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GENETIC DIFFERENTIATION AMONG ORAON AND MUNDA POPULATIONS OF PURNIA DISTRICT, BIHAR (INDIA)

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ABSTRACT : A genetic study was carried out in Oraons and Mundas of Purnia district (which are migrant of Chotanagpur plateau) using four genetic loci (ABO blood groups, Rh blood group, PTC taste ability and colour blindness). Oraons manifested highest frequency of blood group A while Mundas manifested highest frequency of blood group B. The frequency of blood group AB was lowest both in Oraons and Mundas. The distribution of PTC among the population under present investigation was bimodal. The anti mode in them lies between solution number 5 and 6. In Oraons the frequency of non taster gene was less (28.7%) than that of Mundas. The frequency of Rh negative in Oraons and Mundas were found to be 5.94% and 4.45% respectively which is as per other Scheduled Tribes in India. The frequency of colour blindness was 4.45% in Oraons and 5.44% in Mundas. The genetic distance study with other local populations shows that Oraons are more close to Brahmins, while Mundas are more close to Santhal and Dhobi, which clearly indicates gene flow. Gene diversity analysis revealed that these populations are at an early stage of micro genetic differentiation.

Key words : *Tribal Population, Gene diversity, Genetic distance, Heterozygosity, Endogamous, Purnia district.*

INTRODUCTION

In last decades, many genetic studies have been carried out in Indian population groups. These studies showed a considerable genetic variability among them. One of the Indian regions for which up to now only a few genetic data are available in Bihar, particularly, north Bihar which is inhibited by many populations of different ethnic and linguistic characteristics. Tribal populations of North Bihar are migrants of Chotanagpur plateau. No systemic research work has been done on these tribes with reference to their genetical aspects. Keeping this aim in mind the present work was undertaken which deals with the genetical status of two migrant tribal populations - Oraons and Mundas based on four loci -

1. Blood group,
2. Rh Blood group
3. PTC taste ability
4. Colourblindness

The genetic affinities of these tribal populations with other local populations have been also computed.

MATERIAL AND METHODS

For the present work two tribal populations namely Oraons and Mundas were selected. These populations were selected as they are migrants of Chotanagpur plateau and are the major tribal population of the district. The data were collected by door to door survey method from the randomly selected sample from the population living in different villages of Purnia East, Dhamdaha and Amour blocks of Purnia district. The subjects were adults (more than 18 years of age). The frequency of four Mendelian traits (Blood group, Rh Blood group, PTC taste ability and Red-Green colourblindness) with monogenetic inheritance were estimated. The standard methodology was followed for the estimation of specific phenotypes as given below :

a. ABO blood group by slide agglutination method using antisera A and B.
b. Rh blood group - by slide agglutination method using antisera Rh(D).
c. PTC taste ability - by using method of grade dilution as suggested by Harris and Kalmus (1949a)
d. Red-Green colourblindness using Ishihara colour plates.

The frequency of allele was calculated according to Mourant *et al.* (1976) and genetic distance was calculated according to Nei's (1973a,b)

RESULTS AND DISCUSSION

ABO blood groups : In the present investigation blood group A was found highest in the Oraons and blood group B in the Mundas of the Purnia district. The frequency of blood group AB was found lowest in both Oraons and Mundas (10.9% and 11.9% respectively). The allele frequencies of A, B and O in the two groups were as follows : 0.21, 0.34 and 0.43 (in Mundas) and 0.26, 0.23 and 0.50 (in Oraons). Thus there is much variation in the frequency of blood O in both the groups.

However, several workers have reported predominance of blood group B in Oraons and A in Mundas of Chotanagpur plateau (Sarkar,1949; Kirk *et al.*,1962 and Sharma,1976). Bhatia *et al.* (1986) have reported predominance of blood group A in the Oraons of Ambikapur (M.P.). Piplai *et al.* (1985) have reported pre-dominance of

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blood group B in the migrant Oraons of Jalpaiguri district of West Bengal. Lehman and Ikin (1953) has also reported predominance of blood group B in the immigrant labourers of Andman (South).

