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Genetic Diversity of Some North Indian Populations of Different Faiths

Gulshan Ara and Mohammad Afzal

Introduction

The science of population genetics deals with Mendel's law and other genetic principles as they affect entire populations of organisms. Population genetics also includes the various forces that result in evolutionary changes in species through time. By defining the framework within which evolution takes place, the principles of population genetics are basic to a broad evolutionary perspective on biology. From an experimental point of view, evolution provides a wealth of treatable hypotheses for all other branches of biology. Many oddities in biology become comprehensible in the light of evolution: they result from shared ancestry among organisms, and they attest to the unity of life on earth.

Population genetics attempts to describe how the frequencies of the alleles, which control the trait, change over time. To study frequency changes, we analyse populations rather than individuals. Furthermore, because changes in gene frequencies are at the heart of evolution and speciation, population and evolutionary genetics are often studied together.

One of the purposes of population genetics is to study the mechanism of origin and maintenance of genetic variability. The genetic variability is studied in terms of polymorphism of various genetic markers as genetic polymorphism, which is defined as the occurrence in the same population of two or more alleles at one locus, each with appreciable frequency (Cavalli-Sforza and Bodmer 1971). Scholars of population genetics agree that a natural selection and stochastic processes are responsible for the maintenance of this genetic polymorphism in the human population.

Gene frequency data are very useful for studying the genetic relationship and evolution of human population. The comparison of gene frequencies for one or two loci is not reliable since each locus has a different distribution. Only when a large number of loci are examined, the genetic relationship becomes clear (Cavalli-Sforza and Edwards 1964). This is particularly because the inter-populational genetic variation is very small, compared with the intra-populational variation at the gene level (Lewontin 1972; Nei and Roychoudhury 1972, 1982). However, if a large number of loci are examined, even small differences can be detected with sufficient accuracy. If there are gene frequencies for a number of loci in a population, the heterozygosity for an individual locus can be calculated and the average heterozygosity per locus for a population is obtained. The average heterozygosity indicates the magnitude of genetic variation that exists within a population.

The genetic differentiation between a pair of populations is usually measured by a quantity called the genetic distance, which is a function of the gene frequency. There are several different measures of genetic distance.[1] Once the genetic distance is estimated for a group of populations, their genetic relationships can be studied using dendrogram, principal component analysis, etc. (Cavalli-Sforza and Bodmer 1971; Nei 1973; Sneath and Sokal 1973).

In India, the Hindu population constitutes the largest community and the second largest is the Muslim population. In the present study, we took both populations, Muslims as well as Hindus. The history of Hindu population goes back to the Aryans who moved into the Northwest of India. They imposed a caste system to organise the new society created by their arrival. They initially put together a hierarchy of four *varnas* (i.e., castes), which later was expanded to include a fifth category. The caste system is a rigid class structure based on Hinduism which is confined to India. The caste hierarchies most often quoted include the Brahmans (those engaged in sacrifices and priestly functions); the Kshatriyas (rulers and warriors); the Vaishyas (merchants, farmers, and tradesmen); the Shudras (labourers, craftsmen, and service professionals).[2] On the other hand, Muslims belong to two major sects: Sunnis and Shias, while each sect has different *biradaris*, grouped under Ashraf and Ajlaf (Ansari 1960). The former comprise of high-rank Muslims like Syeds, Sheikhs, Pathans, and Moghuls, while the later comprise Qureshis, Ansari, and Saifis, etc. Later on, Arzals were also recognised, which comprise sweepers and other groups of lower occupation. Though Islam does not distinguish the groups on any material grounds, the social isolation might have led to a differentiation of the groups over many generations including differences in their gene pools (Aarzoo and Afzal 2007; Ara et al. 2008, 2011a, 2011b).

In the present study, our aim was to investigate the genetic and biochemical variation among two main communities of the North Indian population, viz. Hindus and Muslims by using enzyme markers, Glucose-6-Phosphate Dehydrogenase (G6PD) and Adenylate Kinase (AK), to find their genetic structure and differentiation.

Materials and Methods

Collection of Sample

The survey was conducted from April 2011 to June 2011 in Aligarh. The Aligarh city of Uttar Pradesh (U. P.) is situated between latitude 27° 28′ and 28° 10′ north and longitude 77° 29′ and 78° 36′ east. The total area is 34.05 km^2. Aligarh has almost a dry climate throughout the year. During the winter, the temperature is very low.

Laboratory Method

About 3 ml of blood was collected in a vial containing 0.3 ml of 10% EDTA and the blood was brought to the laboratory and kept frozen for not more than three hours.

