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Gene Diversity among Some Muslim Populations of Western Uttar Pradesh,India

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ABSTRACT The present paper deals with the distribution of ABO, Rh (D) and PTC tasting ability markers to study the genetic structure and microdifferentiation among Muslim populations of Aligarh.We have undertaken a survey of the allele frequencies of the ABO, Rh (D) and PTC tasting ability for different endogamous Muslim groups viz. Syed, Sheikh, Pathan, Ansari and Shia. For ABO only Pathan and Ansari showed significant differences in allele frequencies, while other combinations showed non-significant values. For the Rh (D) factor, Syed and Sheikh showed the least different values. All the populations showed non-significant differences for the marker PTC tasting ability. The average of the D_{ST} and G_{ST} values for the three markers were found to be 0.020 and 0.035, respectively. The Pathan and Ansari populations separate earlier than the sheikh, as well as Syed and Shia cluster which might have been the migrants to Indian population from outside quite later.

INTRODUCTION

The populations of India and other South Asian countries offer great opportunities to study socio-cultural and genetic variability. Perhaps, nowhere in the world people in a small geographic area are distributed as such in a large number of ethnic, castes, religious and linguistic groups as in India and other South Asian countries. All these groups are not entirely independent; people belong concurrently to two or more of these groups. People of different groups living side by side for hundreds or even thousands of year try to retain their separate entities by practicing endogamy.

History testifies that Greeks, Parthians, Sakas (Scythians) and Pahlavas including the Kushans were the first to come in after the Indo-Aryan civilization entered its settled course. The Huns came in somewhat larger numbers at the close of the Gupta epoch. These successions of peoples from outside India were assimilated into Hindu society. On the west coast, Jews and Parsis came after fleeing from their own homelands. Arabian Muslims, Persian Muslims, Turks and Afghans, whose total number was very large, came to India from time to time. The Muslim immigration into India began even before the Arab invasions of the Sind quite early in the eighth century A.D. and ended with the establishment of the Mughal Empire in the sixteenth century. This was the last major movement which produced some perceptible changes in the composition and culture of the indigenous population. The Muslims did not accept the Hindu religion but they made converts to their religion. The Europeans—Portuguese, Dutch, French and British started their intrusions from 15th century A.D. onwards and the Indo-European community grew from these infusions. In the east Shan peoples from Southeast Asia entered eastern part of India (Assam).The *Navayat,* a sect of Muslims are reported to have migrated from Arab in Konkan on the western coast about 600 years ago and later moved to Hyderabad, Madras, and other places 200 years ago.

The discipline of Biological Anthropology (or Human Biology) incorporates study of biology and environmental factors, as well as the forces of micro-evolution leading to macro-evolution, which ultimately influences the biological structure of human populations. Serological and biochemical characters are inherited in simple Mendelian fashion and are easily investigated. Determined at the time of conception, they are usually least affected by external environment. However, it may be mentioned here that these discrete characters in human populations are subject to a number of evolutionary forces and are not entirely free from the effect of environmental screening. Factors like mutation, natural selection, inbreeding, genetic drift and miscegenation are known to play an important

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role in producing gene frequency differences in different human populations.

The unit of study in understanding variations in man is a 'breeding population' also referred to sometimes as a 'Mendelian population'. The impact of the population approach on the subject of human variation has been to focus attention on 'breeding populations' as biologically and evolutionarily integrated units and to describe them in terms of their characteristic frequencies and resulting implications thereof..

In the present paper an attempt has been made to study the genetic polymorphisms in some Muslim populations of western Uttar Pradesh and their genetic relationships.

MATERIALS AND METHODS

Muslims of India make up more than 12% of the population (Shariff, 1998). They belong to two major sects: Sunnis and Shias, while each sect has different Biradaris, grouped under Ashraf and Ajlaf (Ansari, 1959), the former comprises higher rank Muslims, like Syed, Sheikh, Pathan and Moghul whereas Ajlaf include Qureshi, Saifi, Ansari and others of lower occupation (Ahmad, 1978). A large number of Ajlafs may also be converts from local indigenous populations of other faiths.

