Fisher's exact p between populations
	Number observed	(%)	Number observed	(%)	
Lutheran					
a+b—	—		0	0	
a+b+	—		3	2.8	0. 109**
a—b+	115		103	97.2	
Total	115		106		
Lewis					
Le+	22	26. 5	18	16.9	
Le—	93	73. 5	88	83.1	0. 06
Total	115		106		
Kell					
KK	0	0	0	0. 0	
Kk	0	0	1	0.9	0. 473**
kk	115	100. 0	104	99.1	
Total	115		105		
Duffy					
a+b—	85	73. 9	52	49.1	
a+b+	30	26. 1	40	37.7	16. 14*
a—b+	0	0	14	13.2	
Total	115		106		
χ^2		0. 758		1.911	
JK					
a+b+	44	38. 3	32	30.2	
a+b—	45	39. 1	47	44.3	1. 94
a—b+	26	22. 6	27	25.5	
Total	115		106		
χ^2		5. 230		0.878	
6PGD					
AA	78	69. 6	112	88.2	
CA	32	28. 6	15	11.8	12. 47*
CC	2	1. 8	0		
Total	112		127		
χ^2		0. 034		0.019	
AP					
AA	5	4. 4	12	9. 5	
BA	42	36. 5	53	41.7	3. 85
BB	68	59. 1	61	48.0	
CB	—		1	0. 8	
Total	115		127		
χ^2		0. 219		0.018	

Table 1. Continued.

System	Tibetans		Himachalis		χ^2 or Fisher's exact p between populations
	Number observed	(%)	Number observed	(%)	
PGM$_1$					
1-1	50	43.5	55	56.7	
2-1	53	46.1	26	26.8	5.6
2-2	12	10.4	16	16.5	
Total	115		97		
χ^2	0.139		12.49*	$p<0.025$	
ADA					
1-1	99	86.8	105	88.2	
2-1	15	13.2	14	11.8	0.12
2-2	—		0	—	
Total	114		119		
χ^2	0.018		0.013		
EsD					
1-1	18	40.0	70	56.0	
2-1	18	40.0	51	40.8	0.047**
2-2	9	20.0	4	3.2	
Total	45		125		
χ^2	2.10		0.276		
AK					
1-1	115	100.0	98	77.8	
2-1	—	—	26	22.2	2×10^{-9} **
2-2	—	—	—		
Total	115		126		
χ^2	0.0		0.276		
PGI					
1-1	113	100.0	124	98.4	
3-1	—	—	2	1.6	0.227**
3-3	—	—	0		
Total	113		126		
χ^2	0.0		0.1		
G6PD					
BB (normal)	112	97.4	120	94.5	
Def	3	2.6	7	5.5	0.210**
Total	115		127		
Hp					
1-1	0		3	3.1	
2-1	44	39.6	28	28.6	1.47
2-2	67	60.4	67	68.3	
Total	111		98		
χ^2	6.7*	$p<0.01$	0.01		

χ^2 * Significant. ** Fisher's exact probability.

Table 2.   Gene frequencies for Tibetan and Himachali populations of Himachal Pradesh.

	Tibetan	Himachali		Tibetan	Himachali
p_1	0.152	0.212	*K*	0.000	0.005
p_2	0.000	0.016	*k*	1.000	0.995
q	0.252	0.292	*Fy*a	0.869	0.679
r	0.596	0.480	*Fy*b	0.131	0.321
CDE	0.006	0.000	*Jk*a	0.583	0.524
CDe	0.595	0.518	*Jk*b	0.417	0.476
Cde	0.007	0.017	*PGD*A	0.839	0.941
cDE	0.302	0.168	*PGD*C	0.161	0.059
cDe	0.012	0.069	*AP*A	0.226	0.303
cde	0.077	0.228	*AP*B	0.774	0.693
MS	0.176	0.241	*AP*C	0.000	0.004
Ms	0.559	0.368	*PGMI*1	0.665	0.701
NS	0.042	0.138	*PGMI*2	0.335	0.299
Ns	0.223	0.253	*PHI*1	1.000	0.992
M	0.735	0.609	*PHI*3	0.000	0.008
N	0.265	0.391	*ADA*1	0.934	0.941
S	0.218	0.379	*ADA*2	0.066	0.059
s	0.782	0.621	*EsD*1	0.600	0.764
p+	0.426	0.514	*EsD*2	0.400	0.236
p−	0.574	0.486	*AK*1	1.000	0.889
Lu a	0.000	0.014	*AK*2	0.000	0.111
Lu b	1.000	0.986	*Hp*1	0.198	0.173
Le+	0.143	0.089	*Hp*2	0.802	0.827
Le−	0.857	0.911			

both the populations are listed in Table 2. The genetic systems LDH, MDH, PGM locus II and SOD were found to be monomorphic.