It has been reported that there is a considerable relation between geography and the distribution of blood group. Blood groups are affected by environmental selection, temporal variation and geographical isolation (Das,1991 and Pandey *et al.*,1993,1995). Oraons and Mundas have migrated to Purnia from Chotanagpur plateau nearly 250 years ago. It might be possible that the frequency of blood group A in Oraons and B in the Mundas of Purnia is due to geographical isolation. Bittles and Smith (1991) have reported changes in A and O allele frequencies against distance from North to South commencing from the north and most Peninsula (Bangore). They further reported considerable correlation between genetic and geographic distance matrices. Purnia district is located at a distance of 350 km in the North of Chotanagpur plateau. Thus variation in the blood groups in the Oraons and Mundas of present investigation might be due to the geographical distance. Sharma *et al.* (1985) have reported higher frequency of blood group O while in other studies high incidence of blood group B has been reported in Kond tribes of Orissa. They pointed out that these minor variations are evidently due to geographical isolation, despite common ancestry which supports present finding.

It has been reported that identical gene frequencies of small isolation population become different with the time because of genetic drift (Wright,1934). According to him smaller the population, the greater will be importance of genetic drift. With a change in environmental conditions, the small population may develop superior pool of genes which would give it an advantage over its ancestors. Thus the chance of variation in gene quantity brought through genetic drift can have evolutionary significance. Oraons and Mundas are migrants and are present in small population. Further their mating take place in the same geographical area of Purnia district. They are strictly endogamous. Thus it can be concluded that the higher frequencies of blood group A in the Oraons and B in the Mundas of the present investigation might be due to

Table. 1 Frequency of ABO blood group, Rh, PTC Non-taster, Red-green colour blindness in 10 populations of Purnia district.

		ABO Blood Group						
Caste Tribes	**N**	**A**	**B**	**AB**	**O**	**Rh Negative**	**P.T.C. Non-taster**	**Red-Green Colour blindness**
Bania	190	36	70	28	56	30	58	49
		18.9%	36.8%	14.7%	29.5%	1.6%	30.5%	2.6%
Chamar	368	80	150	15	123	1	69	8
		21.7%	40.8%	4.1%	33.4%	0.3%	18.7%	2.2%
Muslim	34	50	82	30	142	15	98	11
		16.4%	27%	9.8%	46.7%	4.9%	32.2%	3.6%
Mushar	325	103	81	35	106	8	83	19
		31.69%	24.92%	10.76%	32.6%	2.46%	25.33%	5.86%
Tharu	190	50	37	15	88	0	112	5
		26.49%	19.1%	7.95%	46.36%	00%	58.94%	2.65%
Santal	350	96	141	45	68	2	118	7
		27.42%	40.32%	12.9%	19.35%	0.65%	33.87%	1.94%
Dhobi	175	55	69	15	36	10	83	10
		31.38%	39.33%	8.37%	20.92%	5.86%	47.7%	5.86%
Munda	202	52	90	24	36	9	68	11
		25.7%	44.5%	11.9%	17.9%	4.45%	33.6%	5.44%
Oraon	202	70	60	22	50	12	58	9
		34.6%	29.7%	10.9%	24.8%	5.94%	28.7%	4.45%
Brahmin	208	72	54	15	67	15	60	4
		34.6%	26%	7.2%	32.2%	7.2%	28.8%	1.9%

Table. 2 Allele frequencies in various caste and tribal populations of Purnia district Bihar.

Allele	**Bania**	**Chamar**	**Santal**	**Musahar**	**Tharu**	**Muslim**	**Munda**	**Oraon**	**Dhobi**	**Brahmin**
ABO*A	0.1801	0.1426	0.2311	0.2389	0.1858	0.1378	0.2164	0.2651	0.2358	0.2404
ABO*B	0.2947	0.2643	0.3208	0.1960	0.1454	0.1995	0.3498	0.2319	0.2915	0.1849
ABO*O	0.5251	0.5931	0.4480	0.5650	0.6688	0.6627	0.4338	0.5031	0.4727	0.5747
RH*D	0.6026	0.8271	0.9216	0.8431	1.000	0.7779	0.7889	0.7563	0.7610	0.7315
RH*d	0.3974	0.1729	0.0784	0.1569	0.000	0.2221	0.2111	0.2437	0.2390	0.2685
PTC*T	0.4475	0.5670	0.4194	0.4977	0.3593	0.4322	0.4642	0.4782	0.3113	0.4629
PTC*t	0.5525	0.4330	0.5806	0.5023	0.6407	0.5678	0.5358	0.5218	0.6887	0.5371
CB*N	0.9526	0.9783	0.9829	0.9415	0.9737	0.9638	0.9455	0.9554	0.9429	0.9808
CB*D	0.0474	0.0217	0.0171	0.0585	0.0263	0.0362	0.0545	0.0446	0.0571	0.0192

chance variation of gene quantity brought through genetic drift, which might be selective advantage in their present environmental conditions. Such type of variations in blood groups has been found in the Dunkers of Eastern of Pennsylvania who had emigrated over 200 years ago from West Germany (Glass,1953).

