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Gene Diversity Analysis and Microdifferentiation Process in North Indian Muslim Populations

Ruqaiya Hussain, Ahsana Shah, Mohd Fareed, Mohammad Afzal *

Abstract

Indian population is well known for its genetic diversity, ethnicity and microdifferentiation process. The present work deals with the distribution of A_1A_2BO, Rh (D), PTC tasting ability and Red green Colorblindness to study the genetic structure, fitness and microdifferentiation process among different Muslim populations of North India. We have undertaken a survey of the gene frequencies of the four markers in six endogamous groups: Syed, Sheikh, Pathan, Ansari, Qureshi and Saifi. For A_1A_2BO only, the Syed and Ansari showed significant differences while other combinations showed nonsignificant values. All the populations showed nonsignificant differences for the PTC marker except Pathans of which interpopulational differences were seen. Pooled heterozygosity was highest for A_1A_2BO being 0.6899 and lowest for Colorblindness, 0.0727. The average of the DST and GST values for the four markers were found to be 0.00698 and 0.0176, respectively. A dendrogram was constructed using the UPGMA and NJ clustering method. It shows that Syed and Sheikh are the more recent populations, followed by Pathan, then Ansari and the oldest ones are Qureshi. The results of the genetic distance analysis can throw some light on origin, migration and genetic relationship among different endogamous groups of Muslim Populations.

Keywords: Gene diversity; Heterozygosity; A_1A_2BO, PTC tasting ability; North Indian Muslim Population.

Introduction

India is a vast country with enormous social and cultural diversity due to its large population size, complex ethnic history and unique migratory events. The origin of culturally and genetically diverse population of India has always been a subject of debate among anthropologists and geneticists. Despite recent large scale- efforts in discovering human genetic variation, India's vast reservoir of genetic diversity remains unexplored. The people of Indian subcontinent are divided into a large number of endogamous groups consisting of different castes, languages, religions and tribes and it is said to be the melting point of various ethnic groups. Many of the castes are large and widely distributed with further subdivisions or castes within them. These subcastes vary in size, mating pattern and even adaptive strategies (Malhotra 1984).

Linguistically population of India is classified into four major classes 'viz. Indo-Aryan, Dravidian and Austro Asiatic and Tibeto Burman. The Indo-Aryan forms the largest group and comprises much of the north and northwest region of the sub-continent.

* *Human Genetics and Toxicology Lab., Section of Genetics, Department of Zoology, Aligarh Muslim University, Aligarh, Uttar Pradesh, India, 202002;* Corresponding author. Prof. Mohammad Afzal, e-mail: afzal1235@rediffmail.com

In India, majority of the total population (82%) practices Hinduism. The Indian population is structured into 40,000 endogamous groups, of which 37,000 groups belong to the Hindu caste system (Malhotra 1984). Approximately 12% of the Indian population is Muslim, forming the largest religious minority group in India. Hindu population constitutes the largest community and the second largest is the Muslim population. The Indian population also includes Christians, Sikhs, Jains, Buddhists and Parsis. Throughout the ages many population groups have migrated toward India along north eastern and north western routes (Hunter 1897). A look at the ethnic history of India reveals that Indians belong to two different categories: the Dravidians (aborigines) and the Aryans or Sanskrit speaking groups (with mixed groups known as the Musalmans (Hunter 1897). The caste system in India has its origin in the verna system, with its language, state, and religious base; hence caste differentiation can be studied from these three points of views (Karve 1961). The caste system reflects the Indian occupationally and religiously defined hierarchies.

North India is a loosely defined region in the northern part of India. It has a diverse culture. The people of North India are predominantly Indo-Aryan and include various ethnic groups. In North India, the state of Uttar Pradesh is historically important because of its old centers of population, learning and administration. It is the fifth largest state of India with an area of 243.286 km^2. Because of Islamic influence for centuries, Uttar Pradesh becomes the heartland of Indian Muslims, becoming home to 32 million Muslims, nearly one-third of India's total Muslim population (Census of India 2001). The Aligarh city in Uttar Pradesh is situated between latitude 27°28' to 28°10' North 77°29' to 78°36' east longitude and its total area is 34.05 km^2. Aligarh has almost a dry climate throughout the year. The annual average rainfall in the district is 594.1mms and maximum temperature recorded is 44°C.