Blood groups

Several ABO investigations on Tibetans have been reported (Mourant *et al.*, 1976). One earlier study showed an exceptionally high frequency of the *A* gene (46%) (Tennant, 1936), but all other investigations including our present study show a very narrow range of *A* gene frequency (15–17%). Like many other mongoloid populations, the *A2* gene is absent in Tibetans. Both the *A1* and *A2* gene frequencies in Himachalis are within the range reported for Indian populations from north-west India. The *B* gene was 25% in Tibetan and 29% in Himachalis, but the variation of *A* and *O* genes provide significant difference between these two populations ($\chi_3^2 = 9.9$; p < 0.02).

For the Rh system in both the populations the commonest Rh-haplotype found was $CDe(R1)$ but the differences in frequencies of the Rh-haplotypes $cDE(R2)$, $cDe(R1)$ and cde (r) are very prominent (30, 1, and 8% in Tibetans, and 17, 7, and 23% in Himachalis). Overall, the distribution of Rh haplotype showed highly significant heterogeneity between these two populations ($\chi_5^2 = 28.57$, p < 0.0001). In the MNSs system the frequency of M and S were found to be 74 and 22% in Tibetans while it was 61 and 38% in Himachalis. Although the MS haplotype in Tibetans (18%) is low compared to the Himachalis and other Indian populations, but this value extends to the top end of the MS haplotype frequency range found in the neighbouring mongoloid populations (1–14%). Once again for this system the chi-square test shows significant genetic heterogeneity between the two populations studied ($\chi_5^2 = 24.85$; p < 0.0002).

Information regarding other blood group systems, P, Lutheran, Kell, Duffy and Kidd, is scarce in the mongoloid populations of Cis-Himalayan and north-eastern region of India. Some comparison with mongoloid groups from the far-east is possible. The P+1 frequency in Tibetan and Himachalis were 43 and 51% respectively, and for this system the difference between both populations is significant ($\chi_1^2 = 24.6$; p < 1 × 10^{-5}). Whilst the Himachalis' frequencies are compatible with the Indian region the P+1 frequency in Tibetans is higher compared to several mongoloid groups listed from far-east and south-east Asia (Mourant et al., 1976). Lu^a and K positive are either infrequent or absent in India. Both these genes are found to be absent in Tibetans, but in Himachalis the low gene frequency values for these systems are compatible with most of the other Indian populations. The Fy^a gene value in Tibetans is high (87%), a characteristic feature of mongoloid populations. The Fy^a gene frequency in Himachalis is low (68%) and the difference between the two populations is statistically significant ($\chi_1^2 = 16.14$, p < 9 × 10^{-4}). The frequency of Jk^a gene in Tibetan and Himachalis is 58 and 52%, respectively. The Tibetan value is once again higher compared to the several mongoloid groups. In the Lewis system percentage observed frequency of Le^a+ antigen was 27 and 17% in Tibetans and Himachalis, respectively. Both these frequencies are well within range described for Cis-Himalayan region.

Serum protein

The frequency of Hp^*1 gene was 20% in Tibetans and 17% in Himachalis. There was no case of anhaptoglobinaemia in either group. A similar low value of Hp^*1 gene was found in several neighbouring mongoloid populations, however in comparison with the Hp^*1 gene frequency in Filipinos, Japanese and Koreans the Tibetan frequency is low.

Red cell enzymes

Several of the mongoloid populations of the Himalayan region showed a high frequency of the Canning gene ($6PGD-C$). The frequency of PGD^*C is 16% in

Tibetans, compatible with Bhutanese and Nepalis but significantly different from the present sample of Himachalis ($\chi_1^2=12.47$, $p<0.0005$). The frequencies of *AP*A*, *PGM*1* and *ADA*1* were found to be 23, 67, and 93% in Tibetans and 30, 70 and 94% in Himachalis. For these systems there was no significant heterogeneity between the two populations studied. The *AK2* gene in mongoloid populations is generally absent, however one example of AK 2-1 variant has been reported in Taiwan Chinese (Shih *et al.*, 1968). The AK system was monomorphic in Tibetans but an 11% *AK*2* gene frequency in Himachalis was typical of the Indian populations. There was no PGI variant in Tibetans but a very low frequency of *PGI*3* allele was found in Himachalis (0.08).

