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Genetic Diversity Among the Six Mongoloid Populations of North Eastern India

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ABSTRACT A study of five genetic markers, namely, A_1A_2BO, Rhesus, MN, haemoglobin and G-6-PD has been carried out in the six Mongoloid populations of North Eastern India. The study reveals genetic heterogeneity between the populations of Assam (Ahoms and Kacharis) and Arunachal Pradesh (Nishis, Apatanis and Adis) and Nagaland (Nagas). Genetic proximity between the populations of Arunachal Pradesh and Nagaland suggests their common ethnic origin. However, the Ahoms and Kacharis exhibit the admixture of gene pools. High prevalence of G-6-PD deficiency and abnormal haemoglobin E genes probably provide some selective advantage against the malaria endemic bioenvironment in the North Eastern region of India.

Polymorphisms of many genetic traits are now considered to be useful tools for the differentiation of human populations. Unlike morphological polymorphisms, serological and biochemical polymorphisms are independent of the influences of environment. Genetic polymorphism is useful to trace ancestory, admixture and affinity of different groups of people. This is done by using gene frequency data of a number of genetic loci. Evolutionary forces like selection, 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.

The North-Eastern region of India presents ample scope for the genetic studies of human populations. There are a large number of tribal groups in the region which are genetically still virgin and present fascinating features of biological importance. They mostly belong to Mongoloid ethnic stock and practise endogamy. The present study deals with the genetic variations and similarities with respect to five genetic loci among the six endogamous populations of North-Eastern India. The study is focussed on understanding the genetic interrelationship between these population groups on the basis of gene frequency distribution.

MATERIAL AND METHODS

Intravenous about 2ml. of blood was collected from each subject in ethylene diamine tetra-acetic acid (EDTA) coated vials from unrelated healthy individuals. Blood samples were collected from different places namely, Itanagar (Arunachal Pradesh) for Nishis, Adis and Apatanis, Dibrugarh (Assam) for Ahoms and Kacharis, and Kohima (Nagaland) for Nagas in North-Eastern India.

Tests for A_1A_2BO, Rhesus and MN blood groups were performed using control for each group cells by the glass concavity technique (Bryant, 1982). The glucose-6-phosphate dehydrogenase (G-6-PD) deficiency was studied by fluorescent spot screening test (Dacie and Lewis, 1984) and subsequently confirming for hemizygous females by the methaemoglobin reduction test (WHO Report, 1967). The abnormal haemoglobin was detected by performing the sickling test and electrophoresis on cellulose acetate strips following the standard techniques as described by Dacie and Lewis (1984).

RESULTS AND DISCUSSION

From the gene frequency distribution of A_1A_2 BO blood groups, it is apparent that A gene predominates over B in all the six populations (Table 2) showing thereby an affinity with the Mongo-

loid origin. The subtype A_2 of A blood group occurs in the Indian populations with a lower frequency than in European populations. The frequency of A_2 gene does not generally exceed 2.5% (Roychoudhury, 1983). However, the present study shows this variation from O to 3.7% (Table 2), A_2 gene being completely absent in Apatani and Naga populations.

In general, higher incidence of B than A gene is a characteristic of the people of Indian sub-

Table 1: Distribution of serogenetic markers in the six Mongoloid populations of North Eastern India

