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Genetic Structure Among Nine Population Groups of Jammu and Kashmir, India

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ABSTRACT Heterozygosity values show that the different caste groups of Dogras, and Gujjars from Jammu region are more heterozygous than the population groups of Kashmir and Ladakh regions. But nevertheless, among the nine population groups of Jammu and Kashmir, only a small fraction of the total gene diversity accounts for the interpopulational genetic variation whereas the major portion of the total diversity is due to intrapopulational variation. In the dendrogram constructed using genetic distance (D) matrix the two distinct clusters are formed – the Tibetans, Bodhs and Baltis with Mongoloid affinities forming one, whereas the population groups of Kashmir and Jammu regions who are having Caucasoid elements forming the another. The differentiation of the two tribal groups—Bodhs, Baltis, and Tibetans of Ladakh from the population groups of Kashmir and Jammu, could well be due to their mongoloid affinities as demonstrated by several genetic marker systems (high frequencies of *Ms, CDe* and EsD^2; and low frequencies of *cde*, P^a, ADA^2, AK^2 *and* GLO^1)

Polymorphism of many genetic traits are now considered to be useful tool for the study of differentiation of human populations and to trace ancestry, admixture and affinity of different groups of people, using gene frequency data for a number of genetic loci. Evolutionary forces like selection, mutation, migration and genetic drift play an important role in changing the gene frequencies of different population groups. However, human populations living side by side for hundreds or even thousands of years try to retain their separate entities by practising endogamy.

Once a group of populations has been investigated for a set of genetic characters and for the similarities and differences in terms of gene frequencies of various genetic characters, the extent of variation, mechanisms of maintenance of population differences in gene frequencies, and finally the relationship among various population groups could be analysed.

Genetic variation among nine population groups of Jammu and Kashmir investigated from the three geographical divisions—Ladakh, Kashmir and Jammu, has already been reported (Bhasin and Khanna, 1992 a, b, c; Bhasin et al., 1992 a, b, c). In the present paper, further analysis has been attempted using various population genetic structure models, utilizing gene frequency data from 11 genetic marker systems among them.

MATERIAL AND METHODS

For the present study, a total of 1075 blood samples was collected from nine population groups—Bodhs and Tibetans of Leh District (292 samples), Baltis of Kargil District (99 samples); Kashmiri Muslims and Kashmiri Pandits of Srinagar District (155 samples); Gujjars and Dogra caste Groups - Brahmans, Rajputs and Ramdasias of Jammu District (529 samples). The field works were conducted in 1988 and 1989.

Blood group analysis was done following the standard serological techniques and directions suggested by the manufacturers of various antisera: Biotest, West Germany (Anti -A, -B, -K, -M, -N, -S, -C, -E, -c, and -e) and Associated Laboratories, Bombay (Anti -A_1, and -D).

For the typing of red cell enzymes, horizontal electrophoresis was carried out using methods described by Harris and Hopkinson (1976) for acid phosphatase (AP) and glucose phosphate isomerase (GPI); Scott and Fowler (1982) for glyoxalase I (GLO I); Murch et al. (1986) for adenosine deaminase (ADA) and adenylate kinase (AK); and Wraxall and Stolorow (1986) for phosphoglucomutase locus 1 (PGM_1) and esterase D (EsD).

The gene and chromosome frequency calculations have been done after Mourant et al. (1976) and for test of significance (G-test) G numbers of integers after Woolf (1957) have been used.

The degree of gene diversity, pattern of gene differentiation and genetic relationships among the nine population groups of Jammu and Kashmir have been studied using the following population structure models:

Average heterozygosity (Nei, 1973)

Coefficient of gene differentiation (Nei, 1973)

Wahlund's variance (Wahlund, 1928)

Nei's genetic distance measure (Nei, 1987)

Chi-square (G-test) for genetic differentiation.

RESULTS AND DISCUSSION

The gene/chromosome frequencies observed for the eleven genetic markers comprising blood group systems—A_1A_2BO, MNSs, Rhesus and Kell; and red cell enzyme systems-AP, ADA, AK, EsD, GPI, GLO I, PGM_1, are listed in table 1.

A_1A_2BO System

It has been observed that among the three scheduled tribes investigated, the Bodhs and Baltis are showing high frequency of gene *A* than Gujjars, whereas gene *B* is present almost with similar but comparatively higher frequencies among these groups. In the caste groups, the frequency of gene *B* is high among Dogra Ramdasias than other groups studied whereas the frequency of gene *A* is almost similar among the caste groups except Kashmiri Pandits.

From the distribution of A_1A_2BO blood group gene frequencies observed in the present study, it has been observed that among Baltis and Dogra Brahmans, the frequencies of *A* and *B* genes are almost equal, whereas in rest of the population groups, the gene *B* frequency is higher than gene *A* (Fig. 1). The gene A_2 is present in rather high frequency among Baltis, Dogra Brahmans and Dogra Rajputs (over 4 per cent) and Kashmiri Muslims (3.36 per cent).

When compared with the distribution of A_1A_2BO frequencies among the neighbouring populations, it has been observed that the Bodhs, Baltis and Tibetans of Ladakh region are showing similarities with the population groups with Mongoloid affinities inhabiting Himalayan region, South East and Far East Asia, whereas the caste groups of Kashmir and Jammu regions, Kashmiri Muslims and Gujjars are falling closer to the population groups of plains of North India, Middle and Lower Himalayan regions as well as South West Asia.

MNSs System

Among the Scheduled Tribe groups Bodhs and Baltis, the frequencies of gene complexes (chromosomes) *MS* and *NS* are low and that of *Ms* and *Ns* slightly high as compared to Gujjars. The three Dogra caste groups are showing almost similar MNSs frequency distribution, whereas the Kashmiri Pandits show differences for the frequencies of *Ms* and *Ns* with the Dogra caste group. The Muslim

Table 1: Gene/chromosome frequency distribution among population groups of Jammu and Kashmir

System/Gene/ Chromosome	*Gene / Chromosome Frequencies*								
	Ladakh Division			*Kashmir Division*		*Jammu Division*			
	Bodhs	*Baltis*	*Tibetans*	*Kashmiri Muslims*	*Kashmiri Pandits*	*Gujjars*	*Dogra Brahmans*	*Dogra Rajputs*	*Dogra Ramdasias*
BLOOD GROUP SYSTEMS									
A_1A_2BO									
n	185	98	107	122	33	113	147	121	148
A_1	18.10	18.35	17.24	12.31	14.45	11.92	16.92	17.15	19.94
A_2	2.99	4.72	0.56	3.36	0.00	1.55	4.29	4.05	1.28
B	24.13	23.65	23.08	21.61	25.67	26.20	21.98	27.66	28.82
O	54.78	53.28	59.12	62.72	59.88	60.33	56.81	51.14	49.96
MNSs									
n	165	98	107	121	33	93	105	121	105
MS	15.93	16.80	12.21	22.15	26.63	20.94	23.69	21.52	27.35
Ms	53.40	50.55	65.35	41.07	30.94	48.41	36.78	42.12	36.94
NS	2.89	6.95	1.85	11.04	8.23	7.21	12.31	7.48	7.93
Ns	27.78	25.70	20.57	25.73	34.19	23.43	27.21	28.88	27.88
Rhesus									
n	88	95	107	121	33	93	145	118	105
CDE	7.25	7.99	8.03	2.12	1.82	3.57	5.09	5.46	1.80
CDe	62.07	42.53	44.45	48.29	49.34	38.90	44.24	36.28	61.06
CdE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Cde	0.00	0.00	6.86	0.00	9.44	0.00	5.50	11.65	0.00
cDE	19.46	25.69	27.48	15.65	11.81	10.41	10.27	9.62	9.63
cDe	3.29	3.19	7.47	9.94	3.38	10.90	7.49	12.95	7.00
cdE	0.00	0.00	0.00	0.00	0.00	0.00	4.98	6.53	0.00
cde	7.94	20.60	5.70	24.00	24.20	36.22	22.43	17.51	20.51
Kell									
n	79	9	107	121	33	86	104	71	104
K	0.00	0.00	0.00	0.80	0.00	0.00	1.00	0.70	0.50
k	100.00	100.00	100.00	99.20	100.00	100.00	99.00	99.30	99.50
RED CELL ENZYME SYSTEMS									
Acid phosphatase (AP)									
n	179	96	107	122	33	86	105	71	105
P^a	22.91	30.21	16.82	24.59	33.33	37.79	33.33	28.71	33.33
P^b	77.09	69.27	83.18	75.00	66.67	59.88	65.24	69.72	66.19
P^c	0.00	0.52	0.00	0.41	0.00	2.33	1.43	2.11	0.48
Adenosine deaminase (ADA)									
n	185	99	107	121	33	86	105	71	105
ADA^1	92.43	91.92	95.33	87.19	89.39	88.37	85.71	85.91	83.81
ADA^2	7.57	8.08	4.67	12.81	10.61	11.63	14.29	14.08	16.19
Adenylate kinase (AK)									
n	185	99	107	120	33	86	105	71	105
AK^1	96.76	97.47	98.59	93.75	95.45	86.05	89.52	95.77	89.05
AK^2	3.24	2.53	1.41	6.25	4.55	13.95	10.48	4.23	10.95

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tem/Gene/ romosome	Gene / Chromosome Frequencies								
	Ladakh Division			Kashmir Division		Jammu Division			
	Bodhs	Baltis	Tibetans	Kashmiri Muslims	Kashmiri Pandits	Gujjars	Dogra Brahmans	Dogra Rajputs	Dogra Ramdasias
lerase D (EsD)									
	185	99	107	121	33	86*	105	71	105
D^1	71.62	76.77	62.15	75.62	81.82	78.49	83.33	74.65	76.19
D^2	28.38	22.23	37.85	24.38	18.18	20.93	16.67	25.35	23.81
ucose phosphate isomerase (GPI)									
	184	99	107	122	33	86	105	71	105
I^1	98.64	97.98	96.26	100.00	100.00	100.00	100.00	99.30	100.00
I^3	1.36	2.02	3.74	0.00	0.00	0.00	0.00	0.70	0.00
yoxalase I (GLO I)									
	185	99	107	122	33	86	105	71	105
O^1	15.68	18.18	8.88	20.49	25.76	29.65	18.09	25.35	21.90
O^2	84.32	81.82	91.12	79.51	74.24	70.35	81.91	74.65	78.10
iosphoglucomutase locus 1 (PGM_1)									
	182	98	107	122	32	86	105	71	105
GM_1^1	68.68	67.35	73.83	71.72	82.81	62.79	66.19	67.60	70.95
GM_1^2	30.50	32.65	25.70	27.46	17.19	37.21	33.81	30.98	28.57
GM_1^6	0.82	0.00	0.47	0.00	0.00	0.00	0.00	0.00	0.00
GM_1^7	0.00	0.00	0.00	0.82	0.00	0.00	0.00	1.41	0.48

nclude rare gene EsD^3 with frequency of 0.58 per cent.

oups-Kashmiri Muslims and Gujjars are also owing similar pattern of MNSs distribution.