The incidence of G6PD deficiency in Himachalis was found to be 6% while in Tibetans it was 3%. There are several reports of similar incidences of G6PD deficiency in mongoloid populations from the far-east and south-east regions (Mourant *et al.*, 1976).

DISCUSSION

Eight genetic loci (ABO, Rh, MNSs, P, Fy, 6PGD, EsD and AK) show conclusive heterogeneity whereas in several other systems the gene frequency differences are considerable. This pattern of genetic heterogeneity suggests that the impact of the mongoloid genepool to modify the genetic structure of Caucasoid populations living in the interior of HP is slight. However, the mongoloid influence to modify the local gene pool is more prominent in the population living near the border region (Papiha *et al.*, 1984).

The serogenetic difference between the two populations are in accordance with their racial affiliation, however the comparison of the Tibetan with other mongoloid populations of the Cis-Himalayan and others for the eastern region also showed genetic variability for certain genetic systems (*e.g.* P and MNSs). For its interpretation further information can be derived by examining together the genetic systems studied. Such information may be assessed by the amount of departure from Hardy-Weinberg equilibrium of frequencies of homozygous and heterozygotes in each population (Wright, 1965).

The F_{IS} values for ten common loci in Tibetans and Himachalis are given in Table 3. Six out of ten loci for Tibetan genes showed negative F_{IS} values and two showed negative values in Himachalis. The mean F_{IS} over ten loci is -0.005 in Tibetans and $+0.086$ in Himachalis. The later population seems to be moderately inbred, however the Tibetan sample may represent refugees from various parts of Tibet thus suggesting an outbreeding in this group. The difference found in the gene frequencies in the genetic systems in Tibetans compared with the other mongoloid populations may be due to the nature of the sample studied.

Genetic relationship of Tibetans

In order to analyse the genetic relationship, several multivariate methods are

Table 3. F is analysis for Tibetans and Himachalis.

System	Tibetans		Himachalis	
	F_{IS}	χ^2	F_{IS}	χ^2
Rh(C)	0.1603	2.96	0.0168	3.60
Rh(E)	0.1239	1.76	0.1335	2.82
MN	0.1037	1.24	−0.0629	0.51
Ss	−0.0733	0.62	0.0155	0.02
6PGD	−0.0591	0.39	−0.0627	0.50
ADA	−0.0704	0.56	0.0625	0.46
Duffy	−0.1499	2.59	0.1339	1.90
Jk	0.1977	4.49*	0.1112	1.31
PGM	−0.0347	0.14	0.3605	12.6*
Hp	−0.2472	6.78*	0.0036	0.00
Mean for 10 loci	−0.0049		+0.0865	

* Significant.

available. However uniform data for several genetic markers on the mongoloid populations of Cis-Himalayan regions and for others far-east or south-east Asian, is not available. In nineteen populations from the above regions the data for ABO, MNSs and Rh systems were collected, however, for 9 of these mongoloid groups additional data for Kell, Duffy, 6PGD, AK, AP, PGM and AP systems were available (Bhasin et al., 1986; Windhof and Walter, 1983; Mourant et al., 1968; Harvey et al., 1978; Singh et al., 1986; Das et al., 1987; Rouger et al., 1982; Mya-tu et al., 1971; Bhattacharjee, 1975; Bajatzadeh and Walter, 1969; Lin, 1975, and Watanabe et al., 1974). We have thus computed two kinship matrices one based on three genetic systems for twenty populations and the other on the information provided by ten polymorphic systems for ten populations.

Of the groups of multivariate statistics that represent kinship, the index of Harpending and Jenkins (1973) is particularly useful. The Harpending R matrix is based on the mean standardised deviation of gene frequency in each group from the total mean (r_{ii}) and of the average covariance of the gene frequencies in a pair of subpopulations relative to the mean (r_{ij}). In this way the frequencies of k genes from the subgroups are transformed in a single value matrix of scaled gene frequency covariance where the r_{ij} element of the R matrix is:

$$r_{ij} = \sum_k \frac{(p_{ik} - \bar{p}_k)(p_{jk} - \bar{p}_k)}{\bar{p}_k(1 - \bar{p}_k)}$$

where P_{ik} is the frequency of allele k in group i, and $\bar{p}_{ik}$ is the mean frequency of allele k over all groups.