Muslims of India make up more than 12% of the population, yet their genetic structure has not been well investigated. Muslims comprise a distinct community with their regional, linguistic and ethnic identity (Shariff 1998; Aarzoo and Afzal 2007).

Muslims belong to two major sects: Sunnis and Shias, while each sect has different biradaries, which are grouped under Ashraf and Ajlaf (Ansari 1959). The former comprise of higher rank Muslims like Syeds, Sheikhs, Pathans and Moghuls while the latter comprise Qureshis, Ansaris, Saifis. A large number of the Ajlaf may also be converts from local indigenous population of other faiths (Ahmad 1978; Afzal and Sinha 1983).

While Islam does not distinguish the groups on any material grounds, the social isolation might have led to differentiation of the groups over many generations, including the differences in the gene pools. The study of gene pool may throw some light on their origin, ancestry, adaptations and the fitness of the population (Kirk 1985; Basu 1982). The present study is an attempt to investigate the genetic structure, polymorphism and microdifferentiation process among different endogamous groups of Muslim populations of Uttar Pradesh (Aligarh).

Materials and Methods

Population and Sample Collection

The survey was conducted during September 2011 to February 2012 for A_1A_2BO, Rh, Colorblindness and PTC taste ability loci. The sampling of blood was done at random and from healthy unrelated individuals. The survey on classical markers was deemed necessary to know the ethnicity of the population of area. Households were selected by door to door contact by the investigator. Populations studied are Syed, Sheikh, Pathan, Ansari, Qureshi and Saifi. The samples were collected from the Upper Court, Civil Lines, AMU Campus, Sir Syed Nagar and Jamalpur areas of Aligarh.

Laboratory Analysis

The gene frequency of A_1A_2BO blood group, Rh factor, PTC tasting ability and Red-green Colorblindness were calculated from the tests conducted on the individuals as per standard protocols. Slide agglutination method was followed for blood group testing. Sub-typing of A and B blood group was done (Race and Sanger 1968). Taste sensitivity to PTC was studied by serial dilution method of Harris and Kalmus (1949). Ishihara's color plates were used for noting Red green colorblindness (Ishihara 1980).

Statistical Analysis

Phenotypes were recorded for each trait and gene frequencies were calculated according to Hardy-Weinberg law using a gene counting method. Heterozygosity for a given locus was calculated using the genotype frequencies (for heterozygous genotype). The level of Heterozygosity was calculated using the formula:

$$\text{(i)} \quad H=1-\sum Xi^2$$

Chi-square (χ^2) has been used for the measurement of the size of the discrepancy between observed and expected values (at particular degree of freedom {df} for 5% level of significance).

$$\text{(ii)} \quad (\chi^2)=\sum [\text{observed value- expected value}]^2 / \text{expected value}$$

Gene diversity was calculated using Nei's (1973) methods of gene diversity analysis in subdivided populations (Nei 1973).

$$\text{(iii)} \quad HT = HS + DST$$

Genetic distance (D) was determined using (Nei's 1972) formula. The normalized identity of gene between the X and Y with respect to all loci is defined as follows Nei, (1972):

$$\text{(iv)} \quad I=Ia/\sqrt{I^{aIb}}$$

$$\text{(v)} \quad D= -1n\ I$$

The dendrogram was drawn as per UPGMA clustering method using Phylip, version 3.6a3 (Felsenstein 1993) and NJ cluster.