The serum was separated on the day of collection by centrifuging for five minutes at 3.000 rpm. The red cells were washed three times in 0.145 M saline; the washed cells were lysed by addition of an equal volume of distilled water and the haemolysates frozen.

Enzyme Markers

Electrophoresis for Glucose-6-Phosphate Dehydrogenase

The electrophoresis was performed by using 13% hydrolyzed starch gel and the following buffers.

(a) Gel buffer (tris chloride, sodium EDTA, dilution in water).
(b) Tank buffer (gel buffer, sodium chloride).

1 Sanghvi (1953); Cavalli-Sforza and Edwards (1964); Latter (1973); Nei (1973).
2 Karve (1961); Singh (1998); Basu (2003); Majumder (2001a, 2001b).

Sample application: The haemolysates was applied on Watman no. 3 filter paper, inserts, 10 cm from cathode end. The electrophoresis was performed for 17–18 hours at 4 °C. Staining was performed by using Glucose-6-Phosphate (Na^+ salt), tetrazolium compound (such as MTT), phenazine methosulphate, NADP in tris-HCl buffer.

Electrophoresis for Adenylate Kinase

The electrophoresis was performed by using 10–12% hydrolyzed starch gels and the following buffers.

(a) Tank buffer (citric acid, sodium hydroxide).
(b) Gel buffer (L-Histidine monohydrochloride).

Sample application: The haemolysate was applied on Watman no. 3 filter paper inserts at the centre of the gel. The electrophoresis was performed at 5 volt/cm for 16 hours at 4 °C. Staining was done by using Adenosine 5^{I}-diphosphate ADP (disodium salt).

Statistical Analysis

The unit of study in population genetics is gene rather than the genotype or phenotype. Thus to characterise the present population groups from Aligarh, phenotypic data, after applying the chi-square tests, were reduced to allele frequency data for the estimation of measures of genic variation, genetic differentiation, and genetic distance.

Allele Frequency Calculations

G6PD System

$$p = \frac{a + 2c + d}{a + b + 2(c + d + e)},$$

$$q = \frac{b + d + 2e}{a + b + 2(c + d + e)},$$

where
a = total number of normal (SS) males,
b = total number of deficient (ss) males,
c = total number of normal (SS) females,
d = total number of heterozygous (Ss) females,
e = total number of deficient (ss) females.

AK System

Allele frequency of AK was computed by the Hardy Weinberg law. If the alleles for a normal genotype are represented as *AA* and the alleles for rare homozygote as *aa*, according to the Hardy-Weinberg law, the frequency of the homozygotes *aa* is q^2 and the frequency of the other two genotypes are p^2 and $2pq$ respectively.

The Chi-Square Test

The chi-square test for goodness of fit was applied to test the significance of deviations between the observed and the expected phenotype numbers.

$$\text{Chi-square } (\chi^2) = \sum \frac{(\text{number observed} - \text{number expected})^2}{\text{number expected}}.$$

The contingency chi-square test was performed for inter-population and inter-group (Hindu and Muslim) comparisons.

Genetic data analysis: The phenotypes were recorded for each tract and each sample, and the gene frequencies were calculated according to the Hardy-Weinberg law using a gene-counting method. Heterozygosity, gene diversity parameters, and the genetic distance were calculated using the following equations:

(i) $H = 1 - X_i$,

with X_i = frequency of ith allele.

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

(ii) $H_T = H_S + D_{ST}$.

The genetic distance was determined using Nei's (1972) formula.

The normalised identity of gene between *X* and *Y* with respect to all loci is defined as follows (Nei 1972):

(iii) $I = \frac{J_{XY}}{\sqrt{J_X \cdot J_Y}}$.

The genetic distance *D* between *X* and *Y* is defined as

(iv) $D = -\ln I$.

The dendrogram was constructed using the UPGMA clustering method, Phylip Version 3.63 (Felsenstein 1993).

F_{ST} test

$$F_{ST} = 1 - \frac{H_S}{H_T}.$$

Results

The survey was conducted for 585 individuals, out of which 275 (47.01%) were Muslims and 310 (52.99%) were Hindus.