The second property of the R matrix is that diagonal elements (r_{ii}) its mean across all subpopulations is an estimate of R_{ST}, similar to Wright's F_{ST}, and can be shown:

$$r_{ii} = \frac{1}{s} \sum \frac{(\bar{p}_{ik} - \bar{p}_k)^2}{\bar{p}_k(1 - \bar{p}_k)}$$

where s is the number of subpopulations, r_{ii} could be weighted by multiplying with wi (weight of sample size). The distance measure (d^2_{ij}) calculated from the R matrix can be given as:

$$d^2_{ij} = r_{ii} + r_{jj} - 2r_{ij}$$

The R matrix measuring kinship among the twenty populations using data of ABO data and haplotype frequencies of MNSs and Rh systems is given in Table 4, and the R matrix of ten populations using information from ten available genetic systems is given in Table 5. In both these matrices the Tibetans show negative values compared to Filipinos, Koreans, Japanese, Ainu and Chinese populations,

Table 4. Harpending R matrix of 20 Mongoloid populations, calculated from

		1	2	3	4	5	6	7
1.	Tibetan	3.1						
2.	Meities	0.3	4.4					
3.	Lepcha (Sikkim)	0.9	−0.5	2.1				
4.	Bhutias (Sikkim)	0.4	−0.7	1.0	1.1			
5.	Sherpas (Sikkim)	0.9	−0.8	−0.4	0.7	4.1		
6.	Ahoms (Assam)	0.3	0.1	0.4	0.4	1.7	2.8	
7.	Karibs (Assam)	−0.1	0.3	−0.3	−0.6	−1.1	−0.4	2.1
8.	Boro Kacharis (Assam)	−0.9	0.4	−0.5	−0.9	−1.8	−0.6	2.4
9.	Filipinos	−1.4	−0.9	0.1	−0.3	2.0	−0.4	0.9
10.	Bhutanese	1.3	−0.2	1.6	0.9	0.4	0.3	−0.1
11.	Korean (China)	0.6	0.7	−0.6	0.0	0.2	−0.1	−0.9
12.	Korean (China)	−1.7	−1.4	−1.7	−1.4	−1.8	−2.2	−0.4
13.	Japanese	−0.1	−0.3	0.9	0.8	−0.7	−0.4	−0.6
14.	Taiwanese	0.0	1.6	−0.8	−0.7	−2.1	−1.4	−0.1
15.	Chinese (Macau)	−2.6	−0.5	−1.9	−1.3	0.4	−0.4	−0.7
16.	Burmese	−0.5	−0.4	−0.7	−0.3	1.3	1.0	1.2
17.	Ainu (Japan)	−0.9	−1.3	−0.3	0.6	0.2	−2.3	−3.5
18.	Chutiyas (Assam)	0.4	−0.8	0.3	0.5	1.7	1.5	0.2
19.	Khasi (Meghalya)	0.4	0.6	0.1	−0.6	−0.6	0.4	1.4
20.	Chinese (Mainland)	−0.4	−0.7	0.1	0.3	−0.3	0.0	0.4

Mean diagonal element $r_{ii} = R_{ST}$ (unweighted) = 0.041.

suggesting low affinity of Tibetans with these groups. The affinity of Tibetans is more distinct with the neighbouring mongoloid populations of the Cis-Himalayan region.

The contribution of the particular alleles to this pattern of relationship can be summarised by plotting the first two eigenvectors of the R matrix superimposed on the S matrix (Harpending and Jenkins, 1973). In Figs. 1 and 2 the position of the Tibetans is particularly associated with the Lepchas, Bhutias and Sherpas of Sikkim and the Bhutanese due to the MS, cde, $PMG1*2$ alleles. The genetic distance calculated from the R matrix (Table 6) and the dendrogram obtained from the distance matrix using the complete linkage method (Everitt, 1974) showed the same pattern for Tibetans (Fig. 3).

The genetic differentiation (R_{ST}) among twenty mongoloid genes calculated from the diagonal element of the R matrix is 0.041, and for ten populations is 0.032. This difference is perhaps due to the addition of further systems, however these two R_{ST} values suggest that the effect of random subpopulation differentiation among mongoloid groups is only moderate.

gene frequency data of ABO, Rhesus and MNS blood groups (value $= \times 10^{-2}$).