Results

Phenotype frequency

In A_1A_2BO blood group, the most frequent blood group is O (i.e. 30.05%), the second one is A_1 (26.32%), A_1B (20.03%), B (17.68%), A_2(3.33%) and the least frequent group is A_2B (2.5%). The frequency of phenotypes for this marker for the entire group follows the trend, i.e. $O>A_1>A_1B>B>A_2>A_2B$. The highest frequency of Rh-ve individuals is found in Saifi (18%), while in other populations it ranges from 12 to 18%. The incidence of Colorblindness was highest among Saifi (8%) while in other five populations this value ranges from 1-6% (Table 1). It is observed that the phenotype frequency for PTC tasters among Pathan was found to be 60.62% (highest among all group studied). The non-tasters are 39.3% among Pathan while 57.14% among Saifis (Table 2).

Allele frequency

In ABO blood group, I° shows highest frequency in all the six population groups. Ia^2 has lowest frequency. Saifi showed the highest I° and lowest Ia^2 frequency. The Ansari have the highest I^b allele frequency, which is beneficial for malarial protection in the Indian sub-continent. The Ansari also have the highest Ia^2 allele frequency, and may have a lower population group. Syeds have the highest Ia^1 allele frequency while the lowest is found in Saifi. All the populations follow the trend $I°>I^b>Ia^1>Ia^2$. For the Rh system, D allele has the highest frequency in Pathan and lowest in Saifi. For the Colorblindness frequency of Xc is highest in Saifi population and lowest in Syed (Table 3). For the PTC loci, T allele has lowest frequency in Saifi population and highest frequency in Pathan population (Table 4).

The Chi-square differences weas significant among Ansari in case of A_1A_2BO blood groups ($\chi2 = 12,28$, df $= 5$, $p< 0.025$) and remaining populations shows non-significant differences. In case of Rh(D) all populations have non significant value of $\chi2$. Colorblindness differences was significant among Saifi ($\chi2 = 3.88$, df $= 1$, $p > 0.05$) while other population shows non-significant differences. For PTC trait only Pathan have significant value of $\chi2$

and remaining populations have non-significant differences ($\chi 2 = 4.905$, df = 1, $p < 0.025$ for Pathan). The $\chi 2$ difference in allelic frequencies of marker for different populations was non-significant because there is no rigid caste system in Muslims, only biradaries are there.

Heterozygosity

Pooled heterozygosity was highest for A_1A_2BO and lowest for Colorblindness. It was found to be 0.6899 and 0.0727 respectively. All the population groups showed the comparatively higher level of heterozygosities over most of the loci except Colorblindness locus in which frequency of heterozygosity is comparatively low in all groups (Table 5).

Gene Diversity

The measures of gene diversity are presented in (Table 6 and Figure 3). The total (H_T) among the six population groups (0.3975) has been analyzed into components i.e intra-population gene diversity (Hs=0.3905) and inter-population gene diversity (D_{ST}=0.00698). This shows that gene diversity between populaion groups is much lower than the gene diversity within the population groups. The coefficient of gene differentiation, or relative diversity, is rather low for the Rh, Colorblindness and PTC loci (<0.01). The pooled H_T, Hs, and D_{ST} all are found to be the highest for A_1A_2BO blood group and lowest for Colorblindness, while pooled G_{ST} is highest for A_1A_2BO and lowest for Rh (D) factor.

Genetic Distances

The Nei's genetic distances are shown here (Table 7) which is presented in the matrix form. On the basis of their genetic distances, dendrogram was constructed (Figure 1and 2) using UPGMA clustering method, Phylip version 3.63 and NJ Cluster, was used to estimate the "genetic affinity" between the six populations of Muslims of U.P. It shows Syed and Sheikh make one cluster and join with Pathan and they together join with Ansari, Qureshi and Saifi make one cluster, joining with the rest of the population to their ancestor. Thus, Syed and Sheikh are the most recent populations followed by Pathan, then Ansari and the oldest ones are Qureshi. The trend is exhibited in both UPGMA diagram and NJ cluster.