Phenotype Frequencies

G6PD (X-Linked)

The frequency of phenotype SS is quite high, i.e., 96.24% for males and 96.48% for females among Muslims, and 96.18% for males and 94.77% for females among Hindus, and for combined groups 96.21% for males and 95.59% for females. Muslims have 0.70% females and Hindus have 1.96% females which are intermediate (Ss). Muslims consist of 3.76% males and 2.82% females, which are deficient for G6PD. For Hindus 3.82% males and 3.27% females are deficient. Males are more deficient than females, i.e., 3.79% and 3.05% respectively for combined groups. Hindus are more G6PD deficient as compared to Muslims. Among all the four Muslim populations only one heterozygote female is found, i.e., in Sheikhs; while in Hindus three

Table 1: Distribution of G6PD among Various Populations of Aligarh City, India.

Populations	**Tested**	**Sex NO. (%)**	**Glucose-6-Phosphate Dehydrogenase**				
			Phenotypes			**Allels**	
			(SS)	**(Ss)**	**(ss)**	**S**	**s**
Syed	72 (12.31)	M-35 (48.61) F-37 (51.39)	34 (97.14) 35 (94.59)	0 (0.00) 0 (0.00)	1 (2.86) 2 (5.40)	0.9541	0.0459
Sheikh	65 (11.11)	M-25 (38.46) F-40 (61.54)	25 (100) 38 (95.00)	0 (0.00) 1 (2.50)	0 (0.00) 1 (2.50)	0.9714	0.0286
Pathan	80 (13.67)	M-45 (56.25) F-35 (43.75)	43 (95.56) 34 (97.14)	0 (0.00) 0 (0.00)	2 (4.44) 1 (2.86)	0.9652	0.0348
Ansari	58 (9.91)	M-28 (48.27) F-30 (51.72)	26 (92.86) 30 (100.00)	0 (0.00) 0 (0.00)	2 (7.14) 0 (0.00)	0.9772	0.0227
Brahmin	85 (14.53)	M-47 (55.29) F-38 (44.71)	44 (93.62) 36 (94.74)	0 (0.00) 1 (2.63)	3 (6.38) 1 (2.63)	0.9512	0.0488
Bania	78 (13.33)	M-35 (44.87) F-43 (55.13)	34 (97.15) 40 (93.02)	0 (0.00) 1 (2.32)	1 (2.85) 2 (4.65)	0.9504	0.0496
Rajput	94 (16.07)	M-49 (52.13) F-45 (47.87)	48 (97.96) 45 (100.00)	0 (0.00) 0 (0.00)	1 (2.04) 0 (0.00)	0.9928	0.0072
Jatav	53 (9.06)	M-26 (49.06) F-27 (50.94)	25 (96.15) 24 (88.89)	0 (0.00) 1 (3.70)	1 (3.85) 2 (7.41)	0.9250	0.0750
Muslims	**275** **(47.01)**	**M-133 (48.36)** **F -142 (51.64)**	**128 (96.24)** **137 (96.48)**	**0 (0.00)** **1 (0.70)**	**5 (3.76)** **4 (2.82)**	0.9664	0.0336
Hindus	**310** **(52.99)**	**M-157 (50.65)** **F-153 (49.55)**	**151 (96.18)** **145 (94.77)**	**0 (0.00)** **3 (1.96)**	**6 (3.82)** **5 (3.27)**	0.9590	0.0410
Combined	**585**	**M-290 (49.57)** **F-295 (50.42)**	**279 (96.21)** **282 (95.59)**	**0 (0.00)** **4 (1.36)**	**11 (3.79)** **9 (3.05)**	0.9625	0.0375

In 8 different populations (Chi-Square = 8.441523 df = 30 p < .997516).
Between Muslims and Hindus (Chi-Square = 1.370791 df = 6 p < .975).

heterozygote females are present, i.e., one in Brahmin, one in Bania, and one in Jatavs. The G6PD deficiency has zero frequency for males of Sheikh, females of Ansari, and females of Rajput (Table 1).

AK

The frequency of AK (1–1) is 90.08%, that of AK (2–1) is 9.57% and of AK (2–2) is 0.17% for combined groups. The frequency of AK (2–2) is zero for Muslims and 0.32% for Hindus, that of AK (2–1) is 7.24% for Muslims and 11.29% for Hindus, again AK (1–1) is 92.36% and 88.39% for Muslims and Hindus, respectively. The AK (1–1) is most common among Ansaris, i.e., 94.83% and least common in Rajputs (79.79%), while AK (2–1) is the highest among Rajputs (19.15%) and the lowest among Ansaris (5.17%), AK (2–2) is totally absent in all populations studied except Rajputs, i.e., 1.06% (Table 2).