Overall, it is observed that the Ladakh ivision groups with their high *Ms* and low S frequencies show a pattern of *MNSs* distbution which is distinctly different from that population groups of both Kashmir and mmu Divisions, which are rather homoneous with regard to this blood group system ig. 2).

There is high frequency of gene *M* among e population groups of India and South West sia, though still higher frequency of this gene is been observed among the population oups with Mongoloid affinities of Himalayan gion, South East Asia and Far East Asia. imilar pattern of distribution has been found nong the population groups of the present udy. Similarly, rather high frequencies of gene complex *Ms* and low frequencies of gene *S* have been found among the population groups with Mongoloid affinities of Himalayan region, South East Asia, Far East Asia and also Ladakh (present study). On the other hand, among the population groups of Kashmir (Kashmiri Muslims and Kashmiri Pandits) and Jammu (Gujjars and Dogra caste groups) regions (present study), caste groups and communities of the plains of North India, Middle and Lower regions of Himalayas, South and South West Asia, the gene S is observed to be more frequent and gene complex *MS* is relatively less frequent.

Rhesus System

Among the Scheduled Tribe groups, the frequency of *CDe* is quite high (62.07 per cent) and that of *cde* is low (7.94 per cent) among Bodhs, whereas among Baltis and Gujjars, the

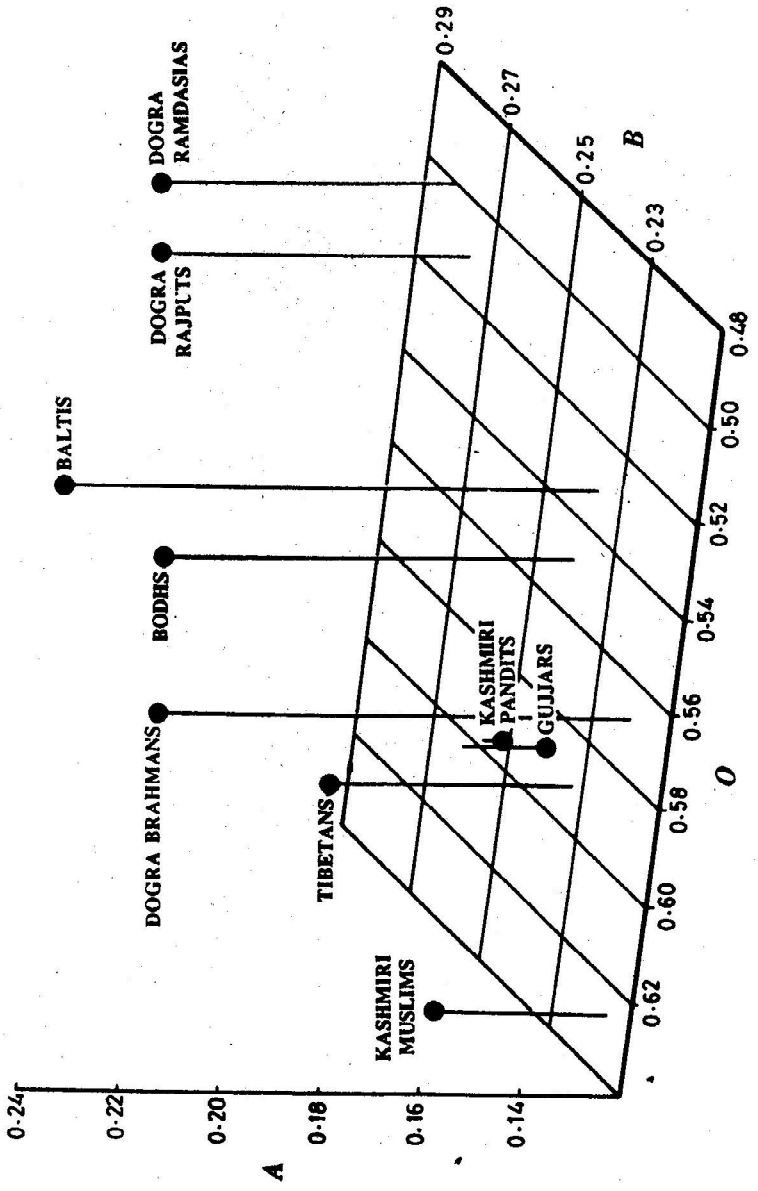

Fig. 1. Distribution of A_1A_2BO gene frequencies among nine population groups of Jammu and Kashmir

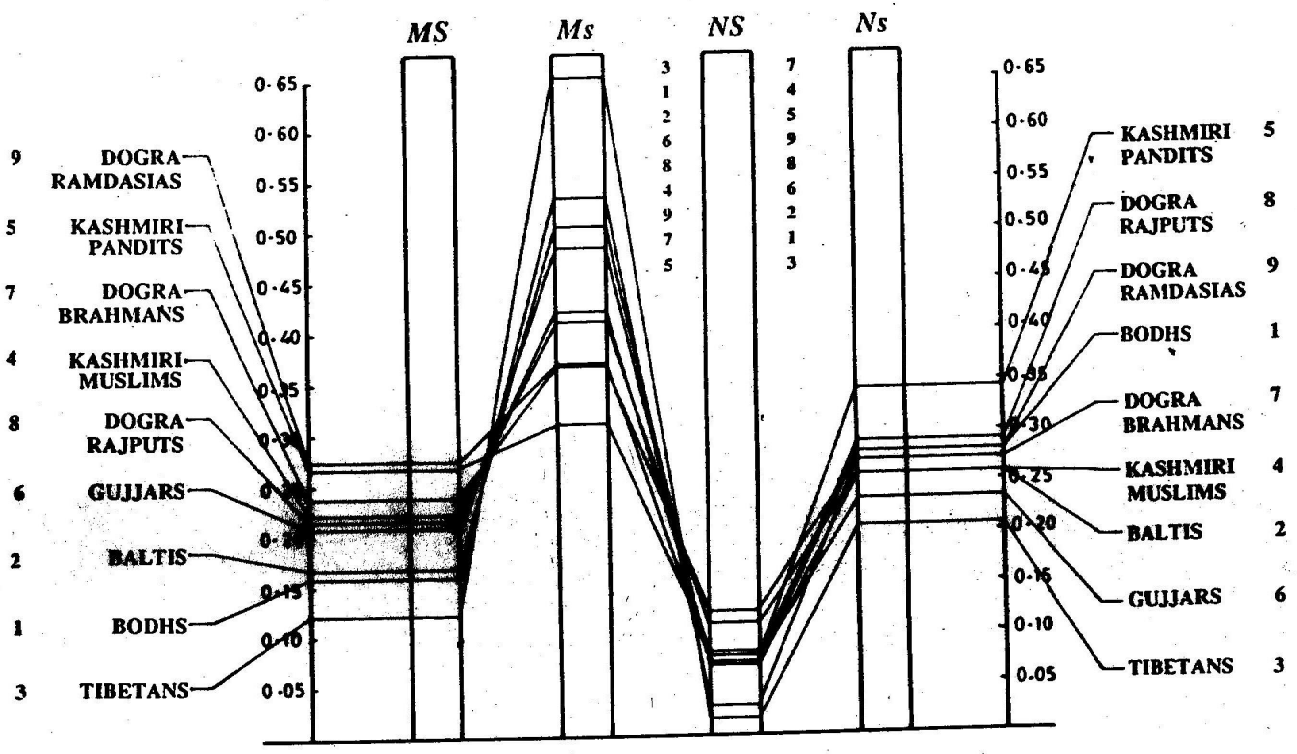

Fig. 2. Distribution of MNSs frequencies among nine population groups of Jammu and Kashmir

frequency of *CDe* chromosome is 42.53 and 38.90 per cent and that of *cde* 20.60 and 36.22 per cent, respectively. The frequency of *cDE* is above 20 per cent among Bodhs and Baltis and about 10 per cent in Gujjars, whereas *cDe* is low among Bodhs and Baltis (3.29 and 3.19 per cent, respectively) as compared to Gujjars (10.90 per cent). Among the caste groups the frequency of chromosome *CDe* is 49.34 and 44.24 per cent and that of chromosome *cde* 24.20 and 22.43 per cent among Kashmiri Pandits and Dogra Brahmans, respectively. The chromosome *Cde* is observed among both these groups–9.44 per cent in Kashmiri Pandits and 5.50 among Dogra Brahmans, and *cdE* is observed 4.98 per cent in Dogra Brahmans. Among Dogra Rajputs the frequencies of chromosomes *CDe* and *cde* are low (36.28 and 17.51 per cent, respectively) whereas in Dogra Ramdasias - a Scheduled Caste group, the frequency of *CDe* is quite high (61.06 per cent) and *cde* is present with a frequency of 20.51 per cent.

It is observed that the frequency of *CDe* is less than 50 per cent among all the population groups except Bodhs (62.07 per cent) and Dogra Ramdasias (61.06 per cent). The frequency of chromosome *cde* is less than 10 per cent among Bodhs and Tibetans and more than 20 per cent in rest of the groups with the exception of Dogra Rajputs (17.51 per cent); Gujjars stand out with their exceptionally high *cde* frequency (36.22 per cent). The chromosome *CDE* is present among all the groups but rather high frequencies (about 8 per cent) are observed among the population groups from Ladakh Division. Similarly, the frequency of chromosome *cDE* is high among population groups of Ladakh (Fig. 3).

Thus, from the distribution of Rhesus chromosome frequencies, it has been found that in the population groups with Mongoloid affinities of Himalayan region, Far East and South East Asia, a high frequency of chromosome *CDe* and low frequency of *cde* have been observed and a similar pattern has been observed among the population groups of Ladakh in the present study. On the other hand, the caste groups of Kashmir and Jammu regions, Kashmiri Muslims and Gujjars of present study show relatively lower incidence of *CDe* and high incidence of *cde* chromosomes, which depicts their similarities with the population groups of the plains of North India, Middle and Lower Himalayan regions as well as South West Asia.