Discussion

The present work is a beginning to explore the genetic structure, fitness and microdifferentiation process of present Muslim populations of North India and their adaptive value. Some studies on Muslim populations have been attempted earlier in Uttar Pradesh. These are described here for comparison. Our studies show some differences from earlier studies on Muslim populations of North India. The endogamous groups of Muslims in different regions are heterogeneous with respect to the gene frequencies of ABO blood groups (Roychoudhury 1981, 1982). There are significant differences in allelic frequency between different subgroups for this marker. Biradari wise breakup is available for ABO, Rh, PTC and Colorblindness in UP (Srivastava 1974) and MP for some groups (Khan et al., 1985). Our study is comparable with ABO frequencies reported in some earlier studies of other caste groups of UP. Majumdar (1943) reported the distribution of ABO blood groups in the Shia Muslim populations of Jaunpur in which the percentage of different types reported were *B,* 34%, *O*, 36%, *A*, 25% and *AB*, 5%. The overall picture for Sunni Muslim from Madhya Pradesh has the following frequencies: *A*, 19.1%, *B*, 22.4%, and *O*, 58.4% (Khan et al., 1985).

Normally, the distribution of ABO blood group varies from one population to another. In many other studies, blood group O has been found to be the most common blood group. In the Caucasians in the United States, the distribution is group O, 47%, group A, 41%, group B, 9% and group AB, 3% (Seeley et al., 1998). Among Western Europeans about 42% are group A, 9% group B, 3% group AB and the remaining 46% group O. For blacks in United States, the distribution is group O, 46%, group A, 27%, group B, 2%, and group AB, 7% (Seeley et al., 1998). Similarly, in Pakistan, blood group O is the most common 35%, blood group A is 24%, blood group B is 33% and blood group AB is 8%. In Lagos Nigeria, blood group O is 55.3%, blood group A, 25.3%, blood group B, 16.7% and blood group AB, 2.7% (Adeyemo et al., 2006).

For A_1A_2BO blood group, studies have been done on few Muslim populations and data reported for distribution of ABO subtypes in different Muslim and Hindu populations of UP has the following frequencies: O, 30.69%; A_1, 24.64%; A_1B, 20.21%; B, 18.88%; A_2, 3.97% and A_2B, 1.60%, which are nearly close to our values. 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 present study, the frequency pooled show allele O to be 59.0%, B, 21.7%, A_1, 19.4%, and A_2, 1.2% which are little higher as compared to studies reported on different Muslim populations of UP by (Ara et al., 2011).

The frequency of ABO blood group varies from race to race. The allelic frequencies of the total population of the world is found to be O = 62.3%; A = 21.5% and B = 16.2%. American blacks generally have frequencies of A, B, AB and O blood groups of 27%, 20%, 4%, and 49% respectively (Conteras and Lubenko 2001).

The Rh distribution also varies within any group of population. The recessive allele (d) ranges from as high as 40% to its virtual absence in Chinese Australian aborigines, Negrito etc. Exceptionally high incidence of Rh negatives yielding frequency of recessive allele (d) in the range of 50 to 60% have been reported in Basque (Europe) and Berbers of Moracco (Mourant et al., 1976).

The variation in frequency of the Rh negative gene (i.e., Rh d) is 15-30% in the majority of the Indian population compared to 35-45% in Europeans and 0-10% in Asian population (Roychoudhury 1983). For the Rh system the overall frequencies for D and d are 80.71% and 19.29% respectively (Tyagi and Hamid 1968), which correspond to 61.62% and 38.38% in our case.

The average frequency of t allele among Indian populations is 53.4 percent (varies from 8.8% among scheduled caste of Andhra Pradesh to 89.2% in Munda of Ranchi, Bihar) while in European populations it varies from 25 to 57% which is little higher but similar to that of South west Asian (Bhasin and Walter 2001). For the Ansari from Bihar, the frequency of the *t* allele is 71% (Afzal and Sinha 1983), which is 69.17% to the present study.

