

Genetic Variation in Some Endogamous Population Groups of North Bihar

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ABSTRACT Based on four genetic systems (ABO and Rh blood groups, PTC taste sensitivity and colour blindness), gene diversity and genetic distances have been estimated among six endogamous population groups of Bihar, viz. the Brahmin, Mushar, Oraon, Kharwar, Kayastha and Muslim of northern Bihar. A small fraction of gene diversity accounts for the inter-population genetic variation, whereas the major portion of the total diversity is due to intra-population variation. In the dendrogram constructed using genetic distance matrix, the Oraons and Kharwar are placed in one cluster, while Brahmin, Mushar and Muslim form the other cluster along with the Kayastha.

INTRODUCTION

Humans are the product of biology as well as culture. Subgroups constitute the population. A human population arises through a common ancestral stock. Each population has its own genetic characteristics. Some of the groups retain their genetical identity by practicing endogamy, while others fuse together by interbreeding thus giving rise to a mosaic distribution of genetical characteristics.

Human biological variations are related to the ethnic and ecological background of population. The genetic similarities within the population show the common origin, or the admixture of the gene pools. Keeping this aim in mind the present work was undertaken which deals with the genetic variation among six endogamous populations inhabiting the Kosi Zone of North Bihar.

MATERIAL AND METHODS

Data were collected from door-to-door survey method from the members of six endogamous populations selected for the present

study viz., the Brahmin (208), Kayastha (228), Muslim (217), Oraon (117), Kharwar (171) and Mushar (325). In no case were two persons belonging to the same family subjected to test. The Mendelian traits of ABO blood groups, Rh and PTC taste ability and red-green colour blindness were studied. The standard methodology was followed for the detection of ABO blood groups by slide agglutination method using anti-A and anti-B; Rh blood-by slide agglutination method using anti-Rh(D); PTC taste ability by using the method of Harris and Kalmus (1950); Red-Green colour blindness by using Ishihara colour plates. Allele frequencies were calculated according to Mourant et al. (1976). Genetic distance was calculated using the formulae given by Nei (1972).

RESULTS AND DISCUSSION

The Kayastha showed highest incidence of blood group O, while Oraon showed highest frequency of blood group A and Kharwar showed highest frequency of blood group B (Table 1). Mandal (1992) has reported high frequency of blood group B among Bania, Rajput and Yadav of Uttar Pradesh and Singh and Sinha (1988) among Dusadh and Mushar of Bhagalpur, Bihar.

It is interesting to note that with their rather high A allele frequency (0.323) and a rather low B allele frequency (0.175) the tribal Oraon stand out from all other population groups investigated here. However an extremely high frequency of the B allele observed among Kharwar (0.459) is surprising (Table 2).

The incidence of the Rh system is also interesting. The Oraon once again differentiate

Table 1: Distribution of the ABO and Rh(D) blood groups, PTC taste blind and colour-blindness in six population groups of North Bihar

Population group	ABO blood groups				Rh(D) negative	PTC non-tasters	Red-green colour-blind
	O	A	B	AB			
Brahmin	67 (32.21)	72 (34.62)	54 (25.96)	15 (7.21)	15 (7.21)	60 (28.85)	4 (1.92)
Mushar	106 (32.62)	103 (31.69)	81 (24.92)	35 (10.77)	8 (2.46)	82 (25.23)	9 (2.77)
Kayastha	90 (39.47)	52 (22.81)	58 (25.44)	28 (12.28)	12 (5.26)	57 (25.00)	2 (0.88)
Oraon	28 (23.93)	52 (44.44)	26 (22.22)	11 (9.40)	0 (0.00)	22 (18.80)	5 (4.27)
Kharwar	18 (10.53)	36 (21.05)	108 (63.16)	9 (5.26)	10 (5.85)	72 (42.11)	6 (3.51)
Muslim	75 (34.56)	55 (25.35)	72 (33.18)	15 (6.91)	12 (5.53)	49 (22.58)	7 (3.23)

from the rest with complete absence of Rh negatives in them, while in the remaining populations the frequency of this phenotype ranges from 0.27-7.21% (Table 1). Singh and Sinha (1988) have reported Rh incidence 4.8% in Chamars and 4.7% among Mushars of Bhagalpur, Bihar.

The distribution of PTC tasting ability among the population under investigation was bi-modal. The antimode lies between the solution numbers 5 and 6. The frequency of non-taster allele (*t*) was high among Kharwar, Brahmin, Mushar and Kayastha (Table 2). Such high frequencies of the *t* allele have also been

reported in different other castes of Bihar (Tripathy, 1969; Dash Sharma, 1976; Pandey et al., 1993).

The incidence of colourblindness was highest among the Oraon (4.27%), followed by Kharwar (3.51%), Muslim (3.23%), while it was lowest among Kayastha (0.88%) (Table 1). Singh and Sinha (1988) reported an incidence of 2.2% in the Chamar and 2.7% in Mushar of Bhagalpur, Bihar.