Kell System

It has been observed in the present study that the gene *K* is completely absent from each of the population groups of Ladakh region (Bodhs, Baltis and Tibetans), whereas in both Kashmir and Jammu regions, this gene is present among the Kashmiri Muslims (0.8 per cent) and all the three Dogra caste groups (range 0.5 to 1.0 per cent) (Fig. 4).

From India, the reports available on the the Kell system are few. However, it has been found that the distribution of gene *K* observed among the population groups of Kashmir and Jammu regions in the present study fits well within the range described for North Indian populations. Whereas, among the population groups of Ladakh region, the gene is completely absent as also observed among other population groups with Mongoloid affinities.

Acid Phosphatase (AP) System

In the present study, the frequency of gene P^a has been observed high among all the caste groups of Kashmir and Jammu regions, Kashmiri Muslims, Gujjars, and Baltis of Ladakh (range 24.59 - 37.79 per cent) as compared to the Bodhs and Tibetans of Ladakh (22.91 and 16.82 per cent, respectively). The gene P^c is absent among Bodhs, Tibetans and Kashmiri Pandits, whereas among rest of the groups, its frequency ranges from 0.41 per cent (Kashmiri Muslims) to 2.33 per cent (Gujjars) (Fig. 5).

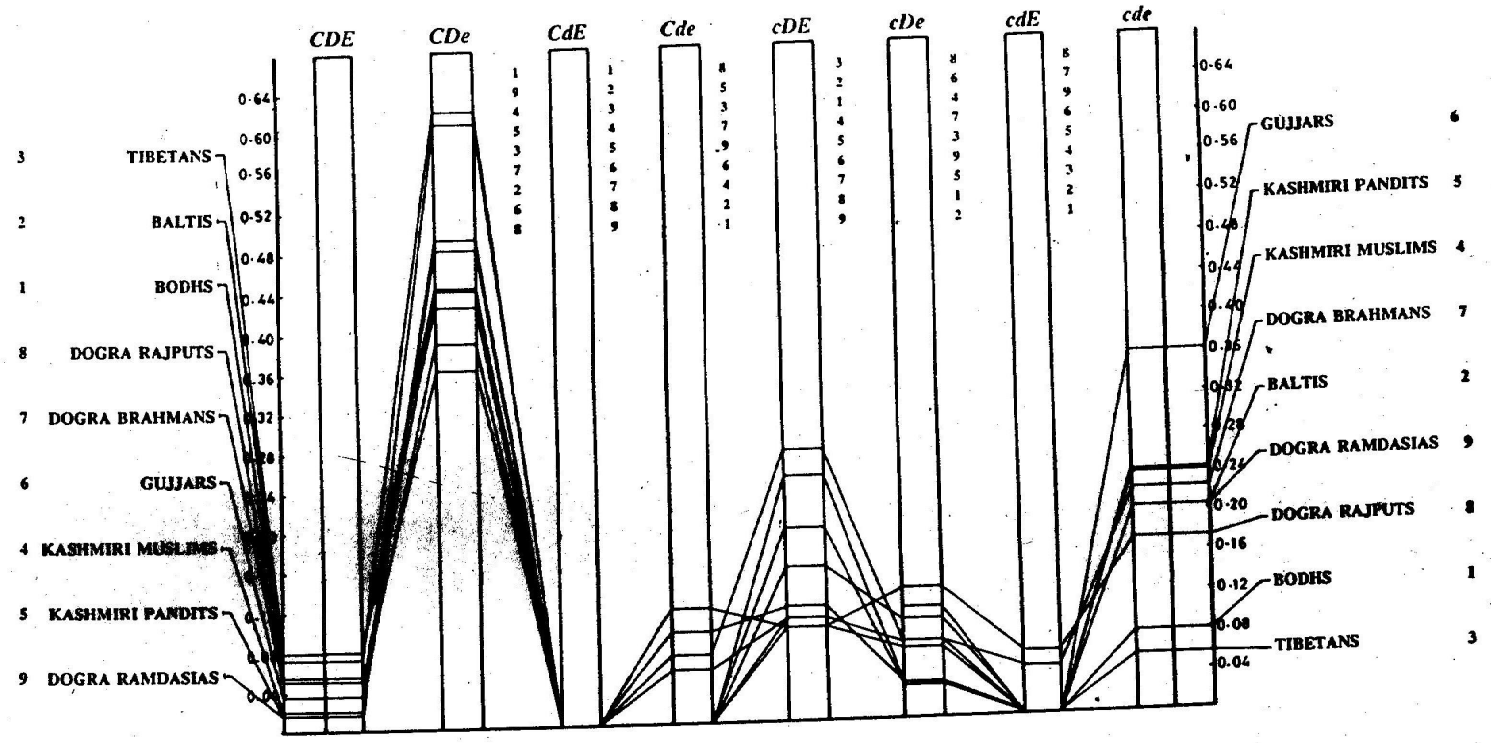

Fig. 3. Distribution of Rhesus chromosome frequencies among nine population groups of Jammu and Kashmir

It has been observed that among the Bodhs and Tibetans, the frequency of gene P^a is low and gene P^c is absent; similar pattern has been found among other population groups with Mongoloid affinities reported from the Himalayan region, Far East and South East Asia. On the other hand gene P^a is quite frequent and P^c is usually present among the population groups of Kashmir and Jammu regions and Baltis of Ladakh (present study), as well as in population groups from the plains of North India, Middle and Lower Himalayas and South West Asia.

Adenosine Deaminase (ADA) System

Among the Scheduled Tribes, the frequency of ADA^2 is almost similar among Bodhs and Baltis (about 8 per cent) but in Gujjars, it is somewhat higher (11.61 per cent). Among the caste groups, the frequency of ADA^2 is almost similar among Dogra Brahmans and Dogra Rajputs (14.29 and 14.08 per cent, respectively), whereas among Dogra Ramdasias it is a little higher (16.19 per cent) and in Kashmiri Pandits it is lower (10.61 per cent) (Fig. 6).

The ADA^2 incidence is low among the present population groups of Ladakh region and other population groups with Mongoloid affinities from the Himalayan region and Far East Asia, as compared to the population groups of Kashmir (Kashmiri Muslims and Kashmiri Pandits) and Jammu (Gujjars and Dogra caste groups) regions, as well as the plains of North India, Middle and Lower Himalayan regions and South West Asia.

Adenylate Kinase (AK) System

In the present study, the gene AK^2 is present among all the nine population groups of Jammu and Kashmir (Fig. 7), though its frequency is comparatively low among the population groups of Ladakh region (1.41 - 3.24 per cent), a little higher among the population groups of Kashmir region (4.55 and 6.25 per cent) and still higher among the population groups of Jammu region (more than 10 per cent, barring Dogra Rajputs). Among the Scheduled Tribes, the frequency of AK^2 is low and almost similar in Bodhs and Baltis (3.24 and 2.53 per cent, respectively) as compared to Gujjars (13.95 per cent). Among the caste groups, the gene AK^2 frequency is over 10 per cent in Dogra Brahmans and Dogra Ramdasias, while among Kashmiri Pandits and Dogra Rajputs, its incidence is surprisingly rather low (less than 5 per cent). Similar pattern of AK distribution has been reported from North India and neighbouring countries *i.e.* among the population groups with Mongoloid affinities of Himalayan region and South East and Far East Asia, low frequencies of AK^2 gene are found, whereas among the caste groups and communities from North India, the AK^2 gene is very frequent.

Esterase D (EsD) System

Among the population groups of the present study (Fig. 8), the gene EsD^2 frequency varies from 16.67 per cent (Dogra Brahmans) to 37.85 per cent (Tibetans). A rare gene EsD^3 has been encountered among the Gujjars.

Among the Scheduled Tribes, the Gujjars and Baltis are showing lower values of EsD^2 gene (20.93 and 22.23 per cent, respectively) than Bodhs (28.38 per cent). Among the caste groups, Dogra Rajputs and Dogra Ramdasias show similar frequencies of EsD^2 gene (25.35 and 23.81 per cent), which are comparatively higher than those recorded in both Kashmiri Pandits (18.18 per cent) and Dogra Brahmans (16.67 per cent).

Thus, it is evident that Tibetans with their high EsD^2 frequency stand out from all other population groups tested here from Jammu and Kashmir. On the other hand, the values recorded in Kashmiri Pandits and Dogra Brahmans are rather low.

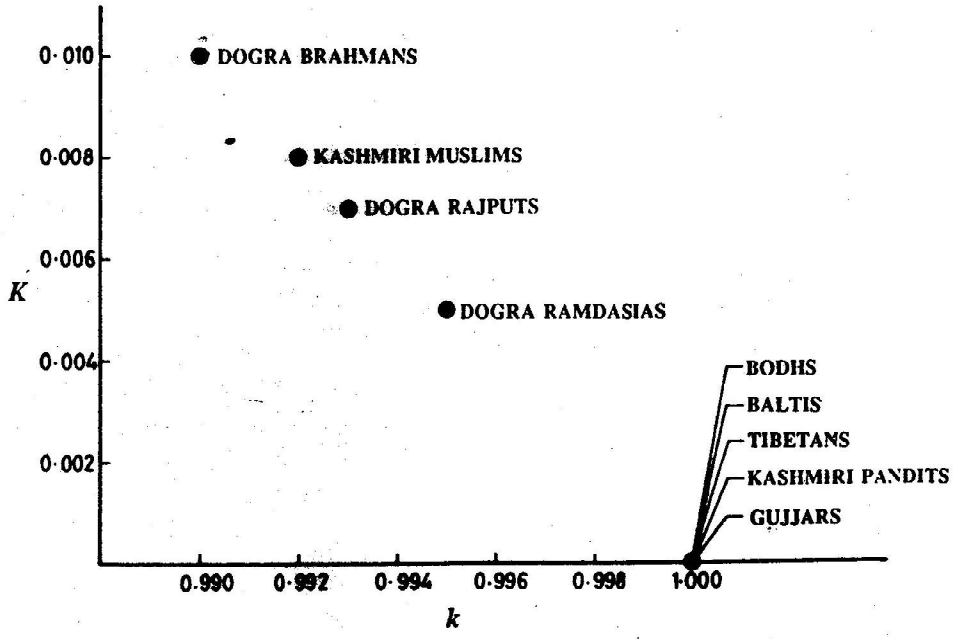

Fig. 4. Distribution of Kell gene frequencies among nine population groups of Jammu and Kashmir

