

A morpho-genetic study of Badhiya Muslims of Purnia District (Bihar), India

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ABSTRACT

Background: The existence of genetic variation in man is caused by many factors along with selection, migration, gene flow and genetic drift. A population is characterized by a set of gene frequencies. Hence, the gene frequency data are essential prerequisite for studying the genetics of any population. As Badhiya Muslims of Purnia district (Bihar) are migrant of other place of India and nothing is known about their genetical status in this new zone, so we proposed to study morpho-genetic variation in them which could provide their genetic affinities with other populations.

Methods: The distribution of morphogenetic traits was studied in Badhiya Muslims of Purnia district (Bihar). For the purpose, a survey was conducted in different villages of Badhiya Muslims and frequencies of different traits were calculated. It was observed that the frequency distribution of various traits among the studied populations shows the homogeneous distribution. Overall, frequencies of these traits were according to Indian trends. However, in certain traits Badhiya Muslims show similarities with Mongoloid traits. It needs further investigation using more serogenetic parameters. For this genetical study data on various parameters were collected from the population of Badhiya Muslims residing in different villages of Purnia district. In no case two persons belonging to the same family were subjected to test the above mentioned Mendelian traits. Standard methodology was used to collect data on various parameters.

Results: It was observed that the frequency distribution of various traits among the studied populations shows the homogeneous distribution. Overall, frequencies of these traits were according to Indian trends.

Conclusion: The allelic frequencies some traits in Badhiya Muslims showed Mongoloid affinities. So, presently, it is difficult to say anything about their genetical status. The data with some more serogenetic markers and morphological characters to be studied in future can throw fresh light on the origin and evolution the population under study.

KEYWORDS

Genetic variation, Consanguinity, Homozygosity, Mongoloids, Caucasoid

INTRODUCTION

Genetic variability is the common feature of many organisms. The existence of genetic variation in man is caused by many factors along with selection, migration, gene flow and genetic drift. By means of many examples Vogel and Motulsky (1986) have shown the importance of these factors for understanding of genetic variation of man. Morpho-genetic variation in human population may be temporal or spatial in studying spatial variation, environment in which a population lives, deserves special consideration. Environment may be geographical, cultural, ethnic and so on.

Populations of the same ethnic origin living in different geographical regions appear to show variation in biological characters among them. People migrate from one geographical area to another and thereby exposed to different environmental condition. The human genetic variations play a significant role in bringing about the diversity in population structure and contribute to the dynamics of human evolution. The genetic similarities between populations show the common origin or admixture of gene pools. The genetic heterogeneity between the populations indicates the diversity or isolation by some unknown barriers.

A population is characterized by a set of gene frequencies. Hence, the gene frequency data are essential prerequisite for studying the genetics of any population. The population diversity could provide an opportunity to study the morpho-genetic variation and similarities among different populations inhabiting the region since they have cohabited for a long time and presumably there might have been gene flow between them, since the existence of genetic variation in man is caused by many factors among which selection, migration, gene flow and genetic drift are the most important (Bhasin *et al.*, 1992). The present paper is to represent certain morpho-genetical traits viz ABO blood groups, Rh blood groups, PTC taste ability, colourblindness, ABH secretion, tongue rolling, tongue folding, ear lobe free or attached), hypertrichosis and cerumen types among Badhiya Muslims of Purnia district which are migrant of other places. Genetic mechanism on morphogenetic trait is still not clear understood as it is seen to occur with variable frequency in different populations and thus are useful in evaluating and analysing evolutionary forces and classification as well (Das and Sengupta 2003).

MATERIALS AND METHODS

To investigate morpho-genetical status of Badhiya Muslims, following parameters have been studied:

- a) ABO blood group system
- b) Rh blood group system
- c) PTC taste ability
- d) Colour blindness
- e) ABH secretion
- f) Cerumen types
- g) Ear lobe
- h) Hypertrichosis.