Rh (D) blood group : Among Indian populations the frequency of allele D is average around 80.3% (Bhasin *et al.*, 1994). It is highest among the scheduled tribe (86.03%) as compared to other ethnic groups. In the present population of Purnia district Rh+ is maximum in Tharu (100%) and minimum in Brahmin (92.8%). In the present investigation, the frequency of Rh negative in Oraoans and Mundas were 5.94% and 4.45% (Table.1 and Fig.1) respectively which was per the other Scheduled Tribes in India.

PTC taste ability : The frequency of allele T among Indian population is 0.457 (varies from 0.108 among Mundas of Ranchi, Bihar to 0.912 in scheduled caste of Andhra Pradesh) which is little low as compared to European but similar to that of South-West Asian populations. The frequency is highest from the island zone as compared to rest of the zones of India-North (0.488), South (0.483), Central (0.389) and West (0.369) India. Among the populations from Himalayan region mostly with Mongoloid affinities, the frequency is highest (0.533) as compared to North Himalayan regions (0.426). The frequency of allele T is low in scheduled tribe (0.451) as compared to other groups with minor differences. It appears that populations with Mongoloid affinities possess high frequency of faster allele T and quite high frequency are observed among the Mongoloids of Asia as compared to Indian tribal groups among whom high frequency of the non taster allele (t) are found. The frequency of allele T is high from island natural region (9.547) and also from the Himalayan mountain complex region (0.545) from where the frequency starts decreasing towards peninsular plateau. From the different climatic regions the frequencies are high in polar, cold, humid and all monsoon type regions and are lowest in tropical Savannah type region (0.377). From East India, the frequency of allele T is quite low from the states of Bihar (0.298, varies from o.108 to 0.490) and Orissa (0.1324, ranges from 0.268to 0.571) from where the frequencies are low among scheduled tribes as compared to rest of the ethnic groups, whereas from the states of Nagaland, Tripura, Meghalaya, Sikkim and Darjeeling district of West Bengal among the populations with Mongoloid affinities the frequencies are quite high (0.702, 0.597, 0.584, 0.694 and about 0.60 respectively). In the present study the frequency of T allele were ranges from 0.47 in Oraons and 0.46 in Mundas (Table.2), which is as per frequency of T allele in Indian population.

Similar high frequencies are observed from Western Himalayan region among populations with Mongoloid affinities from the states of Jammu and Kashmir (Ladakh 0.762). Himachal Pradesh (Gurkhas 0.615, Lahaulies 0.643, Spitians 0.654, Kinnaura 0.606, Ships 0.662, Bodhs 0.656, Savangala 0.605) and Uttar Pradesh Central Himalayan region (different groups of Bhotias about 0.60, Gurang 0.656 among others).

The frequencies of allele T is also quite high among Neware; Sherpas and Tamang combined (0.523, 0.533 and 0.719 respectively, of Nepal and Tibetan (varies from 0.616 to 0.672). the frequency of allele T is low among scheduled tribes from Central India and it is almost similar among all the tribes except Dhurva, in which it is quite low (0.180). the frequency is quite high among different ethnic groups reported from South India (0.483, varies from 0.184 to 0.912) and it is highest among the population groups with Mongoloid affinities from the Himalayan region followed by South Indians.

From West India the frequency of allele T is observed lowest (0.369, varies from 0.249 to 0.536) as compared to other zones and the frequencies are almost similar in both the states of Gujarat (0.368) and Maharashtra (0.371). Among the scheduled castes and scheduled tribes of West India (0.302 and 0.331 respectively) the frequencies are lowest as compared to rest of the groups.

Colourblindness : The frequency of colourblind males among Indian population on average is 3.6% which varies from complete absence to 23.1% (Bhasin *et al.*,1994). In the present populations of Purnia district the incidence of colour blindness ranges from 1.9% to 5.86%. In Oraons and in Munda it was 4.45% and 5.44% respectively (Table.1) which is as for Indian population average of colourblindness.

Bhasin *et al.* (1994) categorized the study available on the population of India and concluded that the difference in incidence of colourblindness in primitive cultures (Scheduled Tribes) is low as compared to castes, scheduled castes and communities.

