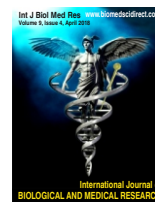




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Original Article

Genetic Characterization on the Rengma Naga, Kohima District, Nagaland

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ABSTRACT

In the present study an attempt was made to study the distribution of ABO, Rh (D), PTC taste sensitivity and colour blindness of the Rengma tribes of Nagaland, India and to understand the population affinities in relation to each other. In the present study blood groupings were done after collection of blood samples and statistical analyses were made. Blood group A (0.4056) shows the highest frequency followed by O (0.4137), B (0.1124) and AB (0.0683) among the Rengma Naga. Allele Rh (d) and Colour blindness was found to be less frequent among Rengma Naga. Whereas, the allele frequencies for PTC taster and non-taster were found to be 0.3475 & 0.6525 respectively.

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1. Introduction

Understanding the genetic structure of any Mendelian human population group is one of the prime concerns of the physical anthropologist, to infer intra and inter genetic variations, through certain genetic traits. Those traits which are less subjected by the environment influences are considered as the obvious choice of such populations' genetic study. Out of such traits the ABO, PTC and Colour blindness is considered to be the bio-chemical tool in the study of human diversity, which is easy to detect and informative at the same time.

The ABO blood groups are the most significant blood factors in clinical transfusions and understanding the importance of blood group is not limited to clinical application alone. The ABO blood groups is also providing to be valuable asset for determining migration pattern, origin and all human population shares the same blood group system, differing only in the frequencies of specific types. According to Khan. et.al. 2004, the blood group frequency distribution is multipurpose and is not only crucial in the medical field, but can also be utilized in genetic research, anthropology and ancestral relation of human.

Anthropological studies have generated numerous biological data among Indian populations and can be used to understand the peopling of India. To the best of my knowledge limited studies on traditional genetic markers has been reported among the Naga Populations. Thus in this study a concerned attempt will be made to elucidate and highlight the importance of bio-anthropological study for better understanding on the patterning of human populations. The present study aims to provide data for genetic markers (blood groups, Rh factor, Colour blindness and tasting ability) of the Rengma Naga of Nagaland and compare them with some other Mongoloid affinities of the region.

According to J.P Mills (1982) the Rengma Naga Point towards Khezhakeno as the place of dispersal along with the Lotha, Angami, Chakhesang and Sema to their present homeland. They are one of the heterogeneous tribes living in the state of Nagaland and Assam with a total population of over 61,000. The headquarter of the people is Tseminyu. They are known and admired by their neighboring tribes as gentle, generosity and humble people. Like the other Naga tribes, Rengma people are considered to have descended from the Mongoloid racial stock and they speak the Sino-Tibetan, Angami-Pochuri and pochuri-Rengma languages, which fall under the Tibeto-Burman language. They practice both Jhum and terrace cultivation. The Main staple food of the people is rice. The present study was carried out among the Rengma inhabiting in Nagaland of different villages under Kohima District.

Materials and Methods

A total of 249 Individuals belonging to the people of Rengma Naga tribe inhabiting presently under Tseminyu of Kohima District were selected for study. They included 125 females and 124 males between the age group of 15-25 years. An effort was made to collect data from biological unrelated individuals. The fieldwork was carried in the month of May in 2017. The blood group analysis was done following the standard slide technique by Lawler and Lawler (1951) and Bhatia (1977). The serial dilution method suggested by Harris and Kalmus (1949) was followed for collecting the data on PTC taste sensitivity and Ishihara chart (1959) was used to collect data on colour blindness.

Results and Discussions

The result of analysis shows the blood group A (44%) is the highest followed by blood group O (36.8%), B (12.8%) and AB (6.4%) among the females. Whereas, blood group O (44.35%) is the highest followed by A (38.71%), B (9.68%) and AB (7.26%) among

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the males as seen in Table 1. The difference in A, B, O and AB blood group prevalence between males and females was found to be statistically insignificant ($\chi^2= 1.89$, d.f 3, $p>0.05$) The allelic frequencies of p, q and r are calculated as 0.2785, 0.0942, and 0.6273 and on applying the test of goodness of fit for Hardy Weinberg Law indicates that the present population is in genetic equilibrium from the genetic point of view ($\chi^2=2.07$, d.f=1, $p>0.05$).

The distribution of Rh (D) blood group in females and males is seen in table 2. As the Rh (D) antigen is concerned, no individual was found to be Rh (d) negative in the present study. Thus, the outcome of the present study indicates that the recessive allele for the D antigen is very rare in the Rengma population and when the recorded values are compared to global data presented by Mourant et al. (1976) and Khattak (2008), the Rh factor data from this study follows the same pattern as found in all the populations till surveyed and has always been reported with a minor Rh(d) type representation which ranges from 0% to 17%. This population include American Indians, Arabs, Bengalis, Africans, Chinese, Eskimos, Mexicans, and Americans. It is also similar to the studies that have been carried out among the Lotha (2.44%) and Kozami (1%) Nagas and other Mongoloid population of North-East India, where the occurrence is absent or if, present in a very low frequency.