For this genetical study data on various parameters were collected from the population of Badhiya Muslims residing in different villages of Purnia district. In no case two persons belonging to the same family were subjected to test the above mentioned Mendelian traits.

i) The standard methodology was followed for the detection of the ABO blood groups by slide

agglutination method using anti A and anti B. Rh blood group was detected by slide agglutination method using anti D.

ii) Phenyl thiocarbamide (PTC) taste ability was studied using method of Harris and Kalmus (1949) and colour blindness was detected by using Ishihara (1959) colour plates.

iii) For ABH secretion saliva specimens were collected by placing a cotton swab under the tongue and when fully soaked the swab was squeezed into a tube by the subject himself. The single tube method of Dunsford and Bowely (1956) was followed for determination of ABH secretion.

iv) For hypertrichosis, unrelated males aged from 17 – 80 were observed. Presence or absence of hairs on four regions (auditory-meatus, the tragus, the lobules and the helix were recorded separately. Methodology of Malhotra (1969) that all men with one or more hair on any part of the ear should be classified as affected was followed.

v) Cerumen type was detected from both the ear canals with the help of a metal stick. The two types of cerumen i.e. wet (sticky type) and dry (hard type) were identified on the basis of their wetness, dryness and colour.

RESULTS AND DISCUSSION

In the present investigation frequency of blood group O was found highest followed by B, A and AB (O>B>A>AB) (Table – 1). Ara *et al.*, (2008) have also reported prevalence of blood group O among Muslims of Western U.P. Higher frequency of blood group O in the population of present investigation might be due to consanguineous marriages as well as short marriage distance. It is well known that consanguinity and short marriage distance leads to homozygosity thereby increasing the chances of expression of recessive alleles. Thus due to consanguinity and short marriage distance the proportions of groups A and B have been reduced while O has been increased. However, Rao and Inbaraj (1979) could not find such an effect among the consanguinity practicing Brahmins of Tamil Nadu and Maharashtra. This may be attributed to differences in the history and marriage structure of the population concerned.

Table 1: Genetic markers among the Badhiya Muslims of Purnia district (Bihar)

Number of tested	System	Phenotypes	Gene Frequencies
509	ABO	O= 193 (38%)	p= 0.1532 q=0.2275 r= 0.6190
		A= 111 (21.8%)	
		B= 170 (33.4%)	
		AB= 35 (6.8%)	
509	Rh	Rh (+ve)= 495 (83.42 %)	D= 0.8342
		Rh (-ve) = 14 (1.658%)	d= 0.1658
428	PTC	Taster = 348 (81.30)	T= 0.4323
		Non taster = 80 (18.69%)	t= 0.4323
402	Colour Blindness	Normal = 396 (98.5%)	C= 0.8775
		Colour Blind = 6 (1.5 %)	c= 0.1225
170	ABH Secretion	Secretors = 122 (71.76)	S=0.47
		Non Secretors = 48 (28.24%)	s= 0.53

Table 2: Morphological traits among Badhiya Muslims of Purnia district (Bihar)

Number	Morphological traits	Classification	Frequency	Allele frequencies
368	Ear lobe attachment	Free	284 (77.17%)	0.5233
		Attached	84 (22.83%)	0.4777
368	Tongue rolling	Rolling	344 (93.48%)	0.7446
		Non rolling	24 (6.52%)	0.2553
368	Tongue folding	Non folding	256 (69.57%)	0.6957
		Folding	112 (30.43%)	0.3043
368	Cerumen type	Dry	252 (68.48%)	0.8275
		Wet	116 (31.52%)	
500	Hypertrichosis	Absent		

The most widely studied ABO blood groups show that in general the allele frequencies of the total population of the world found to be O = 62.3, A = 21.5 and B = 16.2 (Mc Arthur and Penrose, 1950 - 51). The European populations have more than 25 of A allele (varies from 25 to 35) and B allele frequency below 10. Among the population groups of Southwest Asian countries (Saudi Arabia, Jordan, Kuwait, Yemen, Israel, Lebanon, Syria, Iraq, Iran and Afghanistan) the frequencies of alleles A and B are about 23 and 15, respectively except in Afghanistan where the allele B is higher than allele A. (Mourant *et al.*, 1976; Tills *et al.*, 1983). In India, the distribution of allele B frequency is higher (23.3) as compared to allele A (18.6), whereas the frequency of allele O is 58.1. In the present study the frequency of allele B is higher (22.75) as compared to A (15.32) and allele O is 61.90 (Table - 1).