Although Islam does not distinguish among the groups on any material grounds, occupational and social isolation may have led to their differentiation over many generations, including the differences in their gene pools. In the present work, we have used three markers viz.ABO, Rh (D) and PTC tasting ability to study the genetic structure and micro differentiation of Muslim populations of Aligarh, Uttar Pradesh

The Aligarh city in Uttar Pradesh (U.P.) is situated between latitude $27^o28'$ and $28^o10'$ north, and longitude $77^o29'$ and $78^o36'$ east and its total area is 34.05 km^2. Aligarh has almost a dry climate throughout the year. The population of the city (2,990,388 Census of India, 2001) comprises Hindus, Muslims and Christians.

The present survey was conducted during May to December 2005 and the sampling was done at random and from healthy unrelated individuals of different endogamous groups of Muslims of Aligarh (U.P).

Information on caste, age, sex and the solution number was recorded. Pedigrees were drawn for determining the inbreeding status of individuals and only the non-inbred individuals were selected for study.

ABO and Rh (D) Group Typing: Slide agglutination method was followed for ABO and Rh (D) group typing. No sub-typing of A and B group was done.

PTC Tasting: Taste sensitivity to PTC was studied by method of Harris and Kalmus (1949).

Measure of Genic Variation (Heterozygosity): Heterozygosity (H) and coefficient of gene differentiation (G_{ST}) were calculated following Nei (1973).

The genetic relationships among the present Muslim population groups were assessed using the measure of genetic distance (D) proposed by Nei (1972). The parameter D measures the accumulated allele differences per locus or codon differences per unit length of DNA.

A dendrogram was drawn as per UPGMA clustering method using phylip (V 3.63) (Felsenstein, 1993).

RESULTS

In the blood group ABO, the frequency of phenotypes A is high as compared to B among Syed and Shia groups whereas among total Muslims the B (26.02) is little high as compared to A (23.72) and AB is also present in high frequency (15.48) and the O is having highest frequency (34.76) among the combined Muslim population (Table 1).

The Rh (D) -ve phenotype frequency is observed high among various Muslim population groups combine (20.26 percent) which varies from 13.13 percent in Syed to 25.48 percent among Sheikh (Table 2).

The phenotype and gene frequencies of tasting ability are listed in tables 3 and 4. It is observed that the phenotype frequency for non-tasters is observed quite high (35 percent) among total Muslim population groups, which varies from 30.00 percent among Sheikh to 34.58 in Ansari (Table 3).

The χ^2 differences were significant between Pathan and Ansari in case of ABO blood groups (χ^2 =14.2, df =3, p < 0.002 for Pathan; 9.7, df = 3, P > 0.021 for Ansari). In case of Rh (D) factor Syed and Sheikh have smaller difference (χ^2 =3.07, df =1, p < 0.079 for Syed; 2.51, df = 1, P < 0.113 for Sheikh).And for PTC all populations have non significant value of $\chi^{2.}$

The χ^2 difference in allelic frequencies for

Table 1: ABO Blood group among different Muslim populations of Aligarh.

Population	*Observed*	*Phenotypes*				*Allele frequencies*		
		A	*B*	*AB*	*O*	*A*	*B*	*O*
Syed (n=99)	No.	27	24	14	34	0.2347	0.1793	0.5860
	%	27.27	24.24	14.14	34.34			
Sheikh (n=157)	No.	33	35	26	63	0.210	0.1566	0.6334
	%	21.01	22.29	16.56	40.12			
Pathan (n=126)	No.	27	37	33	29	0.2765	0.2439	0.4796
	%	21.42	29.36	26.19	23.01			
Ansari (n=46)	No.	10	17	0	19	0.0845	0.2728	0.6426
	%	21.73	42.50	0	41.30			
Shia (n=179)	No.	47	45	21	66	0.2125	0.1803	0.6072
	%	26.26	25.14	11.73	36.87			
Total (n=607)	No.	144	158	94	211	0.2036	0.2065	0.5897
	%	23.72	26.02	15.48	34.76			

Table 2: Gene Rh (D) factor among different Muslims populations of Aligarh.