Singh and Sinha (1988) reported the incidence of Colorblindness of 2.2% in the Chamar to be 2.7% in Muslims of Bhagalpur, Bihar while in our case the highest frequency of Colorblindness is found in Saifi 8% and in others it ranges from 1-6% of Aligarh UP.

Conclusion

We have studied the patterns of gene diversity between populations, the genetic distances, and the relation of heterozygosity between populations. The extent of genetic divergence (G_{ST}) varies considerably from locus to locus. Gene diversity is the most important measure of genetic variability of a population and can be related to the number of codons different per locus (Nei, 1977). The highest heterozygosity was observed in the Syed (0.6161) and lowest was seen in the Qureshi (0.5441) for A_1A_2BO. Pooled heterozygosity was highest for A_1A_2BO and lowest for Colorblindness. The pooled G_{ST} in A_1A_2BO (0.0176) gives an estimate of the degree of genetic differentiation present among different Muslim populations.

The genetic distance between Syed and Sheikh was the lowest (0.0028) and that between the Syed and Ansari was the highest (0.0864). This (Table 7) suggests a quite different genetic constitution between Ashrafs and Ajlafs. The dendrogram based on genetic distances clearly shows that the, Qureshi and Saifi differentiated from other population groups earlier.

At present the genetic distance and microdifferentiation process have been studied, dendrogram constructed for showing genetic relationship among different endogamous groups of North Indian Muslim populations. Our results also shed some light on genetic composition and fitness of population.

Acknowledgment

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Table 1: Phenotype frequencies of different marker loci for different Muslim populations of North India.

Population	A_1A_2BO Blood Group							Rh factor		Color blindness (in males only)	
	No.	A_1	A_2	A_1B	A_2B	B	O	+ve	-ve	Normal	Color-Blind
Syed	84	32	2	17	0	11	22	72	12	83	1
	%	38.09	2.38	20.23	0.00	13.09	26.19	85.71	14.28	98.80	1.2
	SE	5.2	1.7	4.3	0.0	3.7	4.8	3.8	3.8	1.2	1.2
Sheikh	69	19	3	14	1	13	19	58	11	67	2
	%	27.53	4.34	20.28	1.44	18.84	27.53	84.05	15.94	97.10	2.9
	SE	5.3	2.5	4.9	1.4	4.7	5.4	4.4	4.4	2.0	2.0
Pathan	160	47	2	31	5	22	53	140	20	158	2
	%	29.37	1.25	19.37	3.12	13.75	33.12	87.5	12.5	98.75	1.25
	SE	3.7	0.9	3.1	1.4	2.8	3.8	2.6	2.6	0.88	0.88
Ansari	78	16	5	25	4	11	17	67	11	75	3
	%	20.51	6.41	32.05	5.12	14.10	21.79	85.89	14.10	96.15	3.85
	SE	4.6	2.8	5.3	2.5	3.9	4.7	3.9	3.9	2.2	2.2
Qureshi	68	12	2	10	2	18	24	56	12	64	4
	%	17.64	2.94	14.70	2.94	26.47	36.29	82.35	17.64	94.11	5.89
	SE	4.6	2.0	4.3	2.0	5.9	5.8	4.6	4.6	2.9	2.9
Saifi	50	8	3	5	1	15	18	41	9	46	4
	%	16.0	6.0	10.0	10.0	2.0	30.0	82	18	92	8
	SE	5.2	3.4	3.4	4.2	2.0	6.5	5.4	5.4	3.8	3.8
Total	509	134	17	102	13	90	153	434	75	493	16
	%	26.32	3.33	20.03	2.55	17.68	30.05	85.26	14.73	96.85	3.15
	SE	2.0	0.8	1.8	0.9	1.7	2.0	1.6	1.6	0.77	0.77

No. = number of individuals, Parentheses = percentage (%), SE = standard error.

Table 2: Phenotype frequency of PTC marker loci for different Muslim populations of North India.