Among Indian populations the frequency of allele D averages around 80.3% (Bhasin *et al.*, 1992 ; 1994). It is highest among scheduled tribes (86%) as compared to other ethnic groups. In the present

investigation the frequency of D allele was found to be 83.42% and that of d was 16.58%. (Table -1).

The taste sensitivity to PTC is well established as a population genetic marker. Human on the basis of their ability to taste PTC have been classified as tasters and non-tasters. The tasting ability is due to an autosomal dominant gene T and the inability to recessive gene t. Today it has been well established that the ability to taste PTC exhibits a clear cut monohybrid pattern of inheritance (Mohr, 1951b; Das, 1956). Bhalla (1972) studied Tibet and Ladakh populations for PTC sensitivity and its frequency. They observed that more than 50 percent people of this area could taste this chemical. In the present investigation the frequency of taster was 81.30%. (Table -1). Singh and Singh (2011) have also reported higher percentage of tasters in Hindu and Muslim population of U. P. Bhasin *et al.*, (1994) stated that taster allele T is present in high frequency among Mongoloid populations of East Asia and Indian population with Mongoloid affinities. However, the present population does not belong to Mongoloid group nor it has any

affinity with Mongoloid population. Further, no significant age or sex differences in PTC tasting ability were observed in the present investigation. Such results have been reported by Das (1956) and Pandey *et al.*, (1996).

The sex linked character of colourblindness is widely used as genetic marker for better understanding of human variation. It has been known for a long time that males have much higher frequency of red green colourblindness than females. The frequency of colourblindness is lowest in hunting and gathering societies, with highest frequency in industrial societies (Stein and Rowe, 1978). The defect shows quite a bit of variation in different populations. The frequency of colour blind males among Indian populations on an average is 3.6% which varies from complete absence to 23%. In the present study the frequency colourblindness was found to be 1.5%. Shah *et al.*, (2013) have reported Muslims belonging to caste Sheikh, Pathan, Syed and Moghul shows overall prevalence rate of 5.34 %, 4.58%, 6.89% and 3.70% respectively.

With the study of A, B, AB and O blood groups, it was noted that some persons possess A and/or B antigens which could be detected in aqueous secretions of their eyes, noses and salivary glands. Individuals with such traits are called secretors and those lacking it as non secretors. Secretors have dominant gene 'S' which enable them to secrete their antigens in the body secretions. Non secretors are homozygous for recessive allele's'. The immunological specificity determined by the dominant allele 'S' is largely part of glycosphingolipid molecule (Shen *et al.*, 1968). Nearly 70 – 75% people of the world are secretors. The frequency of allele 'S' in Indian population is 52.4% (varies from 21.6 to 86.3%). It is lowest among scheduled tribes (49.5%) as compared to rest of ethnic groups (community – 51.7%, scheduled castes – 53.2% and caste – 55.5%) (Bhasin *et al.*, 1992 ;1994). In the present population 71.76% were secretors while rest were non secretors (Table -1).