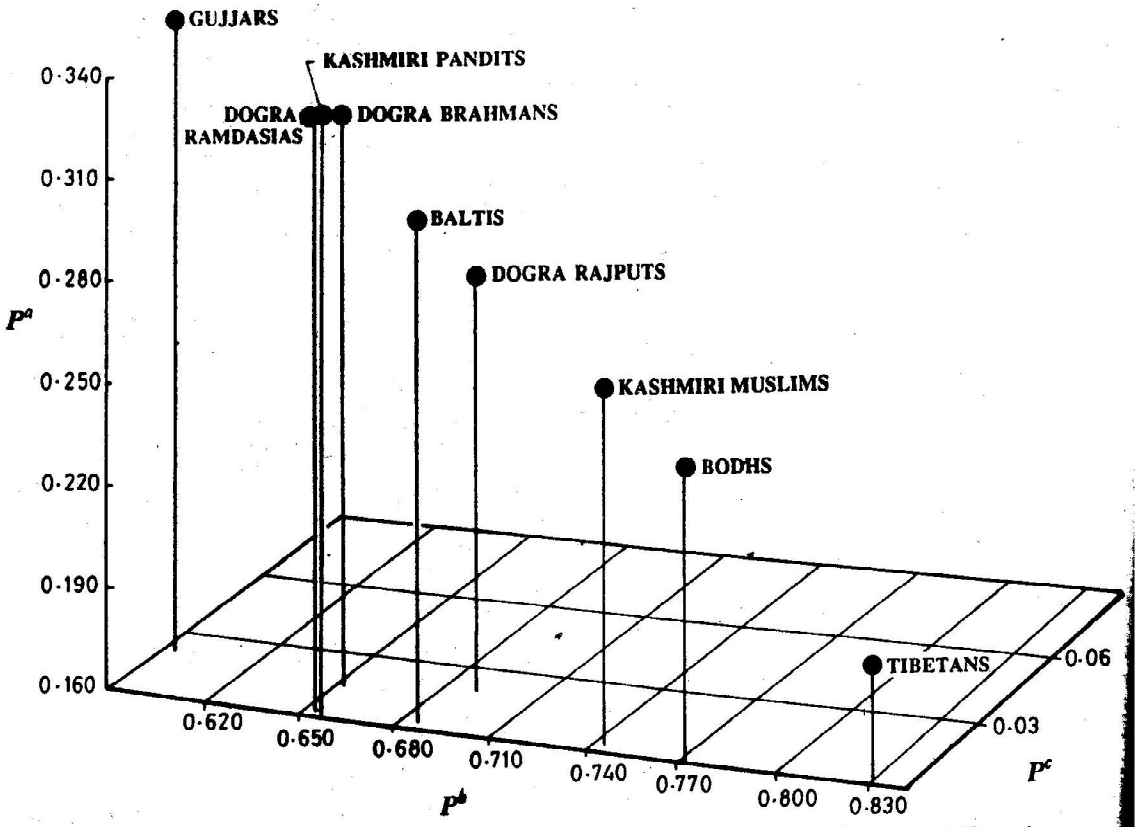

Fig. 5. Distribution of AP gene frequencies among nine population groups of Jammu and Kashmir

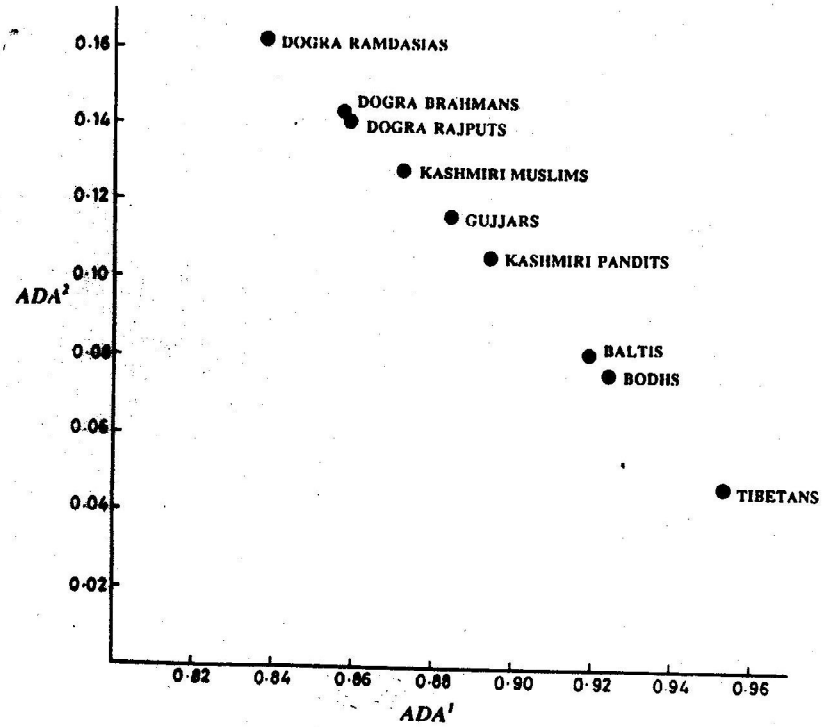

Fig. 6. Distribution of ADA gene frequencies among nine population groups of Jammu and Kashmir

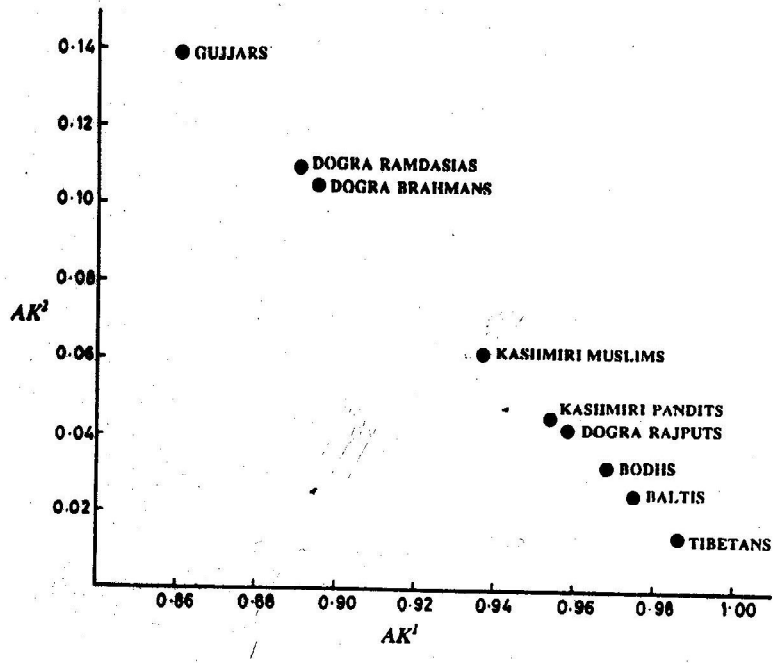

Fig. 7. Distribution of AK gene frequencies among nine population groups of Jammu and Kashmir

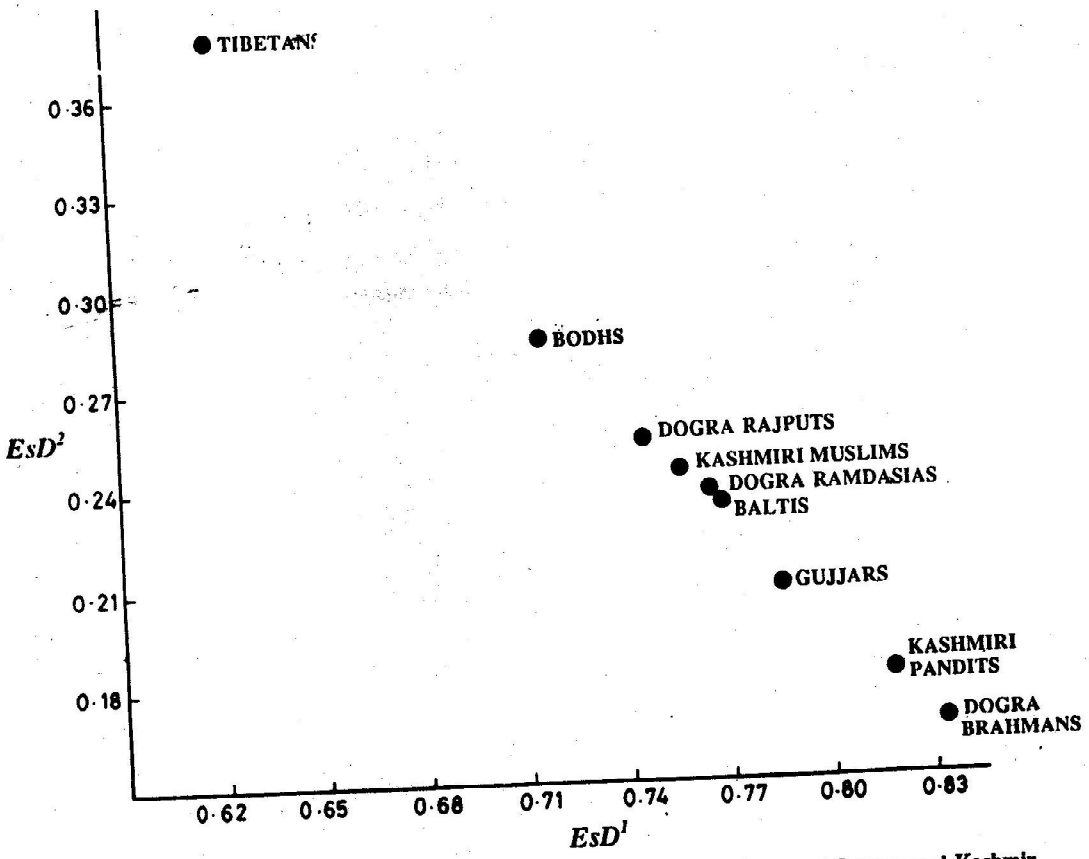

Fig. 8. Distribution of EsD gene frequencies among nine population groups of Jammu and Kashmir