Population	Taster			Non-taster			Total		
	Male	Female	Combined	Male	Female	Combined	Male	Female	Combined
Syed	32	26	58	22	30	52	54	56	110
	59.26	46.43	52.72	40.74	53.57	47.27			
Sheikh	26	26	52	19	25	44	45	51	96
	57.77	50.98	54.16	42.22	49.01	45.83			
Pathan	45	52	97	33	30	63	78	82	160
	57.69	63.41	60.62	42.30	36.58	39.3			
Ansari	19	16	35	31	12	43	50	28	78
	38.0	57.14	44.87	62.0	42.85	55.13			
Qureshi	24	20	44	28	20	48	52	40	92
	46.15	50.0	47.83	53.84	50.0	52.17			
Saifi	15	15	30	22	18	40	37	33	70
	40.54	45.54	42.86	59.46	54.54	57.14			

Table 3: Allele frequency of different maker loci for different Muslim populations of North India.

Population	A_1A_2BO blood group				Rh factor		Colorblindness	
	I^{a1}	I^{a2}	I^b	I^o	D	d	X^+	X^c
Syed	0.2819	0.0228	0.1778	0.5273	0.6222	0.3778	0.9881	0.0119
Sheikh	0.2062	0.0399	0.2209	0.504	0.6008	0.3992	0.9710	0.0289
Pathan	0.2121	0.0108	0.1924	0.5929	0.6465	0.3535	0.9875	0.0125
Ansari	0.1669	0.0643	0.2764	0.5047	0.6246	0.3754	0.9615	0.0385
Qureshi	0.1312	0.0118	0.2536	0.5945	0.58	0.42	0.9412	0.0588
Saifi	0.1134	0.0431	0.2353	0.6050	0.5758	0.4242	0.92	0.08
Total ±SE	0.19485 ±0.017	0.01235 ±0.005	0.21776 ±0.018	0.59045 ±0.02	0.6162 ±0.022	0.3838 ±0.022	0.9685 ±0.008	0.0315 ±0.008

I^{a1}, I^{a2}, I^b and I^o are allele frequencies of blood group A_1, A_2, B and O respectively.
D and d are dominant and recessive alleles of Rh factor.
X^+ and X^c are dominant and recessive alleles of Colorblindness.
SE = standard error.

Table 4: Allele frequency of PTC maker loci for different Muslim populations of North India.

Population	Allele	Male	Female	Combined
Syed	T	0.3617	0.2680	0.3125
	t	0.6383	0.7319	0.6875
Sheikh	T	0.3502	0.2999	0.3230
	t	0.6497	0.7000	0.6769
Pathan	T	0.3496	0.3951	0.3725
	t	0.6504	0.6048	0.6274
Ansari	T	0.2126	0.3454	0.2575
	t	0.7874	0.6546	0.7425
Qureshi	T	0.2661	0.2928	0.2777
	t	0.7338	0.7071	0.7222
Saifi	T	0.2289	0.2615	0.2440
	t	0.7711	0.7385	0.7559
Total	T	0.2996 0.0186	0.3177 0.0189	0.3083 0.0188
	t	0.7004 0.0186	0.6823 0.0189	0.6917 0.0188

SE = standard error.
T and t are dominant and recessive alleles respectively.

Table 5: Observed Values of Heterozygosities at four marker loci for different Muslim populations of North India.

Population	A_1A_2BO Blood Group	Rh Phenotype	PTC Marker	Red-green Color blindness
Syed	0.6161	0.47014	0.4297	0.0235
Sheikh	0.6136	0.4796	0.4373	0.0563
Pathan	0.5782	0.4570	0.4674	0.0246
Ansari	0.6402	0.4689	0.3824	0.07395
Qureshi	0.5441	0.4872	0.4011	0.11072
Saifi	0.5477	0.4885	0.3689	0.1472
Pooled	0.6899	0.5752	0.4095	0.0727

Table 6: Genetic differentiation for different Muslim populations of North India-Estimates of Nei's measures of Gene diversity.