Ear lobes are of two types – free ear lobes (dominant) and attached ear lobes (recessive). Free earlobes are those that hang below the point of attachment to the head while attached ear lobes are attached directly to the side of the head. The frequency of ear lobe attachment are

characteristics for mongoloid-Japanese 67.1%, Chinese: 64.3 % (Lai and Walsh, 1966), Tibetans: 50.4 % (Tiwari and Bhasin, 1969). Muslims on the other hand are of Caucasoid origin, in which the frequency of attached ear lobes is generally much lower (Shah *et al.*, 2012). In Badhiya Muslims the frequency of attached ear lobe was found to be 22.83% (Table -2). Bhowmik (1970) has reported homogeneous distribution of this trait in adult male Hindus and Muslims. Kalia and Gupta (1978) had observed higher incidence of free ear lobes (73.84%) among Punjabis. The frequency of free ear lobes was found to be in the range of 56% to 74% in five endogamous groups of Haryana by Yadav *et al.*, (2000). Chadha and Sandhu (2013) have reported frequency of free ear lobes 63.66% and 53.33% in Mahasha and Bhagat of Jammu and Kashmir respectively.

Hypertrichosis is a Y-linked character (Gates, 1960; Dronamraju, 1960). Occurrence of a large number of males and no female with true hairs, support the Y-linked hypothesis for this trait. Hypertrichosis is seen rather frequently in India, but also occurs in Caucasians, Australian aborigines and Japanese. A large number of studies have been carried out to show the genetics and variability in different populations for this trait.

Little information regarding this trait is available among populations of Negroid and Mongoloid origins. Gates and Vella (1962) studied Mongoloid groups (Lepchas, Bhotias, Tibetan refugees, Khasis and Totos) but not found any individual with hypertrichosis. However, Chakarvarti (1964) reported two individuals having hairy rims among the Totos, a tribe with Mongoloid affinities of Jalpaiguri (West Bengal). It may be inferred that Mongoloid people possesses very low frequency of this trait (Garg, 1980). In the present investigation of 500 unrelated individuals, not a single individual with this trait was recorded. However, presently it is very difficult to say that Badhiya Muslims have any affinities with Mongoloid populations. It needs further investigation as this trait is lacking in Mongoloids.

In human beings ear wax (cerumen) occurs in two forms – wet and dry types. Ear wax types are inherited in a simple Mendelian way: there are two alleles, the one producing sticky type being dominant over that for dry type (Matsunaga, 1962). The two types of ear wax manifested soon after

birth. The dry allele reaches high frequencies among indigenous populations of Asia and American Indians. The wet allele has a high frequency in European populations (Petraakis, 1971). It has been suggested that migration is one of the definite factors responsible for distribution of ear wax. Various factors of natural selection also have been suggested as influencing the distribution of ear wax types. These include differences in the effectiveness of the wet and dry types of ear wax in relationship to ear diseases, correlation with humidity and so on.

High frequency of dry type ear wax in caste groups (Brahmin, Kalita and Kayastha) from India has been reported by Das (1977). Chakarvarti and Chakarvarti (1978) have reported 60.4% frequency of dry type cerumen in the Muslims of Kerala. The frequency of this type of cerumen has been found 86.7% and 67.6% in the Oraon and Santal of Bihar respectively (Sahu and Dyal, 1985). The present study also revealed high frequency of dry (68.47%) type cerumen which is according with the Indian trend.

There are a large number of traits in the behaviour and morphology of which the human species living under varying ecological zones, has been found to demonstrate variation of racial/ethnic and genetic significance. The human tongue of the digestive system is one of the organ which presents variation in its behaviour. Tongue rolling and tongue folding are dominant traits. In the present study, the frequency of tongue rolling was found to be 93.48% while that of non folding was 69.57%. (Table-2). Shah *et al.*, (20012) and Das *et al.*, (1985) have reported higher frequency of tongue rolling in Muslims of Manipur and Assam respectively.

CONCLUSION

In conclusion this study presents gene frequencies of ABO blood groups, Rh, PTC taste ability, Colour blindness, ABH secretion, hypertrichosis, ear-lobe and tongue rolling in the Badhiya Muslims of Purnia district (Bihar). The frequencies of these traits are more or less like Indian trends. However, allelic frequencies some traits show Mongoloid affinities. The data with some more serogenetic markers and morphological characters to be studied in future can throw fresh

light on the origin and evolution the population under study.

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