Allele Frequencies

G6PD

The frequency of S allele is high, i.e., 0.9625 and of s allele is 0.0375 for combined group. The s allele is more common in Hindus (0.0410) as compared to Muslims (0.0336). Among all populations Ansaris have the highest frequency of S allele, i.e., 0.9928; the s allele is highest among Jatavs, 0.0750 (Table 1).

AK

The allele AK^1 has a high frequency, i.e., 0.9486, and of AK^2 it is 0.0495 for combined groups. The frequencies of AK^1 allele are 0.9618 and 0.9403 and of AK^2 allele these are 0.0382 and 0.0596 for Muslims and Hindus respectively. Among Muslims, Ansaris have the highest frequency for AK^1 (0.9741)

Table 2: Distribution of Enzyme Marker Adenylate Kinase among Various Populations of Aligarh City, India.

Populations	**Tested**	**Adenylate Kinase**				
		Phenotypes			**Alleles**	
		(1–1)	**(2–1)**	**(2–2)**	***AK*¹**	***AK*²**
Syed	72 (12.31)	65 (90.28)	7 (9.72)	0 (0.00)	0.9514	0.0486
Sheikh	65 (11.11)	59 (90.77)	6 (9.23)	0 (0.00)	0.9538	0.0461
Pathan	80 (13.67)	75 (93.75)	5 (6.25)	0 (0.00)	0.9687	0.0312
Ansari	58 (9.91)	55 (94.83)	3 (5.17)	0 (0.00)	0.9741	0.0258
Brahmin	85 (14.53)	78 (91.76)	7 (8.24)	0 (0.00)	0.9588	0.0412
Bania	78 (13.33)	71 (91.03)	7 (8.97)	0 (0.00)	0.9551	0.0448
Rajput	94 (16.07)	75 (79.79)	18 (19.15)	1 (1.06)	0.8936	0.1063
Jatav	53 (9.06)	50 (93.34)	3 (5.66)	0 (0.00)	0.9617	0.0283
Muslims	**275 (47.01)**	**254 (92.36)**	**21 (7.64)**	**0 (0.00)**	**0.9618**	**0.0382**
Hindus	**310 (52.99)**	**274 (88.39)**	**35 (11.29)**	**1 (0.32)**	**0.9403**	**0.0596**
Combined	**585**	**528 (90.25)**	**56 (9.57)**	**1 (0.17)**	**0.9486**	**0.0495**

In 8 different populations (Chi-Square = 15.20533 df = 14 p < .887072).
Between Muslims and Hindus (Chi-Square = 1.984879 df = 2 p < .5).

and in Hindus Jatavs have the highest frequency (0.9617); while AK^2 allele has the highest frequency in Syeds (0.0486) of the Muslim groups and Rajputs (0.1063) of the Hindu group (Table 2).

Heterozygosity

G6PD and AK have a low heterozygosity, the pooled heterozygosity for the G6PD is found to be 0.0722 and for AK it is 0.0977. For both the marker loci viz. G6PD and AK Hindus have a larger heterozygosity than the Muslims, for G6PD, Hindus have 0.0786 and Muslims have 0.0649 heterozygosity and for AK, Hindus have 0.1123 and Muslims have 0.0735. For G6PD the highest value of heterozygosity is 0.1387 among Jatavs and the lowest among Rajputs, i.e., 0.0143; for AK the highest heterozygosity is found among Rajputs (0.1902) and lowest among Ansaris (0.0505) (Table 3).

Table 3: Observed Heterozygosity of Different Populations of Aligarh, Using Enzyme Markers G6PD and AK.

Populations	G6PD	AK
Syed	0.0876	0.0925
Sheikh	0.0556	0.0881
Pathan	0.0672	0.0606
Ansari	0.0446	0.0505
Bania	0.0928	0.0790
Brahmin	0.0943	0.0858
Rajput	0.0143	0.1902
Jatav	0.1387	0.0743
Muslims	0.0649	0.0735
Hindus	0.0786	0.1123
Combined	0.0722	0.0977

In 8 different populations (Chi-Square = .1547108 df = 7 p < .995).
Between Muslims and Hindus (Chi-Square = .0010726 df = 1 p < .995).

Gene Diversity

The gene diversity of intra-population (H_s) and inter-population (D_{ST}) indices are 0.0744 for G6PD and 0.0901 for AK (H_s); 0.0010 for G6PD and 0.0012 for AK (D_{ST}), respectively. The coefficient of gene differentiation (G_{ST}) is 0.0133 for G6PD and 0.0131 for AK. The gene diversity of the total population is 0.0754 and 0.0913 for G6PD and AK respectively (Table 4).