Population	*Observed*	*Phenotype Frequency*		*Allele frequencies*	
		Rh + (D)	*Rh - (D)*	*D*	*d*
Syed (n=99)	No.	86	13	0.6376	0.3623
	%	86.86	13.13		
Sheikh (n=157)	No.	117	40	0.4952	0.5047
	%	74.52	25.48		
Pathan(n=126)	No.	94	32	0.4961	0.5039
	%	74.60	25.39		
Ansari(n=46)	No.	37	9	0.5577	0.4423
	%	80.43	19.56		
Shia (n=179)	No.	150	29	0.6507	0.3493
	%	83.80	16.20		
Total (n=607)	No.	484	123	0.5569	0.4431
	%	79.73	20.26		

Table- 3: PTC taster frequency among different Muslim populations

Populations		*Tasters*			*Non-Tasters*		
		Male	*Female*	*Total*	*Male*	*Female*	*Total*
Syed (n=90)	No.	30	30	60	12	18	30
	%	33.33	33.33	66.66	13.33	20.00	33.33
Sheikh (n=110)	No.	35	42	77	13	20	33
	%	31.81	38.18	70.00	11.81	18.18	30.00
Pathan (n=234)	No.	70	72	142	46	46	92
	%	29.91	30.76	60.68	19.65	19.65	39.31
Ansari (n=60)	No.	21	18	39	14	7	21
	%	35.00	30.00	65.00	23.33	11.66	35.00
Shia (n=336)	No.	110	115	225	63	48	111
	%	32.73	34.22	66.96	18.75	14.28	33.03
Total (n=830)	No.	266	277	543	148	139	287
	%	32.05	33.37	65.42	17.83	16.74	34.58

majority of markers for different populations is non-significant (χ^2 = .0211, df 14, p = 0.999 for ABO; 0.5949, df = 9, P > 0.999 for Rh and 0.0211, df = 11, p < 1.00 for PTC). This is because there is no strict caste system among Muslims, only biradaris are there.

Heterozygosity: For the pooled Muslim material heterozygosity value for ABO locus was 0.56; for Rh (D) 0.54 and for PTC 0.48. Pooled heterozygosity was highest for ABO and lowest for PTC (Table 5).

Gene Diversity: The gene diversity indices for total population H_T and intra populational gene diversity, (H_S) are quite high i.e.0.546 and 0.525, respectively (Table 6).The interpopulational gene diversity (D_{ST}) is low i.e. 0.020, and the coefficient of genetic differentiation is 0.035.The pooled H_T, D_{ST} and G_{ST} all are found to be the

Table 4: PTC tasting ability allele frequencies for different Muslim populations of Aligarh.

Population			*Male*	*Female*	*Combined*
Syed	Allele	T	0.4654	0.3876	0.4227
		t	0.5345	0.6123	0.5773
Sheikh	Allele	T	0.4795	0.4320	0.4522
		t	0.5204	0.5679	0.5477
Pathan	Allele	T	0.3702	0.3756	0.3729
		t	0.6291	0.6243	0.6270
Ansari	Allele	T	0.2517	0.5523	0.4083
		t	0.7483	0.4472	0.5916
Shia	Allele	T	0.3965	0.4573	0.4252
		t	0.6034	0.5426	0.5747
Total	Allele	T	0.5713	0.4287	0.4120
		t	0.4288	0.5712	0.5880

highest for Rh (D) and lowest for PTC tasting ability, while pooled H_S is highest for ABO and lowest for PTC tasting ability marker.

Genetic Distance: Using the allele frequency data for the five markers, and Nei's measure of genetic distance was calculated between the present Muslim groups. It was found highest between Syed and Pathan (0.1519) and lowest between Syed and Shia (0.0015).Using Table 7 matrix a dendrogram was constructed as per UGPMA method (Fig.1). It shows Ansari and Pathans to be older Muslim populations as compared to Sheikh, Syed and Shia, the Ashrafs.

DISCUSSION

The most widely studied ABO blood groups show that in general, the allele frequencies of the total population of the world in found to be *O* = 62.3; *A* = 21.5 and *B* = 16.2 (McArthur 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 he allele *B* is higher than allele *A*. (Mourant et al., 1976a; 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 little higher (20.65) as compared to *A* (20.36) and allele *O* is 59, whereas the studies reported on Shia and Sunnii Moslems (Majumdar, 1943) and on Sayyad and Pathan (Srivastava, 1975) frequency of allele *B* is quite high as compared to A.

In most of the people of Europe, the frequency of Rh negative d allele is about 40 percent. In Africans, the allele varies around 20 percent. In

Table 5: Observed heterozygosities at three locus in five Muslim populations of Aligarh, U.P., India.