Locus	H_T	H_S	D_{ST}	G_{ST}
A_1A_2BO	0.6218	0.5993	0.0225	0.0362
Rh	0.4764	0.4753	0.00108	0.00227
PTC	0.4179	0.41461	0.00329	0.00787
Color blindness	0.0738	0.07275	0.00105	0.01423
Pooled	0.3975	0.3905	0.00698	0.0176

H_T = Gene diversity in total population, H_S = Intra population gene diversity, D_{ST} = Inter population gene diversity; G_{ST} = Coefficient of gene differentiation.

Table 7: Matrix to construct Dendrogram, showing Genetic distance for different Muslim populations of North India.

Population	Syed	Sheikh	Pathan	Ansari	Qureshi	Saifi
Syed	0	0.0029	0.0045	0.0864	0.0260	0.0133
Sheikh		0	0.1666	0.0029	0.0205	0.0079
Pathan			0	0.0098	0.0245	0.0131
Ansari				0	0.0197	0.0048
Qureshi					0	0.0170
Saifi						0

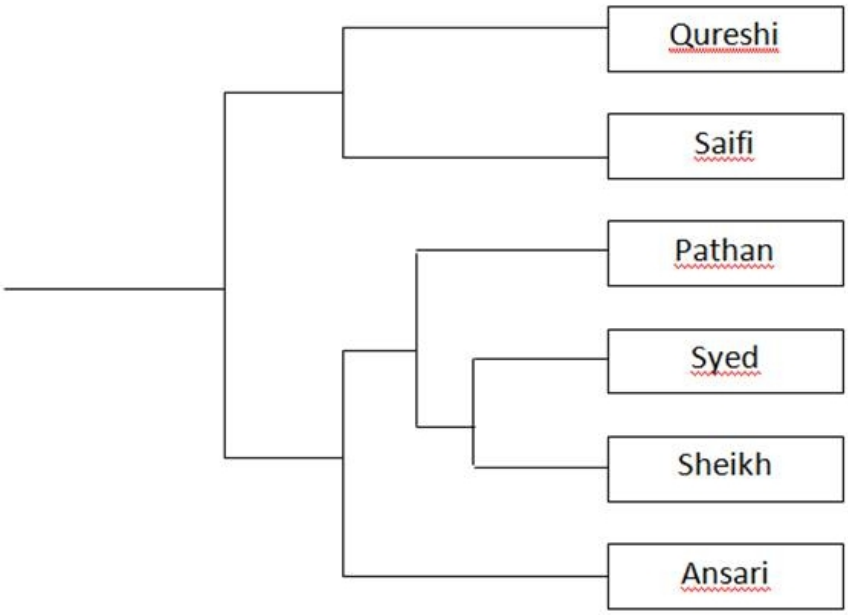

Figure (1) Dendrogram of six population groups of North Indian Muslims, based on the genetic distance of four polymorphic loci (UPGMA) method