8	9	10	11	12	13	14	15	16	17	18	19	20
3.2												
1.6	2.2											
−0.6	−0.6	1.7										
−1.3	−0.6	−0.3	2.8									
−0.1	0.8	−1.7	0.9	6.3								
−0.8	0.3	0.7	0.9	0.1	1.6							
0.3	0.5	−1.1	2.1	1.4	0.6	3.7						
−0.1	0.8	−1.9	0.4	3.5	−0.6	0.6	7.9					
1.1	0.9	−0.2	−0.8	−0.9	−1.0	−1.3	1.2	2.5				
−3.9	−2.3	−0.4	−1.6	4.3	0.2	−1.8	−2.9	−4.0	24.3			
−0.1	−0.2	0.2	−0.9	−2.4	−0.7	−1.5	−0.8	1.3	−1.1	1.9		
2.1	0.4	0.0	−1.5	−0.8	−1.1	−0.3	−0.8	0.2	−1.6	0.1	2.8	
0.5	0.5	−0.1	0.0	−0.5	0.3	0.2	−0.3	0.4	−1.6	0.4	−0.3	0.7

Table 5.   Harpending R matrix of 10 Mongoloid populations using 10 polymorphic
systems (value $\times 10^{-2}$).

		1	2	3	4	5	6	7	8	9	10
1.	Tibetan	1.66									
2.	Lepcha (Sikkim)	0.61	1.53								
3.	Bhutias (Sikkim)	0.29	0.62	1.64							
4.	Sherpas (Sikkim)	0.50	0.25	1.37	3.83						
5.	Filipinos	−1.28	−0.64	−0.59	−1.27	4.69					
6.	Bhutanese	0.86	0.76	−0.26	−0.41	−1.42	2.41				
7.	Korean	−0.96	−1.42	−0.80	−0.97	1.50	−1.38	4.18			
8.	Japanese	−0.60	−0.53	−0.59	−1.32	0.26	0.43	−0.17	1.96		
9.	Ainu	−0.96	−0.81	−1.43	−1.26	−2.51	−0.28	−0.36	0.35	8.28	
10.	Chinese	−0.14	−0.37	−0.26	−0.72	1.27	−0.71	0.37	0.21	−1.03	1.36

Mean diagonal element $r_{ii} = R_{ST}$ (unweighted)=0.032.
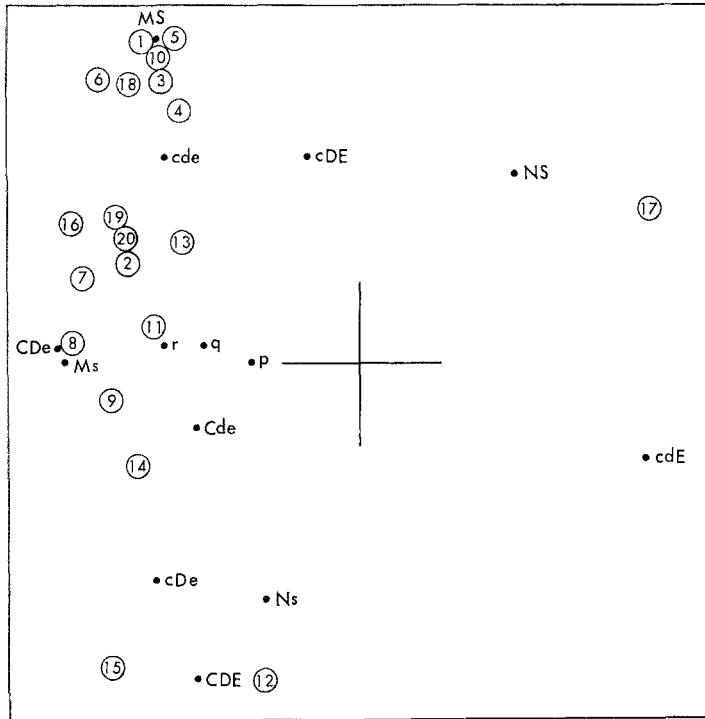
Fig. 1.   Plot of alleles on first two eigenvectors of Harpending's S matrix for 20 Mongoloid
populations (Based on ABO, MNSs and Rhesus blood group systems only).
Mongoloid populations: 1, Tibetan; 2, Meities (Manipur); 3, Lepchas (Sikkim); 4,
Bhutias (Sikkim); 5, Sherpas (Sikkim); 6, Ahoms (Assam); 7, Karibs (Assam); 8,
Boro Kacharis (Assam); 9, Filipinos; 10, Bhutanese; 11, Korean; 12, Korean (China);
13, Japanese; 14, Taiwanese; 15, Chinese (Macau); 16, Burmese; 17, Ainu (Japan);
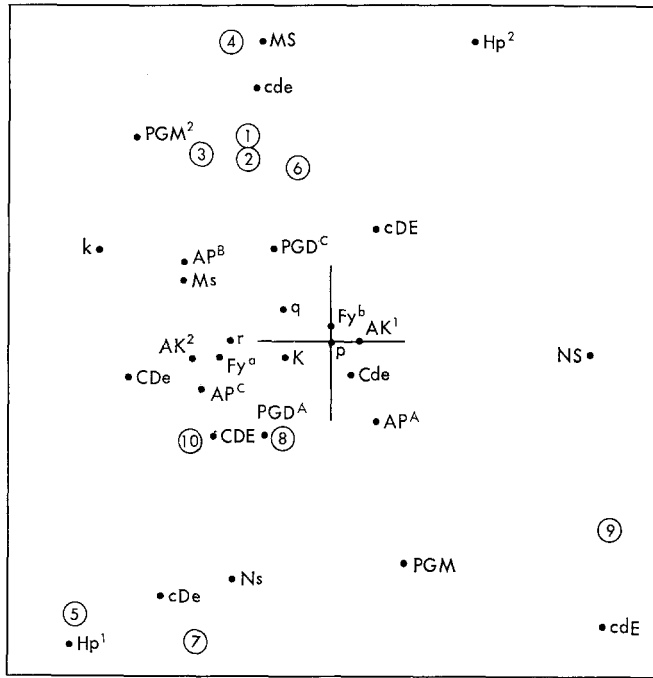18, Chutiyas (Assam); 19, Khasi (Meghalya); 20, Chinese (Mainland).