The allele frequencies of PTC taste sensitivity for taster (T) and the non-taster (t) allele was calculated as 0.3475 and 0.6525 respectively as seen in Table 3. However, it is found to be more than 3 in females and in total sample. This indicates that the distribution of taster and non-taster is statistically bimodal. The difference between the sexes is found to be statistically not significant (student t-test = 0.133, d.f=247, $p>0.05$). On comparison of PTC taste sensitivity with other Naga populations the Rengma Naga differs from the Kozami, Lotha and Angami ($\chi^2=4.2956$, 22.5709, 61.0145). The present colour blindness test (Table 4) among the male subjects may be associated with the theoretical exception, that the frequency of colour blindness occurrence is lower among the females of a population due to the fact that colour blindness is believed to be an X-linked trait and is similar with the other studied population of the Nagas and other Mongoloid populations.

The present finding of ABO on comparison with the other studied Naga populations show a similarity with the Konyak Naga (British research Association) ($\chi^2=1.8289$) despite the close proximal geographical location with the Angami (Seth & Seth) and Lotha (Murry et.al) Nagas it shows a significant difference and also with the Kozami (Zehol & Zehol) and Biates (Haloi). With regard to the PTC taste sensitivity on comparison shows a significant difference with the Angami, Lotha (Murry et.al) and Kozami (Zehol & Zehol) Nagas. More Comparison cannot be carried out due to the unavailability of the reported data on genetic markers among the other Naga Populations. The frequency of Rh negative and the incidence of colour blind are in low frequencies and these are the characteristic of the populations groups with Mongloid affinities from the North-east region of the Himalayas as reported by Bhasin and Walter (2001). Thus, it can be suggested that, it is likely that the Rengma Naga are genetically similar to these Mongloid populations, suggesting the presence of gene flow in the past, if not in the present generation due to the admixture rate.

Table 1: Phenotype and allele frequencies of ABO Blood group of the Rengma Naga, Nagaland

Phenotypes	Total No. (249)						Phenotype Frequency
	Females(125)		Males(124)		Total (249)		
	No.	%	No.	%	No.	%	
O+	46	36.8	55	44.35	101	40.56	0.4056
A+	55	44	48	38.71	103	41.37	0.4137
B+	16	12.8	12	9.68	28	11.24	0.1124
AB+	8	6.4	9	7.26	17	6.83	0.0683

Allele Genotype frequencies: $p=0.2785 \pm 0.03$, $q=0.0942 \pm 0.017$, $r=0.6273 \pm 0.022$

Difference between sexes $\chi^2=1.89$, d.f=3, $p>0.05$

Goodness of fit for Hardy Weinberg Law: $\chi^2=2.07$, d.f=1, $p>0.05$

Table 2: Phenotype and allele frequencies of RH (D) factor of the Rengma Naga, Nagaland

Phenotypes	Total no. (249)					
	Females (125)		Males (124)		Total (249)	
	No.	%	No.	%	No.	%
RH (D)+	125	100	124	100	249	100
RH (D)-	0	0	0	0	0	0

Allele frequencies \pm Standard Error: $d=0 \pm 0.032$; $D=1 \pm 0.032$

Difference between sexes $\chi^2 = 0$, d.f = 1, $p > 0.05$

Table 3: Frequency of PTC taster and non-Taster of the Rengma Naga, Nagaland

PTC Taste Sensitivity	Females (125)		Males (124)		Total (249)	
	No.	%	No.	%	No.	%
Taster	70	56	73	58.9	143	57.43
Non- taster	55	44	51	41.1	106	42.57

Allele frequencies \pm Standard Error: $T=0.3475 \pm 0.0245$, $t=0.6525 \pm 0.0245$,

Difference between sexes (student's t-test) = 0.133, d.f = 247, $p > 0.05$

Table 4: Frequency of Colour Blindness of the Rengma Naga, Nagaland

Phenotypes	Females(125)		Males(124)		Total (249)	
	No.	%	No.	%	No.	%
Red-Green deficiency	2	1.6	5	4.03	7	2.81
Normal	123	98.4	119	95.97	242	97.19

Allele Frequencies: $c=0.1676$, $C=0.8324$

Concluding Remarks

However, it would be wrong for the author to draw any conclusion and say about origin and migration of the population in this small research work, thus for a better understanding of the population, an elaborate and more precise study is needed in particular to the North-East region of India.

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