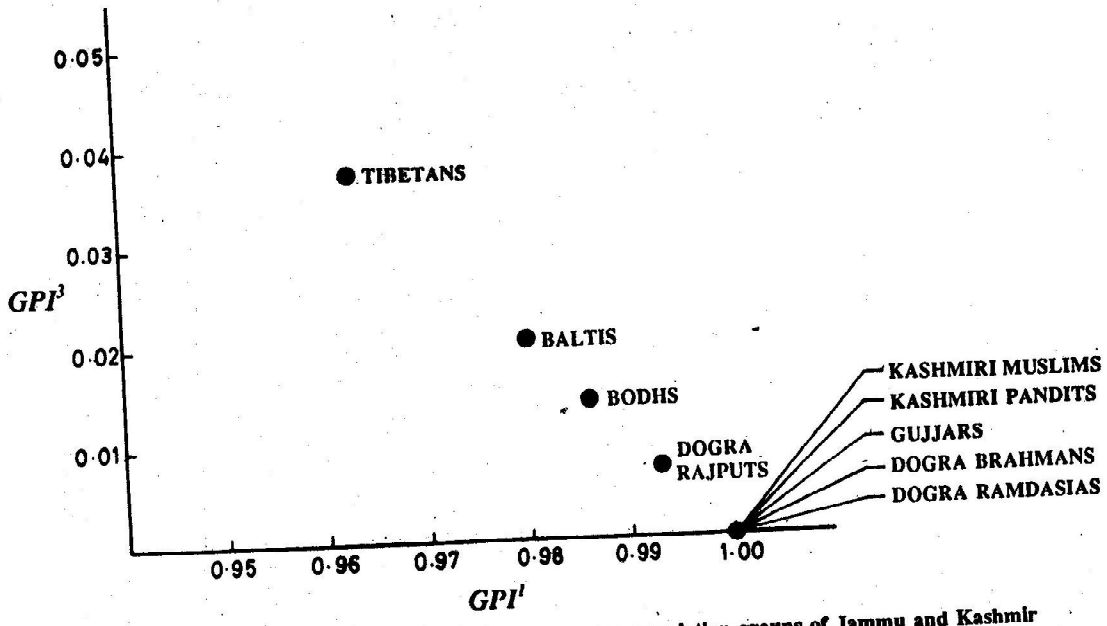

Fig. 9. Distribution of GPI gene frequencies among nine population groups of Jammu and Kashmir

From the distribution of EsD polymorphism among the populations reported in literature, it has been found that the frequency of EsD^2 is higher among the Indian populations than among Europeans, but the population groups with Mongoloid affininties have still higher values as observed Far East Asia and Himalayan regions. Essentially similar pattern has been observed in the present study *i.e.*, the Mongoloid populations of Ladakh are showing higher values for gene EsD^2, whereas the population groups of both Kashmir and Jammu regions are showing frequencies similar to that observed among the caste groups and communities of Middle and Lower regions of Himalayas, as well as the plains of North India.

Glucose Phosphate Isomerase (GPI) System

In the present study, except GPI^3, no other rare gene has been detected; the gene being present in each of the population group of the Ladakh region—Bodhs (1.36 per cent), Baltis (2.02 per cent) and Tibetans (3.74 per cent), but encountered only in Dogra Rajputs (0.70 per cent) outside this region (Fig. 9).

The rare gene GPI^3 is usually present among most population groups of North India and the population groups of the present study are no exception; albeit the absence of the gene in most population groups of Kashmir and Jammu divisions is somewhat surprising.

Glyoxalase I (GLO I) System

Among the population groups of Ladakh region, the incidence of gene GLO^1 is low (8.88 - 18.18 per cent) as compared to that observed among populations of Kashmir (above 20 per cent) and Jammu (range 18.09 - 29.65 per cent) regions, of the present study (Fig. 10).

Among the Scheduled Tribe groups, the Bodhs and Baltis GLO^1 gene frequencies (15.68 and 18.18 per cent, respectively) are rather low as compared with Gujjars (29.65 per cent). Among the caste groups, Kashmiri Pandits and Dogra Rajputs showing somewhat higher GLO^1 frequency (25.76 and 25.3 per cent, respectively), whereas Dogra Brahmans are represented with somewhat lower GLO^1 frequency (18.09 per cent).

Though, the studies available on the GLO I system are few, it has been observed that the population groups with Mongoloid affinities of Himalayan region, South East and Far East Asia are reported with low frequencies of GLO^1 gene and in the present study also among the population groups of Ladakh, a similar pattern has been observed. On the other hand, among the caste groups - Kashmiri Pandits and Dogra caste groups, and the religious groups - Kashmiri Muslims and Gujjars the distribution of the gene has been observed similar to that found among the various population groups of Punjab, Haryana and Delhi.

Phosphoglucomutase Locus 1 (PGM_1) System

In the present study, the frequency of PGM_1^2 varies from 17.19 per cent among Kashmiri Pandits - a caste group to 37.21 per cent among Gujjars - a Scheduled Tribe. Barring Kashmiri Pandits, among remaining population groups of the present study, the PGM_1^2 frequency ranges between 25 and 37 per cent (Fig. 11) which is as observed for other population groups of India. Two rare genes PGM_1^6 and PGM_1^7 have also been detected in the present material; the former was found among Bodhs and Tibetans from the Ladakh region and the latter, among caste groups - Dogra Rajputs and Dogra Ramdasias of Jammu region and Kashmiri Muslims of Kashmir region.

In the distribution of PGM_1 gene frequencies, the present population groups from Jammu and Kashmir are showing similarities with the population groups of the plains of North India and the Middle and Lower Himalayan regions. Rare genes, PGM_1^6 and PGM_1^7 found in the present study, have also been reported earlier among populations of India and other parts of Asia.

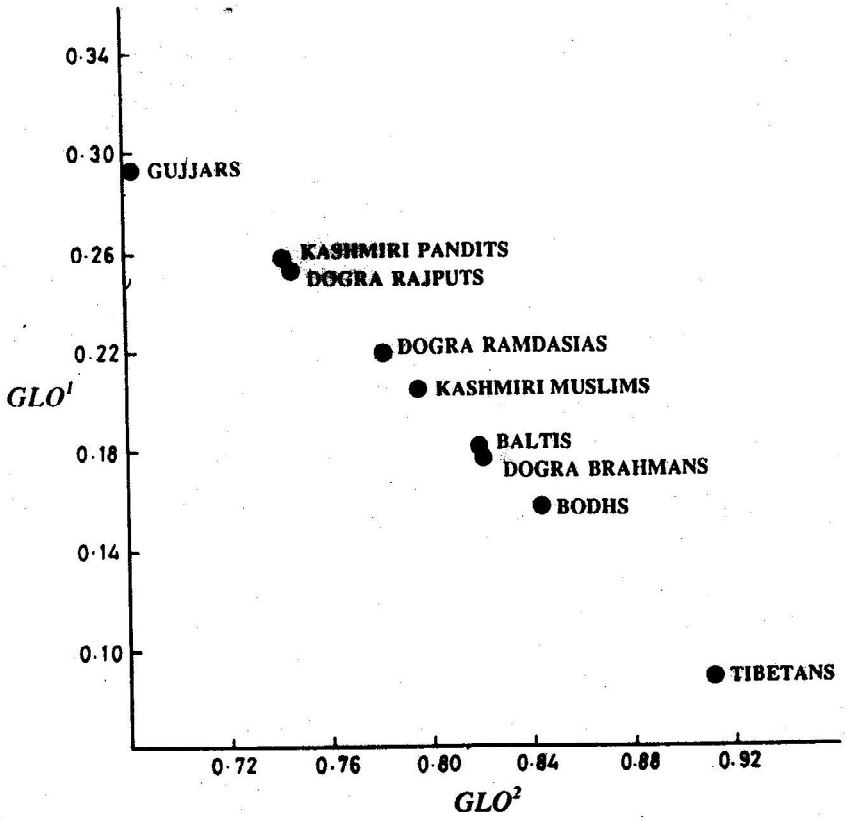

Fig. 10. Distribution of GLO I gene frequencies among nine population groups of Jammu and Kashmir

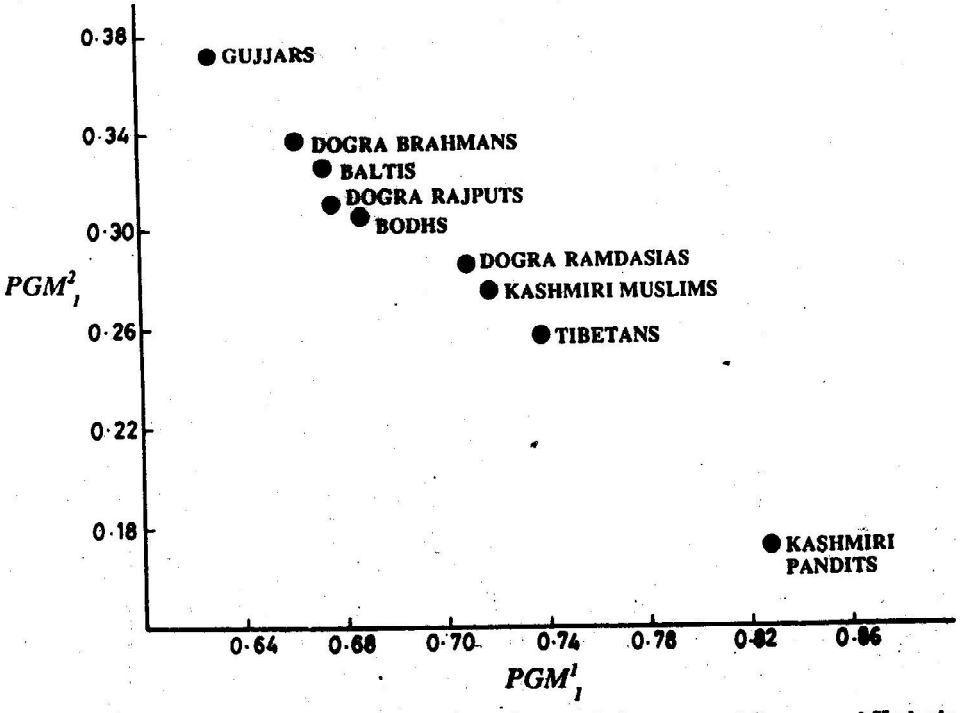

Fig. 11. Distribution of PGM_1 gene frequencies among nine population groups of Jammu and Kashmir

STATISTICAL ANALYSIS

The Chi-square values for inter-group differences among the nine population groups of Jammu and Kashmir for 11 genetic markers are given in table 2.

When compared statistically, the Bodhs and Baltis of Ladakh region exhibit non-significant differences with each other as well as with Kashmiri Muslims, Kashmiri Pandits, Dogra Rajputs and Gujjars, whereas Tibetans show such differences with Bodhs only.

The population groups of Kashmir region: Kashmiri Muslims and Kashmiri Pandits, and Jammu region : Gujjars, Dogra Brahmans, Dogra Rajputs and Dogra Ramdasias do not show any significant inter-group variation.

Heterozygosity

Heterozygosity (H), a measure of genetic variability, is intended to give a compound value of variation from the observed gene frequencies of a population. The H values calculated for each locus among the nine population groups of Jammu and Kashmir are listed in table 3. There is a great variation in heterozygosity values over loci (range 0.007 - 0.679), Rhesus being the most heterozygous locus and Kell, the least heterozygous locus. This heterogeneity in heterozygosity values (Fig. 12) could simply be a genetic consequence of population structure, or it may indicate the effect of natural selection operating among the population groups of the present study.