Fig. 2. Plot of alleles on first two eigenvectors of Harpending's S matrix for 10 Mongoloid populations.
Mongoloid populations: 1, Tibetian; 2, Lepchas (Sikkim); 3, Bhutias (Sikkim); 4, Sherpas (Sikkim); 5, Filipinos; 6, Bhutanese; 7, Korean; 8, Japanese; 9, Ainu (Japan); 10, Chinese.

Table 6. Harpending distance matrix of 10 Mongoloid populations.

	Tibetan	Lepchas	Bhutias	Sherpas	Filipinos	Bhutanese	Korean	Japanese	Ainu
Lepchas	0.019								
Bhutias	0.027	0.019							
Sherpas	0.045	0.049	0.027						
Filipinos	0.089	0.075	0.075	0.111					
Bhutanese	0.023	0.024	0.046	0.071	0.099				
Koreans	0.078	0.086	0.074	0.099	0.059	0.094			
Japanese	0.048	0.045	0.048	0.084	0.061	0.035	0.065		
Ainu	0.119	0.114	0.113	0.146	0.180	0.113	0.132	0.095	
Chinese	0.033	0.036	0.035	0.066	0.035	0.052	0.048	0.029	0.117

In conclusion, the present investigation demonstrates the heterogeneous nature of the genetic constitution of Tibetans compared to local Himachali and several mongoloid groups of far-east and south-east Asia. In their genetic affinity Tibetans
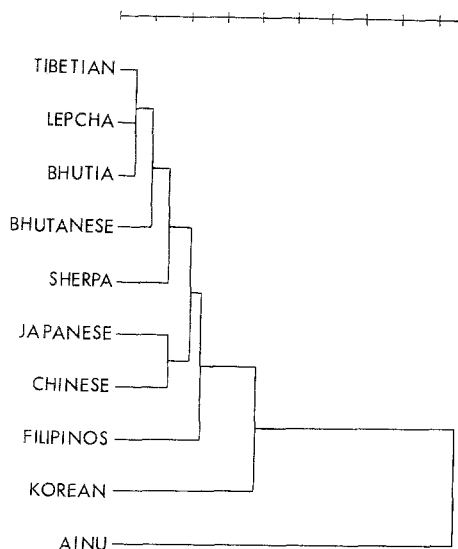
Fig. 3.   Dendrogram plotted from Harpending's genetic distance matrix for 10 Mongoloid populations.

cluster along with their neighbouring mongoloid groups from Cis-Himalayan and north-eastern region of India.   Though there is a possibility of admixture among these groups, racial affinity and selective factors for genetic systems like Rh, MNS, 6PGD and AK seem to play an important role in maintaining the present-day structure of the mongoloid populations of this region.

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