Genetic Markers	*Nishi*		*Adi*		*Apatani*		*Naga*		*Ahom*		*Kachari*	
	No.	*%*	*No.*	*%*	*No.*	*%*	*No.*	*%*	*No.*	*%*	*No.*	*%*
A_1A_2BO Blood Groups												
O	54	45.0	12	33.3	12	40.0	19	43.2	44	35.2	22	27.1
A_1	42	35.0	13	36.1	14	46.7	21	47.7	33	26.4	32	39.5
A_2	0	0.0	1	2.8	0	0.0	0	0.0	3	2.4	2	2.5
B	18	15.0	9	25.0	1	3.3	4	9.1	31	24.8	18	22.2
A_1B	5	4.2	0	0.0	3	10.0	0	0.0	13	10.4	5	6.2
A_2B	1	0.8	1	2.8	0	0.0	0	0.0	1	0.8	2	2.5
Total	120	100.0	36	100.0	30	100.0	44	100.0	125	100.0	81	100.0
Rhesus Blood Groups												
CCDee	64	53.3	24	66.7	12	40.0	10	22.7	75	59.5	50	61.8
CCddee	0	0.0	0	0.0	0	0.0	2	4.5	0	0.0	0	0.0
CcDEE	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0
CcDEe	1	0.8	0	0.0	0	0.0	2	4.5	5	4.0	4	4.9
CcDee	35	29.2	7	19.4	6	20.0	30	68.2	36	28.6	20	24.7
Ccddee	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.2
ccDEE	1	0.8	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0
ccDEe	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0
ccDee	17	14.2	4	11.1	12	40.0	0	0.0	6	4.7	6	7.4
ccddee	2	1.7	1	2.8	0	0.0	0	0.0	1	0.8	0	0.0
Total	120	100.0	36	100.0	30	100.0	44	99.9	126	100.0	81	100.0
MN Blood Groups												
MM	82	68.3	23	63.9	18	60.0	-	-	39	42.8	23	38.3
MN	29	24.2	9	25.0	10	33.3	-	-	45	49.5	33	55.0
NN	9	7.5	4	11.1	2	6.7	-	-	7	7.7	4	6.7
Total	120	100.0	36	100.0	30	100.0	-	-	91	100.0	60	100.0
G-6-PD Deficiency												
Gd^+	100	84.0	29	80.6	25	83.3	40	90.9	115	91.3	72	90.0
Gd^-	19	16.0	7	19.4	5	16.7	4	9.1	11	8.7	8	10.0
Total	119	100.0	36	100.0	30	100.0	44	100.0	126	100.0	80	100.0
Abnormal Haemoglobin (Hb)												
AA	103	88.0	31	88.6	26	89.7	41	93.2	60	48.0	14	17.3
AE	14	12.0	4	11.4	3	10.3	3	6.8	52	41.6	42	51.8
EE	0	0.0	0	0.0	0	0.0	0	0.0	12	9.6	25	30.9
AS	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0
Total	117	100.0	35	100.0	29	100.0	44	100.0	125	100.0	81	100.0

Table 2: Gene frequency distribution in the different population groups

Genetic Markers Gene	*Nishi*	*Adi*	*Apatani*	*Naga*	*Ahom*	*Kachari*
A_1A_2BO Blood Groups:						
A_1	0.219	0.204	0.335	0.280	0.203	0.265
A_2	0.006	0.037	0.000	0.000	0.021	0.035
B	0.106	0.154	0.067	0.047	0.198	0.170
O	0.669	0.605	0.598	0.673	0.578	0.530
Rhesus						
CDE	0.000	0.000	0.000	0.000	0.000	0.012
CDe	0.683	0.764	0.500	0.591	0.762	0.760
Cde	0.000	0.000	0.000	0.000	0.000	0.012
cDE	0.012	0.000	0.000	0.022	0.040	0.000
cDe	0.206	0.130	0.500	0.387	0.123	0.204
cde	0.099	0.106	0.000	0.000	0.075	0.012
MN						
M	0.804	0.764	0.767	-	0.676	0.658
N	0.196	0.236	0.233	-	0.324	0.342
G-6-PD						
Gd^+	0.840	0.806	0.833	0.909	0.913	0.900
Gd^-	0.160	0.194	0.167	0.091	0.087	0.100
Abnormal Hemoglobin (Hb)						
A	0.940	0.943	0.948	0.965	0.688	0.432
E	0.060	0.057	0.052	0.035	0.304	0.568
S	0.000	0.000	0.000	0.000	0.008	0.000

continent (Mourant et al., 1976; Roychoudhury, 1983), but the opposite is also true for most of the tribal populations of North-Eastern India. Similarly, the absence of A_2 gene among the two tribal populations (Apatani and Naga) of North-Eastern India is in conformity with the characteristic of Mongoloid populations. Thus, the Indian populations show regional variations in the gene frequencies of A_1A_2BO blood groups as a result of probably eco-biological adaptation (Balgir and Sharma, 1988a) and the higher incidence of A than B gene among the North-East Indian populations is attributed to the evolutionary phenomenon of natural selection.