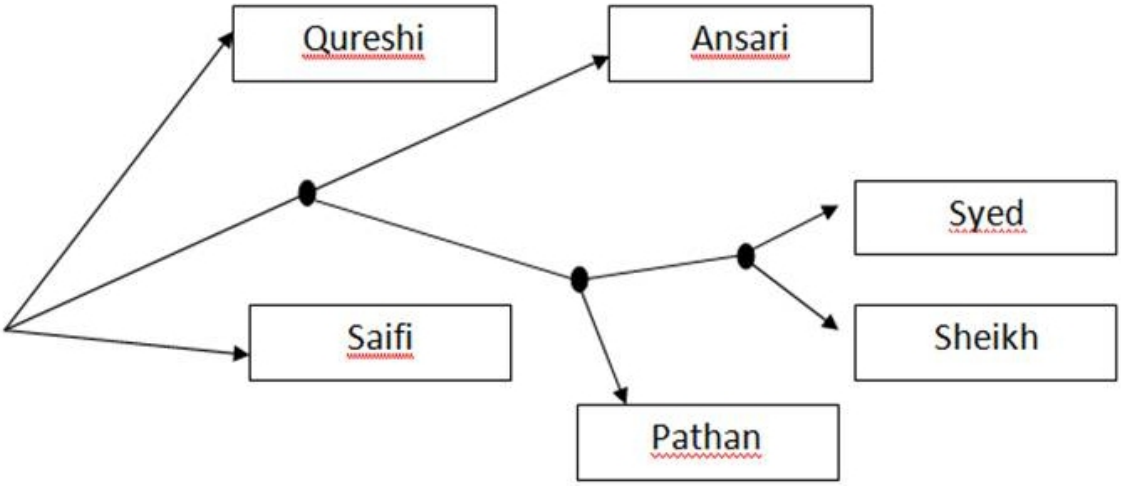

Figure (2) Dendrogram of six population groups of North Indian Muslims, based on the gene frequency data of four polymorphic loci (NJ) method

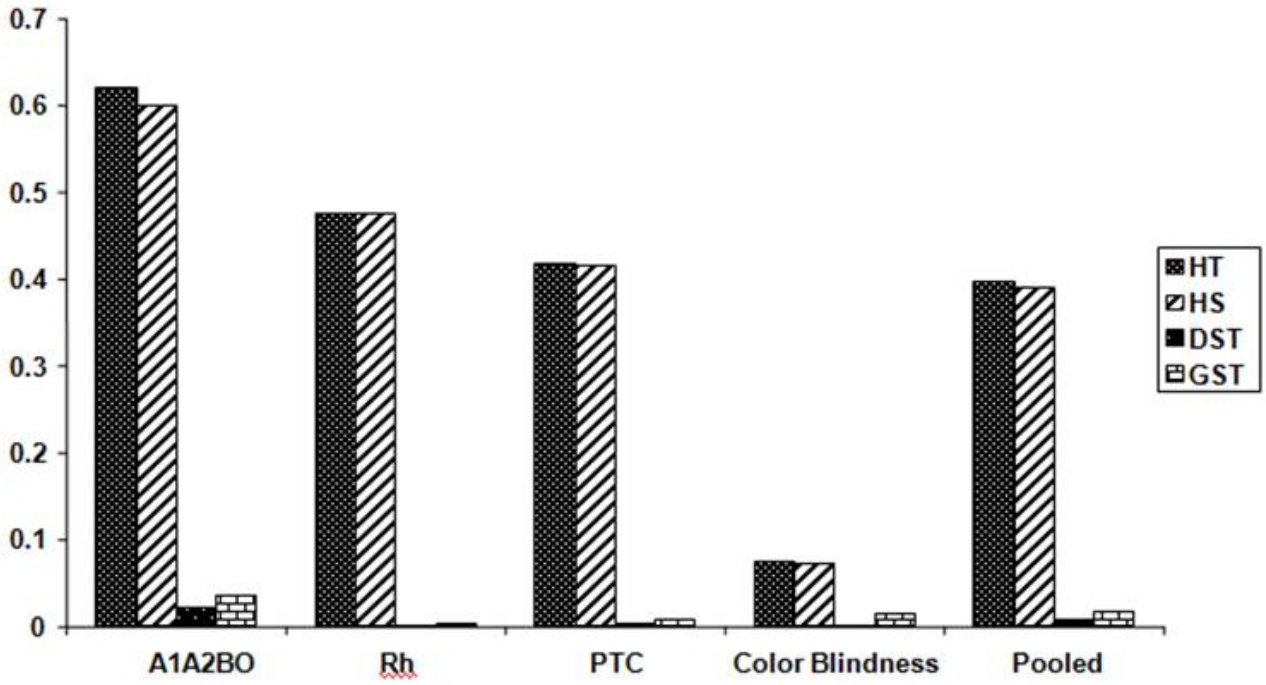

Figure (3) Genetic differentiation in different Muslim populations of North India

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