Genetic diversity : The genetic variation with in a population is usually measured by the average heterozygosity per locus (Nei & RoyChoudhury,1974a,b). By taking the average gene frequencies of all sub- population as representative of the total population (HT) (Table.4) has been calculated as follows :

$$HT = HS + DST$$

Where, HS is the average gene diversity within the sub- population and DST is the average gene diversity between the sub- populations (Nei,1973a,b). The co-efficient of gene differentiation relative to the total population has been calculated as follows :

$$GST = DST/HT$$

In the present study the total gene diversity (HT= 1.484954) among the ten population groups have been analyzed into two components *i.e.*, intra-population gene diversity (HS=1.442479) and inter population gene diversity (DST = 0.042476).This showed that gene diversity between population groups was lower than the gene diversity within the population groups. In the other words only a small fraction of the total gene diversity was due to individual variations within the population groups. Furthermore, it also suggests that, the present population groups were at an early stage of genetic differentiation.

Despite the fact that the present study is based on only four common loci, the results indicated a clear possibility of identifying population structure variables that influence the genetic diversity at the general level. In the case of present study this diversity is related to ethno-historical migration of populations. In case of scheduled caste groups (Chamar and Mushars) endogamy and isolation are possible factors because of dearth of demographic information on population structure variable in these populations. It is difficult to examine the assumptions of Harpending and Ward Model.

Genetic distance : The genetic distance of Oraons and Mundas with other local populations is shown in the Fig.1 and Table.3. From the dendrogram, it is quite clear that : **A)** Oraon, Brahmin, Santhal and Munda separate from the main stock at an early stage of micro-genetic differentiation. **B)** Tharu, Bania and Chamar form one cluster, Muslim, Mushar, Oraon and Brahmin also form one cluster. Likewise, Dhobi, Santhal and Munda also form one cluster. **C)** Oraon and Brahmin manifest lowest genetic distance while Tharu and Munda manifest highest genetic distance. Thus it may be concluded that all these populations have arisen through a common ancestor and change gene frequency among them is due to evolutionary process like Selection, Mutation, Migration, Genetic-drift and Temporal variation. However, these populations retain their separate entity by practicing endogamy. Gene diversity analysis revealed that gene populations are at an early stage of micro-genetic differentiation.

Table. 3 Nei's genetic Distance (D) matrix based on study on the four loci.

Allele	Bania	Chamar	Santal	Musahar	Tharu	Muslim	Munda	Oraon	Dhobi	Brahmin
Bania	0	0.026447	0.041403	0.027346	0.065366	0.017455	0.017369	0.012676	0.019273	0.010565
Chamar		0	0.017675	0.005224	0.028191	0.009748	0.012056	0.009385	0.032681	0.010726
Santal			0	0.010598	0.016587	0.021221	0.007123	0.013432	0.014589	0.020846
Mushar				0	0.015968	0.007353	0.009753	0.004147	0.020198	0.006064
Tharu					0	0.0182	0.03158	0.0300001	0.029433	0.029084
Muslim						0	0.016353	0.009064	0.016604	0.004794
Munda							0	0.004919	0.010997	0.011493
Oraon								0	0.012609	0.002123
Dhobi									0	0.014683
Brahmin										0

Table. 4 Nei's gen diversity analysis in caste and tribal population of Purnia distric, Bihar (India)

Allele	Gene diversity in total population (H_t)	Inter population gene diversity (H_s)	Intra population gene diversity (D_{st})	Coefficients of gene differentiation (G^{st})
ABO	0.598843	0.586956	0.011887	0.01985
Rh(D)	0.318798	0.297784	0.021014	0.065916
PTC	0.493721	0.484624	0.009098	0.018426
CB	0.073592	0.073115	0.0004777	0.006481
Mean				0.027668

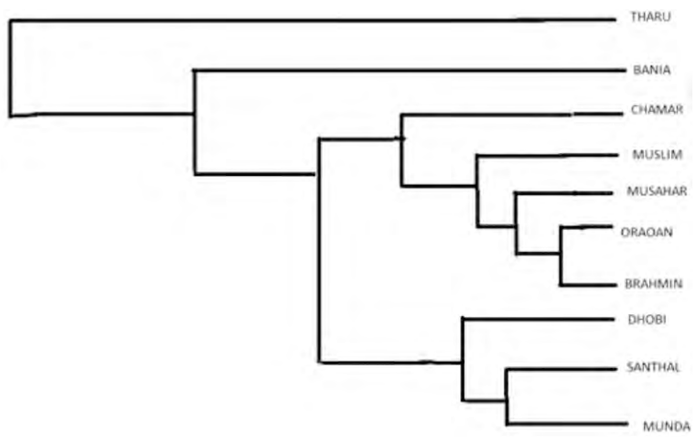

Fig. 1 Showing the relationship between ten endogamous population of Purnia district Bihar.

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