The range of variation for Rh-negative (d) gene is 15 to 30% in majority of the Indian populations as against 35 to 45% in Europeans and 0 to 10% in Mongoloid populations (Roychoudhury, 1983). The frequency of cde gene complex in the present study (Table 2) although shows the Mongoloid affinities, but it is far below the range earmarked for the Indian populations. The high frequency of Cde gene complex and low of cde chromosome in the North-Eastern populations of India (Table 2) is in agreement with the Mongoloid trends of the populations. However, these populations present a local pattern for the dispersal of Rhesus gene complex.

While considering MN blood group locus, it has been observed that the frequency of M gene is generally higher in India than in Europe. The populations of North-Eastern India, showing resemblance with the Mongoloid features, exhibit a higher frequency of M gene and the present study testifies this criteria.

The study of the enzyme G-6-PD, an X-linked genetic marker is interesting one, the deficiency of which shows considerable ethnic and regional variations in India (Balgir, 1989). The deficiency of this enzyme has been reported to be the highest (27%) among the Angami Nagas (Seth and Seth, 1971) in India. Elevated frequencies of this gene in the present populations (Table 2) especially belonging to Arunachal Pradesh (Adi, Apatani and Nishi) indicate the wide spread of this defective gene in the populations of North-Eastern India.

Abnormal haemoglobins in red blood cells may be used as genetic markers for differentiating human populations. Abnormal haemoglobins E and S have been detected in the populations under study of North-Eastern India. The gene frequency of the abnormal haemoglobin E is the highest among the Kacharis (56.8%), followed by Ahoms (30.4%), Nishis (6.0%), Adis (5.7%), Apatanis (5.2%) and Nagas (3.5%) in the decreasing order. High frequency of haemoglobin E gene has also been reported earlier by Deka et al. (1988) among the Kacharis. A case of sickle cell trait has also been detected among the Ahoms for the first time.

The intrusion of various racial and tribal elements from different corners complicated the study of origin, migration and admixture of the people in the North-Eastern region of India. Historical record in this regard is either negligible, rudimentary or fragmentary and the true picture of the origin and migration of the people is still obscure. Based on gene frequency data, an attempt has been made for population synthesis.

The over all evaluation of gene frequency distribution reveals that the Nishis, Adis, Apatanis and the Nagas on the one hand, and Ahoms and Kacharis on the other hand, do not exhibit intra-population genetic variations. They show close genetic proximity with each other. This situation probably is due to either admixture of the gene pools or being belonging to a common ethnic origin and forming fission groups due to intra-group feuds and wars and have emerged as separate entities. However, the Ahoms and Kacharis do not resemble with the Nishis, Adis, Apatanis and Nagas in the over all gene frequency distribution.

The sickle cell gene in the autochthonous inhabitants of Assam is non-existent (Balgir and Sharma, 1988b) and only prevalent in the migrated tea garden populations which have orginated from Orissa, Bihar and Madhya Pradesh. The detection of a sickle cell trait among the Ahoms indicates that the gene flow from the tea garden tribals has started penetrating into the surrounding local populations.

The linkage or association of genetic markers with a disease is a fascinating enquiry. Elevated frequency of polymorphic traits in a population amounts to maintenance of natural balance against some prevalent diseases. The high prevalence of G-6-PD deficiency and abnormal haemoglobin E genes in the populations under study suggests the operation of protection mechanism against the malaria infection. The North-Eastern region as a whole is malaria endemic, especially for forest malaria (prevalent in dense forests) and *Plasmodium falciparum* infection. The high prevalence of these genetic markers gives some sort of selective advantage to the propositi in the North-Eastern region of India.

The North-Eastern region of India being malaria endemic (Dutta et al., 1989), the anti-malarial drugs such as primaquine, sulfapyridine, etc. are frequently administered to the patients for treatment. These drugs produce from mild to severe haemolysis of the red blood cells of G-6-PD deficient patients, resulting in severe anaemia. Moreover, the prevalence of abnormal haemoglobins in the population adversely affect their normal physiology and daily chores. In order to reduce the morbidity and mortality as a result of increased homozygosity of these traits in the population, rendering of genetic counselling is one of the effective measures for the welfare of the society at large. It is, therefore, suggested to create and provide special facilities for genetic counselling in the high risk localities to the affected people.

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