The average heterozygosity values calculated for each of the nine population groups over 11 loci are presented in table 4. These values show little variation from one population group to another (range 0.298 - 0.373), Dogra Rajputs being the most heterozygous and Tibetans the least heterozygous (Fig. 13).

The average heterozygosity for the present sample has been found 34.3 per cent which is more than three times the value recorded by Nei and Roychoudhury (1974) for various ethnic groups (about 10 per cent), using random loci. But this difference is not real and is attributable to the fact that only polymorphic loci were considered in the present study, the proportion of which is one third of the total human genome (Nei and Roychoudhury, 1974). Therefore, the two values given above are in good agreement.

The mean heterozygosity value for the population groups of Ladakh region (0.318) has been found lower than that recorded in population groups of either Kashmir (0.336) or Jammu (0.366) regions. This indicates that the population groups of Ladakh region are genetically less variable than those of both Jammu and Kashmir regions.

Genetic Differentiation

Measures of population differentiation are the measures of genetic variability among local population or larger subdivisions of a species, with respect to known gene frequencies. In the present study, two most common such measures Wahlund's variance (Wahlund, 1928) and a set of gene diversity measures developed by Nei (1973), have been used to analyse the genic differentiation among the nine population groups studied here from Jammu and Kashmir.

Wahlund's Variance

For a diallelic locus, Wahlund's variance (f) is given by

$$f = \frac{\sigma^2 p}{\bar{p}(1-\bar{p})}$$

Where $\sigma^2 p$ is the variance of gene frequency p across subpopulations, and $\bar{p}$ is the mean of p across subpopulations.

The f values calculated for 12 diallelic loci are set out in table 5. It is observed that f values for S, C, D, E, AK^2, EsD^2 and GLO^1 genes are comparatively high (range 0.02093 - 0.04820), and this suggests higher differentiation of these genes among present population groups. Differentiation with respect to other

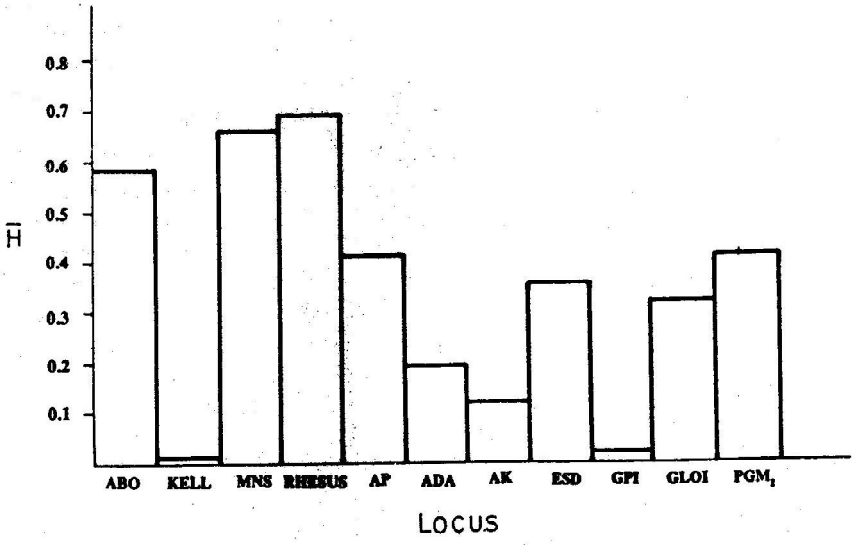

Fig. 12. Distribution of average heterozygosity ($\bar{H}$) at 11 loci among nine population groups of Jammu and Kashmir

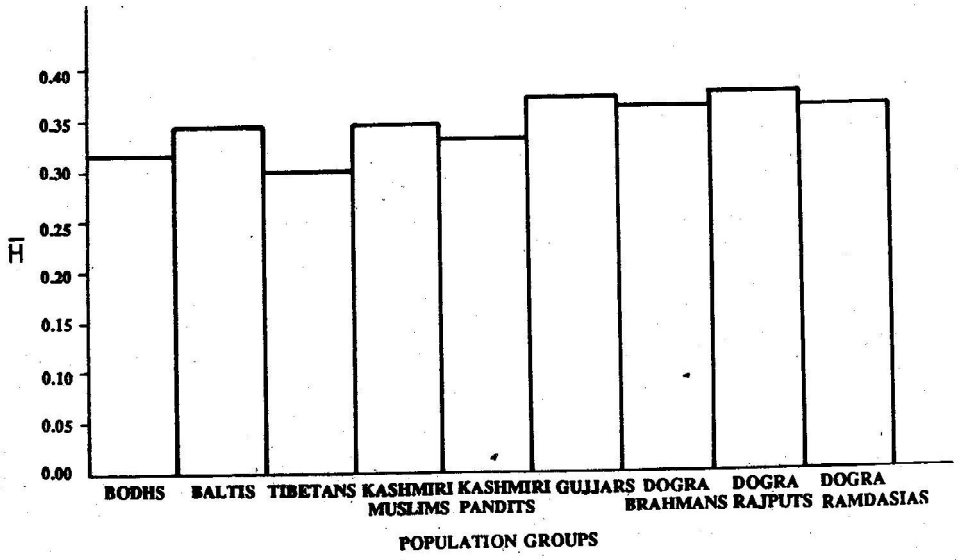

Fig. 13. Distribution of average heterozygosity ($\bar{H}$) in nine population groups of Jammu and Kashmir

able 2: Chi-square values for intergroup differences among nine population groups of Jammu and Kashmir

;ystem	Bodhs X Baltis	d.f.	Bodhs X Tibetans	d.f.	Bodhs X Kashmiri Muslims	d.f.	Bodhs X Kashmiri Pandits	d.f.	Bodhs X Gujjars	d.f.	Bodhs X Dogra Brahmans	d.f.	Bodhs X Dogra Rajputs	d.f.	Bodhs X Dogra Ramdasias	d.f.	Baltis X Tibetans	d.f.	Baltis X Kashmiri Muslims	d.f.
BLOOD GROUPS																				
A_1A_2BO	6.2261	3	1.0466	3	3.9619	3	1.9619	3	7.3455	3	2.9157	3	2.9136	3	2.1365	3	7.1726	3	7.1743	3
MNSs	5.9105	5	9.6300	5	19.3674*	5	15.6730*	5	6.4342	5	24.5222*	5	12.2718	5	21.0065*	5	12.4080*	5	9.2516	5
Rhesus	25.7764*	9	5.9999	10	28.7053*	9	17.5995	10	53.5004*	9	26.1318*	13	27.2453*	13	27.9323*	9	24.8341*	10	20.7397*	8
Kell					1.34681	1					1.6442	1	1.0163	1	0.67021	1			0.1064	1
RED CELL ENZYMES																				
AP	6.3104	3	2.8808	2	1.7236	3	8.6518*	2	21.8601*	4	12.5281*	4	8.5876	4	6.7950	4	10.2952*	3	3.8295	3
ADA	2.4477	2	2.1061	2	4.5774	2	1.2941	2	2.4543	2	6.7580*	2	5.3516	2	10.1618*	2	2.1600	2	3.1087	2
AK	0.2236	1	1.8914	1	3.2987	1	0.2704	1	22.1247*	2	13.5767*	1	0.2979	1	13.5954*	2	0.7008	1	3.6537	1
EsD	1.8043	2	5.7737	2	1.4323	2	2.9602	2	3.5042	2	10.0529*	2	0.5129	2	1.6101	2	10.0233*	2	0.1445	2
GPI	0.3829	1	3.5405	1	3.3888	1	0.9758	1	2.3974	1	2.6618	1	0.4120	1	2.8618	1	1.4181	1	4.9791*	1
GLO I	1.0550	2	5.3459	2	2.2594	2	6.2010*	1	15.6758*	2	1.3755	2	6.1618*	2	4.7464	2	16.9100*	2	0.6514	2
PGM_1	7.3212*	2	3.8144	2	3.2966	2	4.3728	2	3.1476	2	2.9839	2	3.8472	2	3.3882	2	2.9284	2	1.7839	2

Table 2: Contd....

System	*Baltis X Kashmiri Pandits*	*d.f.*	*Baltis X Gujjars*	*d.f.*	*Baltis X Dogra Brahmans*	*d.f.*	*Baltis X Dogra Rajputs*	*d.f.*	*Baltis X Dogra Ramdasias*	*d.f.*	*Tibetans X Kashmiri Muslims*	*d.f.*	*Tibetans X Kashmiri Pandits*	*d.f.*	*Tibetans X Gujjars*	*d.f.*	*Tibetan X Dogra Brahmans*	*d.f.*	*Tibetans X Dogra Rajputs*	*d.f.*
BLOOD GROUPS																				
A_1A_2BO	6.8357	3	6.1591	3	1.6101	3	5.7446	3	4.8693	3	1.0888	3	0.8131	3	4.2043	3	3.1503	3	2.3223	3
MNSs	5.9589	5	2.4528	5	9.7555	5	5.5996	5	11.5279*	5	37.4913*	5	14.9699*	5	15.0772	5	35.9982*	5	23.2132*	5
Rhesus	16.5306	9	27.2788*	8	26.6438*	13	37.9658	13	23.0823*	8	32.9203*	10	21.0297*	10	58.4815*	10	34.7054*	13	32.1192*	13
Kell					0.1269	1	0.1124	1	0.1112	1	0.9093	1					2.0191	1	1.5085	1
RED CELL ENZYMES																				
AP	1.0820	3	6.3305	4	2.1699	4	3.4157	4	3.8140	4	4.6861	3	9.1601*	2	26.0641*	4	17.5394*	4	10.1223*	4
ADA	0.4538	1	1.7676	2	4.6541	2	4.4414	2	6.7510*	2	9.2045*	2	3.3484	1	4.2700	2	10.8299*	2	9.9140*	2
AK	0.7097	1	16.9164*	2	11.2125*	1	0.7830	1	10.6711*	2	7.3239*	1	2.4911	1	22.4013*	1	16.7181*	1	2.8088	1
EsD	0.7497	2	0.6932	2	2.9970	2	0.2974	2	0.02974	2	0.0696	2	10.0647*	2	8.1980*	2	9.8104*	2	22.3786*	2
GPI	1.3750	1	3.5954	1	4.4051*	1	0.9934	1	4.4051*	1	9.6334*	1	4.5436	1	6.8290*	1	8.3137*	1	3.2965	1
GLO I	2.1584	2	9.7584*	2	2.1710	2	2.7153	2	3.5268	2	6.7237*	2	12.0520*	2	29.2297*	2	8.5190*	2	16.5630*	2
PGM_1	7.0479*	2	2.2870	2	0.7213	2	0.1061	2	1.0575	2	0.2532	2	2.3004	2	5.8505	2	3.2351	2	1.5223	2

Table 2: Contd....