Locus	*Syed*	*Sheikh*	*Pathan*	*Ansari*	*Shia*	*Pooled*
ABO	0.5696	0.5303	0.6342	0.5055	0.5243	.5578
Rh(D)	0.4622	0.5000	0.7436	0.4934	0.4812	.53608
PTC	0.4881	0.4956	0.4679	0.4833	0.4890	.4847

Table 6: Gene diversity analysis in five Muslim populations of Aligarh.

Locus	D_{ST}	H_T	H_S	G_{ST}
ABO	0.008	0.5667	0.5587	0.0141
Rh	0.05094	0.5870	0.5361	0.08678
PTC	0.0024	0.4841	0.4817	0.00496
Pooled	0.02045	0.5459	0.5255	0.03528

Table 7: Genetic distance matrix among different Muslim populations of Aligarh.

Populations	*Syed*	*Sheikh*	*Pathan*	*Ansari*	*Shia*
Syed		0.0158	0.1519	0.0161	0.0015
Sheikh			0.0914	0.0139	0.0080
Pathan				0.1214	0.1309
Ansari					0.0099
Shia					

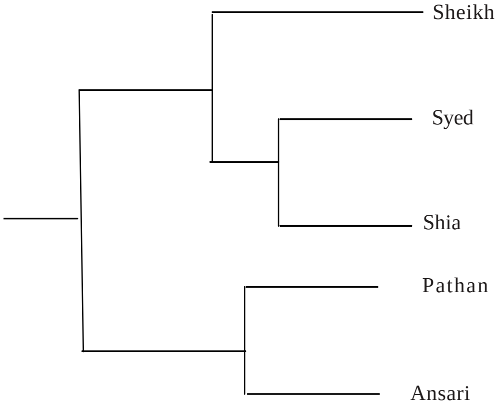

Fig.1. Dendrogram showing genetic relationships among sdifferent Muslim populations of Aligarh.

Asia it is difficult to see any definite trend in the frequency of d and there is a fall in the regions inhabited by peoples who are partly or wholly Mongoloid (Mourant, 1983).

In India, the general frequency of Rh negative allele (d) is observed to be 23 percent. With regard to different zonal regions, the highest value for d is observed among the population groups of South India (29 percent) followed by East, West, North India (25, 24 and 20 percent respectively) (Bhasin et al.,1992, 1994) which is different from 44% in our case. This larger frequency of recessive allele *d* may be due to either the hidden inbreeding in the population or, a smaller sample size or may also be due to weak anti D antibody titre taken for assay.

The frequency of nontaster allele t is about 50 percent among European populations it varies from25 to 57 percent. Among Mongoloid populations of East Asia and South East Asia, the frequency of the *t* allele is very low (about 30 percent ranges from 5 to 45 percent). (Mourant et al. 1976; Roychoudhury and Nei, 1988).

The average frequency of t allele among Indian populations is 53.4 percent (varies from 8.8 percent among scheduled caste of Andhra Pradesh to 89.2 percent in Munda of Ranchi, Bihar) which is little higher as compared to Europeans but similar to that of South west Asian Bhasin et al., 2001).

The extent of genetic divergence (G_{ST}) varies considerably from locus to locus. The pooled G_{ST} value over all loci (0.0353) gives an estimate of the degree of genetic differentiation present among different Muslims populations for ABO locus, the heterozygosity is highest among Pathan i.e. 0.6342 and lowest among Ansari i.e. 0.5055 and for Rh (D) locus, highest among Pathan (0.7436) again and lowest among Syed (0.4622). Whereas for PTC locus, it is highest among Sheikhs i.e. 0.4956 and lowest among Pathan.

The genetic distance between the Syed and Sheikh was the lowest (0.0015) and that between the Syed and Pathan was the highest (0.1519) (Table 7). This suggests a quite different genetic constitution of Pathan and Ansari compared to higher caste groups i.e. Syed, Shia and Sheikh. The dendrogram based on genetic distances clearly shows that the Pathan and Ansari differentiated from other population groups earlier. Meaningful conclusions about the genetic structure of the sub-populations cannot be obtained unless a good number of loci are considered and even sample sizes can be increased further.

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