From the foregoing discussion it is clear that genetic heterozygosity exists among the six population groups investigated here from North Bihar. However assessment of this varia-

Table 2: Allelic frequencies of different genetic markers in six population groups of North Bihar

Population group	ABO blood groups			Rh(D)		PTC tasting ability		Red-green colour blindness	
	O	A	B	D	d	T	t	C	c
Brahmin	0.577	0.239	0.184	0.731	0.269	0.463 ±.035	0.537 ±.035	0.861 ±.024	0.139 ±.024
Mushar	0.563	0.240	0.197	0.843	0.157	0.498 ±.028	0.502 ±.028	0.834 ±.021	0.166 ±.021
Kayastha	0.601	0.191	0.207	0.771	0.229	0.500 ±.033	0.500 ±.033	0.906 ±.019	0.094 ±.019
Oraon	0.502	0.323	0.175	1.000	0.000	0.566 ±.046	0.434 ±.046	0.793 ±.037	0.207 ±.037
Kharwar	0.390	0.148	0.459	0.758	0.242	0.351 ±.037	0.649 ±.037	0.813 ±.030	0.187 ±.030
Muslim	0.595	0.178	0.227	0.765	0.235	0.525 ±.034	0.475 ±.034	0.820 ±.026	0.180 ±.026

Table 3 : Estimates of Gene diversity among six population groups of North Bihar

Locus	H_T	H_S	D_{ST}	D_{ST}
ABO	0.5989	0.5810	0.0170	0.0285
Rh	0.3870	0.3818	0.0051	0.0133
PTC tasting ability	0.5000	4906	0.0094	0.0089
Colour blindness	0.2688	0.2664	0.0024	0.0089
Mean	0.4380	0.4299	0.0085	0.0174

tion can be obtained by applying some statistical measures such as heterozygosity and genetic distance, for which further analysis have been performed.

Heterozygosity

The genetic variation within a population is usually measured by the average heterozygosity per locus (Nei and Roychoudhury, 1974). 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 :

$$H_T = H_S + D_{ST}$$

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

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

The gene diversity analysis among the six population groups is shown in the table 3. The total gene diversity (H_T) among the six population groups (0.4380) has been analysed into two components *i.e.* intra-population gene diversity ($H_S = 0.4299$) and inter-population gene diversity ($D_{ST} = 0.0085$). This shows that gene diversity between population groups is much lower than the gene diversity within the population groups.

In other words, only a small fraction of total gene diversity is due to the differences between the populations groups, while a large part of this diversity is attributable to individual variation within the population groups. This suggests that the present population groups are at an early stage of gene differentiation.

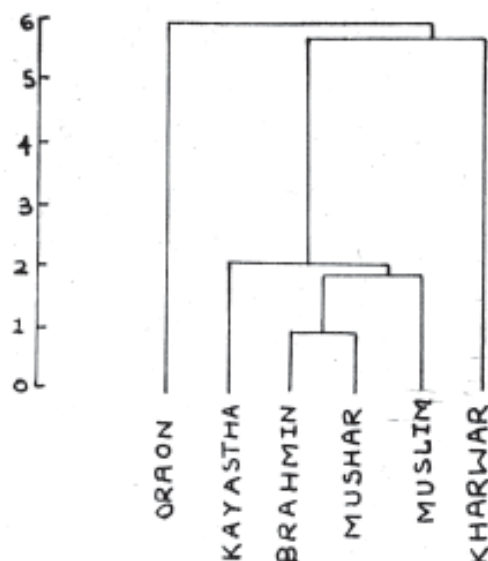


Fig. 1. Genetic distances among six endogamous populations of North Bihar

Table 4: Estimates of Nei's measures of genetic distance (D) among six population groups of North Bihar

Population group	Mushar	Kayastha	Oraon	Kharwar	Muslim
Brahmin	0.0009	0.0020	0.0102	0.0415	0.0057
Mushar	—	0.0027	0.0059	0.0419	0.0018
Kayastha	—	—	0.0140	0.0468	0.0032
Oraon	—	—	—	0.0551	0.0097
Kharwar	—	—	—	—	0.0056
Muslim	—	—	—	—	—

The co-efficient of gene differentiation (G_{ST}) values among the six population groups of Bihar under the study are comparatively high at both the blood group loci. The average G_{ST} value is 0.0067.

Genetic Distance

The genetic distance among the six population groups are shown in the table 4 and in the form of a dendrogram in figure 1. From the dendrogram it is quite clear that :

a) Oraon and Kharwar differentiate from the remaining four groups of early stages.

b) The Kayastha also separate from the common cluster of the four groups at an early stage.

c) The Brahmin, Mushar and Muslim form one cluster, separate.

There are no indications of genetic contact among Brahmin, Mushar and Muslims. Hence one can suppose that their presence in one cluster might either be due to analogous genetic

differentiation process in the past or even by chance.

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