System	Tibetans X Dogra Ramdasias	d.f.	Kashmiri Muslims X Kashmiri Pandits	d.f.	Kashmiri Muslims X Gujjars	d.f.	Kashmiri Muslims X Dogra Brahmans	d.f.	Kashmiri Muslims X Dogra Rajputs	d.f.	Kashmiri Muslims X Dogra Ramdasias	d.f.	Kashmiri Pandits X Gujjars	d.f.	Kashmiri Pandits X Dogra Brahmans	d.f.	Kashmir Pandits X Dogra Rajputs	d.f.	Kashmiri Pandits X Dogra Ramdasias	d.f.
BLOOD GROUPS																				
A_1A_2BO	3.9019	3	1.5866	3	2.1874	3	3.2886	3	5.6207	3	7.3889	3	3.4371	3	3.9589	3	2.3421	3	3.3730	3
MNSs	14.8061*	5	4.0675	5	5.1768	5	5.8798	5	6.9854	5	5.9232	5	6.8702	5	5.3331	5	6.3569	5	6.0100	5
Rhesus	40.4579*	10	5.2642	8	11.8127	7	25.7187*	13	18.8798	13	11.9108	7	14.3209	8	9.7576	13	12.6044	13	8.5793	8
Kell	1.0048	1	0.5062	1	1.3462	1	0.0274	1	0.0146	1			0.2172	1	0.6768	1	0.4326	1	0.2658	1
RED CELL ENZYMES																				
AP	16.0269*	3	3.6401	3	12.8227*	4	6.9809	4	3.3580	4	4.7126	3	4.5341	4	2.6261	4	2.2424	4	2.9763	3
ADA	13.9641*	2	0.5403	2	0.1550	2	0.4253	2	0.2378	2	1.2757	2	0.4327	2	1.0053	2	0.6740	2	1.5601	2
AK	15.6921*	2	0.3006	1	7.5277*	2	2.8703	1	1.074241	2	3.9548	2	4.4195	1	2.4117	1	0.0169	1	2.3327	2
EsD	10.4127*	2	1.1977	2	1.5074	2	4.2365	2	0.3153	2	0.0189	2	0.4454	2	0.1877	2	1.2691	2	0.9439	2
GPI	8.3137*	1							1.5161	1							0.4320	1		
GLO I	15.1128*	2	2.3523	2	6.3811*	2	1.55079	2	1.1972	2	1.6441	2	4.6013	2	6.6182*	2	1.2376	2	4.9391	2
PGM_1	0.5127	2	3.3070	2	4.2467	2	1.9122	2	0.7747	2	0.0773	2	8.5275*	2	6.8038*	2	5.3680	2	3.8519	2

Table 2: Contd....

System	*Gujjars X Dogra Brahmans*	*d.f.*	*Gujjars X Dogra Rajputs*	*d.f.*	*Gujjars X Dogra Ramdasias*	*d.f.*	*Dogra Brahmans X Dogra Rajputs*	*d.f.*	*Dogra Brahmans X Dogra Ramdasias*	*d.f.*	*Dogra Rajputs X Dogra Ramdasias*	*d.f.*
BLOOD GROUPS												
A_1A_2BO	4.8921	3	7.0108	3	8.9249*	3	4.0897	3	4.2966	3	0.3161	3
MNSs	6.4040	5	1.3814	5	4.8472	5	2.7699	5	1.1749	5	1.8535	5
Rhesus	23.3232*	13	30.1475*	13	18.6021*	7	8.6330	13	33.6012*	13	30.9233*	13
Kell	1.6537	1	1.4078	1	0.9045	1	0.0565	1	0.3382	1	0.0843	1
RED CELL ENZYMES												
AP	1,6707	4	4.3771	4	3.5433	4	2.3670	4	2.3444	4	4.8848	4
ADA	0.8049	2	0.4641	2	1.8514	2	0.4929	2	0.2817	2	0.8609	2
AK	2.0462	2	8.9584*	2	1.6572	2	4.9565*	1	2.2255	2	4.7954	2
EsD	2,0928	2	0.8108	2	1.1712	2	4.5400	2	3.5175	2	0.4442	2
GPI			1.4078	1			1.5085	1			1.5085	1
GLO I	7.5529*	2	2.2589	2	3.3786	2	3.7151	2	1.0605	2	1.7633	2
PGM_1	0.6151	2	1.8450	2	3.4740	2	0.5623	2	4.0534	2	0.3851*	2

genes is small, and it appears that there has been little effect of population subdivision on these alleles. The mean f value over the 12 genes (0.02453) gives an estimate of the overall magnitude of gene differentiation among the nine population groups of the present study (Fig. 14).

Nei's Gene Diversity Analysis

By taking the average gene frequencies of all sub-populations as representative of the entire population, the gene diversity of the total population (H_T) has been calculated as follows:

$H_T = H_S + D_{ST}$

Table 3: Heterozygosity in nine population groups of Jammu and Kashmir—estimates by loci

Locus	*Heterozygosity ($\bar{H}$)*
A_1A_2BO	0.589
MNSs	0.662
Rhesus	0.679
Kell	0.007
AP	0.414
ADA	0.195
AK	0.117
EsD	0.362
GPI	0.017
GLO I	0.319
PGM_1	0.415
Mean	0.343

Table 4: Heterozygosity in nine population groups of Jammu and Kashmir - estimates by population groups

Population	*Heterozygosity ($\bar{H}$)*
Bodhs	0.316
Baltis	0.339
Tibetans	0.298
Kashmiri Muslims	0.342
Kashmiri Pandits	0.330
Gujjars	0.371
Dogra Brahmans	0.362
Dogra Rajputs	0.373
Dogra Ramdasias	0.359
Mean	0.343

Table 5: Mean gene frequency, variance and Wahlund's variance among nine population groups of Jammu and Kashmir

Gene	*Mean ($\bar{p}$)*	*Variance (σp^2)*	*Wahlund's Variance(f) $\sigma p^2/\bar{p}(1-\bar{p})$*
M	0.65822	0.00343	0.01525
S	0.28078	0.00610	0.03021
C	0.60000	0.00636	0.02650
D	0.76400	0.00869	0.04820
E	0.21611	0.00760	0.04486
K	0.00333	0.00002	0.00603
ADA^2	0.11111	0.00138	0.01397
AK^2	0.06367	0.00190	0.03187
EsD^2	0.24300	0.00385	0.02093
GPI^3	0.00867	0.00015	0.01745
GLO^1	0.20433	0.00379	0.02331
PGM_1^2	0.29344	0.00326	0.01572
Mean			0.02453

Where H_S is the average gene diversity within the sub-populations, and D_{ST} is the average gene diversity between the sub-populations (Nei, 1973b). The coefficient of gene differentiation relative to the total population (G_{ST}), has been calculated as follows

$G_{ST} = D_{ST}/H_T$

In the present study, the total gene diversity (H_T) among the nine population groups (0.3511) has been analysed into its two components, i.e., intra-populational gene diversity (H_S = 0.3434) and inter-populational gene diverstiy (D_{ST} = 0.0077) (Table 6). This shows that the gene diversity between population groups is much lower than the gene diversity within the population groups. In other words, only a small fraction of the total gene diversity is due to the differences between the population groups while a large part of this diversity is attributable to individual variations within the population groups. Furthermore, it also suggests that the present population groups are at an early stage of genic differentiation.

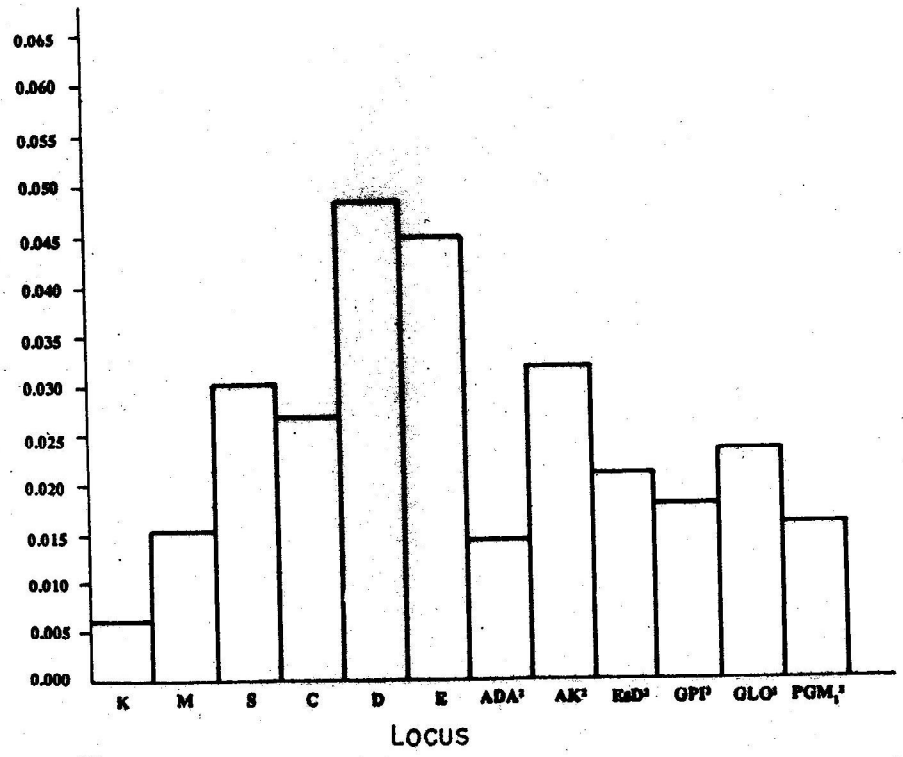

Fig. 14. Distribution of Wahlund's variance (*f*) at 12 diallelic loci among nine population groups of Jammu and Kashmir

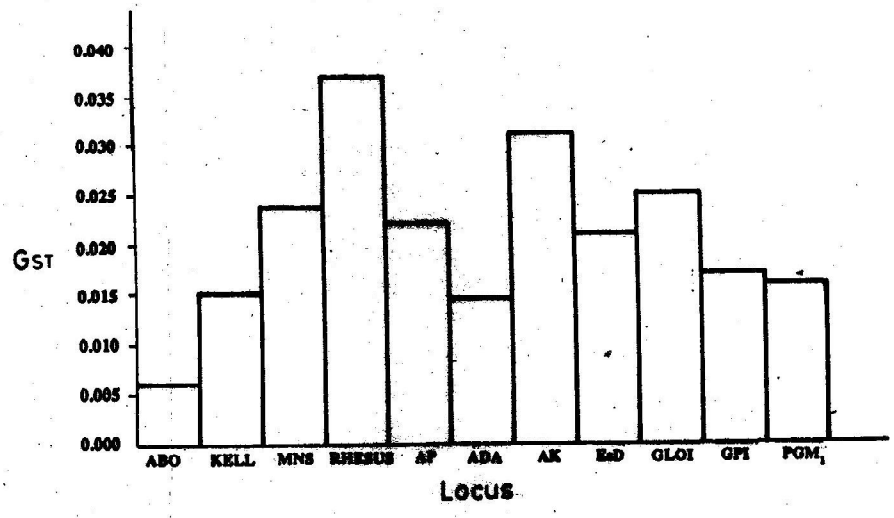

Fig. 15. Distribution of G_{st} (coefficient of gene differentiation) at 11 loci among nine population groups of Jammu and Kashmir

The coefficient of gene differentiation, (G_{ST}) values among the nine population groups of Jammu and Kashmir under study are comparatively high at MNSs, Rhesus, AK and GLO I loci. On the other hand, little differentiation has been recorded at A_1A_2BO, Kell, ADA , AK and GPI loci while figures are moderate for AP, EsD, GPO I and PGM_1 loci (Fig. 15). It has been observed that among the present population groups, the average G_{ST} value over 11 loci (0.0219) (Table 6) is close to the average *f* value (0.0245) over 12 loci.

To test for the selective neutrality of genes, the test proposed by Lewontin and Krakauer, (1973) has been applied to the distribution of *f* values for various alleles in the present study (Table 7). This table shows that the observed variance of *f* (0.00015) is not significantly different from the expected (theoretical) variance of *f* (0.00017). This suggests that the gene frequency variation in these nine population groups is mainly due to the population breeding structure, with little or no selection operating among them.

Genetic Distance

Genetic distance can be regarded as a function of the differences in gene frequencies. It is simply a tool to investigate the relationship among a set of populations, but it may not necessarily establish any exact phylogenetic relationship among them. An idea about the similarity and differences in the gene pools of populations can be obtained only by considering a large number of loci simultaneously. Out of several so called "genetic distance" measures available in the literature, the measure proposed by Nei (1987) has been employed in the present study, since it has a biological meaning attached to it.

The pattern of relationship are based on grouping the populations into clusters such that populations belonging to a cluster are more close to one another than those belonging to different clusters. Such patterns obtained from cluster analysis are usually shown in the form of a dendrogram.

In the present study, the lowest genetic distance (D) (0.00138) has been observed between Kashmiri Muslims and Kashmiri Pandits, and the highest (0.02963) between Tibetans and Gujjars (Table 8). Tibetans show smaller genetic distances with both Bodhs and Baltis than with the other population groups and this suggests that the genetic constitution of the three population groups of Ladakh division is similar but quite different from that of the other population groups investigated from either Kashmir or Jammu division. Both the Kashmiri population groups are showing closeness with the three Dogra population groups and Gujjars. Gujjars are showing low genetic distance with Dogra population group of the present study. Furthermore, the D values recorded among the three Dogra groups in the present study are rather small. However, the genetic distance values among the nine population groups were statistically non-significant (Table 9).

The overall genetic relationship between various population groups of the present study is summed up in the dendrogram constructed from genetic distance matrix following Sneath and Sokal (1973) (Fig. 16). It is clear from this figure that there are two main clusters-one by the population groups of Jammu and Kashmir divisions together and the other by population groups of Ladakh. Thus, early genetic divergence of Bodhs, Baltis and Tibetans from all the remaining population groups of this study is evident.

In the second main cluster, the early divergence of Gujjars from the remaining five population groups of Kashmir and Jammu divisions is also quite apparent. Among latter groups, Kashmiri Muslims and Kashmiri Pandits are placed together in a sub-cluster within this main cluster, while various Dogra caste groups branch away at an earlier stage from both of them.

The dendrogram analysis, therefore, clearly differentiates the three population

Table 6: Estimates of Nei's measures of gene diversity among nine population groups of Jammu and Kashmir

Locus	*Gene diversity in the total population (H_T)*	*Intra-populational gene diversity (H_S)*	*Inter-populational gene diversity (D_{ST})*	*Coefficient of gene differentiation (G_{ST})*
A_1A_2BO	0.5931	0.5894	0.0037	0.0062
MNSs	0.6785	0.6625	0.0160	0.0236
Rhesus	0.7047	0.6787	0.0260	0.0369
Kell	0.0067	0.0066	0.0001	0.0149
AP	0.4237	0.4144	0.0093	0.0219
ADA	0.1979	0.1951	0.0028	0.0141
AK	0.1209	0.1172	0.0037	0.0306
EsD	0.3701	0.3624	0.0077	0.0208
GPI	0.0172	0.0169	0.0003	0.0174
GLO I	0.3271	0.3189	0.0082	0.0251
PGM_1	0.4218	0.4152	0.0066	0.0156
Mean	0.3511	0.3434	0.0077	0.0219

Table 7: Lewontin-Krakauer test for the heterogeneity of *f* values of polymorphic genes in nine population groups of Jammu and Kashmir

Number of groups	*Number of genes*	*Mean f over genes ($\overline{f}$)*	*Observed variance $S^2 f$*	*Theoretical variance*	$S^2 f / \sigma^2 f$
9	12	0.0245	0.00015	0.00017	0.88

Table 8:Estimates of Nei's measure of genetic distance (D) among nine population groups of Jammu and Kashmir

Population	*Bodhs*	*Baltis*	*Tibetans*	*Kashmiri Muslims*	*Kashmiri Pandits*	*Gujjars*	*Dogra Brahmans*	*Dogra Rajputs*
Baltis	0.00320							
Tibetans	0.00544	0.00883						
Kashmiri Muslims	0.00529	0.00241	0.01354					
Kashmiri Pandits	0.01144	0.00653	0.02489	0.00138				
Gujjars	0.01771	0.00708	0.02963	0.00596	0.00792			
Dogra Brahmans	0.01034	0.00387	0.02333	0.00185	0.00186	0.00396		
Dogra Rajputs	0.00863	0.00320	0.01574	0.00247	0.00265	0.00588	0.00196	
Dogra Ramdasias	0.00707	0.00683	0.02362	0.00304	0.00148	0.00803	0.00238	0.00502

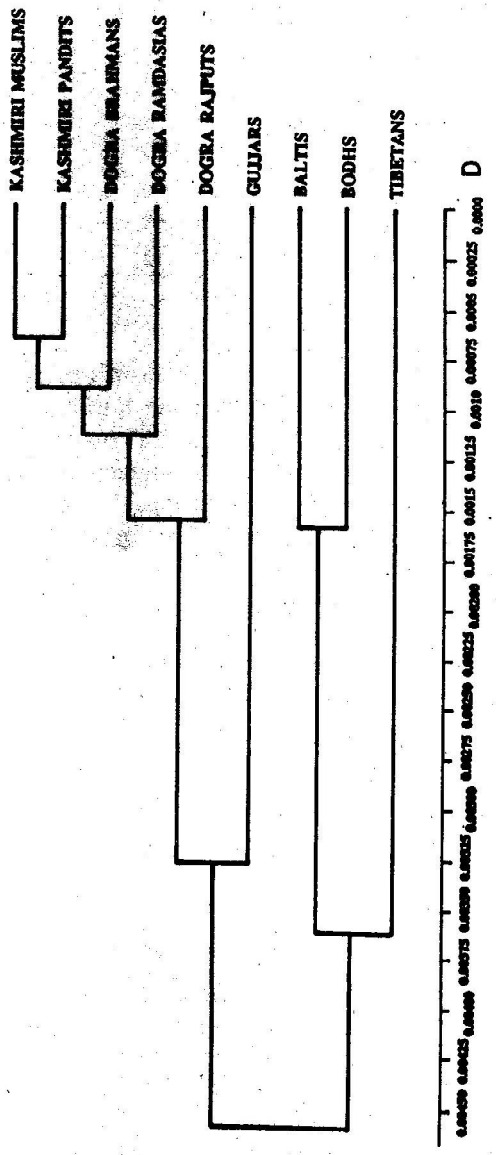

Fig. 16. Dendrogram constructed from Nei's genetic distance measure(D) among nine population groups of Jammu and Kashmir

Table 9: The chi-square values for the test of significance of genetic distance

Population	*Bodhs*	*Baltis*	*Tibetans*	*Kashmiri Muslims*	*Kashmiri Pandits*	*Gujjars*	*Dogra Brahmans*	*Dogra Rajputs*
Baltis	0.3178							
Tibetans	0.5123	0.8863						
Kashmiri Muslims	0.6397	0.4415	1.3535					
Kashmiri Pandits	1.2866	0.9971	1.8918	0.7874				
Gujjars	1.3093	0.7918	2.1500	0.4483	0.9906			
Dogra Brahmans	1.0492	0.7037	1.7741	0.4142	0.5094	0.5260		
Dogra Rajputs	1.0363	0.7816	1.4460	0.6492	0.6007	0.7740	0.3299	
Dogra Ramdasias	0.7909	0.7123	1.7844	0.2831	0.7112	0.4720	0.4214	0.272

Degree of freedom=21

groups of Ladakh from all the population groups of Kashmir and Jammu divisions taken together. Furthermore, close genetic relationship between the two population groups of Kashmir division on one hand, and among the three Dogra caste groups of Jammu division on the other, is also quite clear. Thus, from this analysis there is some evidence for close genetic relationship among the population groups belonging to the same region, irrespective of their caste, religion, linguistic or any other affiliation.

Thus the present study shows that the population groups of Ladakh are not similar to the population groups of either Kashmir or Jammu regions in their genetic constitution. The differentiation of the two tribal groups-Bodhs and Baltis; and Tibetans of Ladakh from the Kashmiri Muslims, Kashmiri Pandits, Gujjars and Dogra caste groups, could well be due to a considerable Mongoloid admixture in the former groups as demonstrated by high frequencies of *Ms, CDe* and EsD^2, and low frequencies of *cde*, p^a, ADA^2, AK^2 and GLO^1.

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