Table 4: Gene Diversity Analysis for Two Individual Loci G6PD and AK in Eight Populations of Aligarh, India.

Locus	D_{ST}	H_T	H_S	G_{ST}
G6PD	0.0010	0.0754	0.0744	0.0133
AK	0.0012	0.0913	0.0901	0.0131

Genetic Distance

For G6PD and AK markers the genetic distance measures in between populations is very small (Table 5). It is the highest between Brahmin and Sheikh (0.02130) and is zero for Brahmin–Bania, Syed–Bania, and Syed–Brahmin (Table 5). It may be mainly due to the smaller sample size of the populations surveyed.

On the basis of their genetic distances, a dendrogram was constructed using the UPGMA method. The Syed and Brahmin form one cluster and Bania and Rajput form another one, joining with Jatav and/or joining with Sheikh, whereas Pathan and Ansari constitute another cluster (Fig. 1). Based on the dendrogram the Syed and Brahmin are older populations.

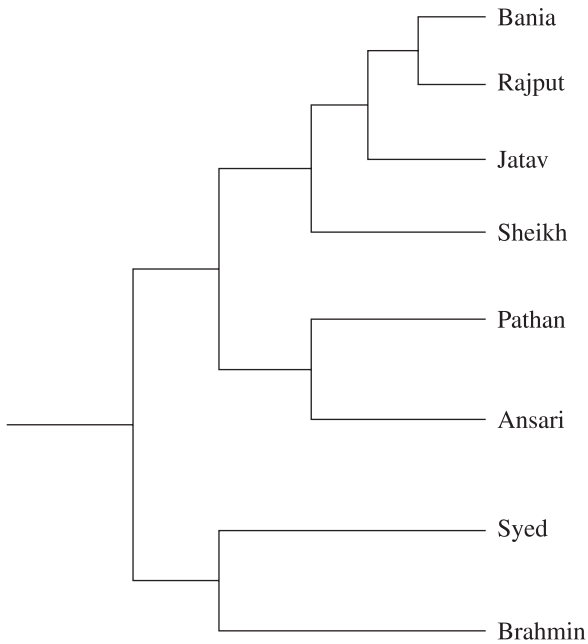

Fig. 1: Dendrogram showing genetic relationship among different populations of Aligarh, North India, using G6PD and AK.

Table 5: Genetic Distance Matrix among Different Populations of North India.

Populations	Syed	Sheikh	Pathan	Ansari	Brahmin	Bania	Rajput	Jatav
Syed		0.00011	0.00014	0.00030	0.00000	0.00000	0.00264	0.00057
Sheikh	–	–	0.00013	0.00016	0.02130	0.00022	0.00211	0.00108
Pathan	–	–	–	0.00007	0.00006	0.00343	0.00325	0.00063
Ansari	–	–	–	–	0.00030	0.00752	0.00343	0.00103
Brahmin	–	–	–	–	–	0.00000	0.00557	0.00267
Bania	–	–	–	–	–	–	0.00308	0.00040
Rajput	–	–	–	–	–	–	–	0.00559
Jatav	–	–	–	–	–	–	–	–

F_{ST} Test

On the basis of the F_{ST} test, Muslims and Hindus were compared, and it was found that the genetic divergence between Hindus and Muslims is very low (Table 6). It may be due to the reason that the North Indian Hindus and Muslims have same ancestors, which again means most of the Muslims of North India have converted from Hindus, thus having a very little divergence. On the other hand, genetic divergence within the groups is comparatively high. For the enzyme markers G6PD and AK, the genetic divergence within Hindus is high as compared to Muslims (Table 6, Fig. 2). This may be due to the fact that the Hindu caste system is very rigid, which means Hindus do not marry among castes, while Muslims have no caste system as such, though *biradaris* are there. Ashrafs (higher occupation Muslims), Ajlaf (lower occupation Muslims), and Arzals (schedule castes and tribes) are ethnically distinct due to their conversions from Hindu caste ancestors. Muslims follow the Indian culture, viz. on the basis of the occupation and castes conversions have been carried out among Muslims, too, for Ashraf, Ajlaf, and Arzal and the marriages between them is not allowed.

Table 6: The Values of Fst to Compare the Genetic Divergence between and within Muslims and Hindus on the Basis of Enzyme Marker Loci.

Markers	Muslims	Hindus	Muslims vs. Hindus
G6PD	0.0020	0.0140	0.00042
AK	0.0027	0.0158	0.00268
Combined	**0.0025**	**0.0152**	**–0.00026**

Discussion

Although 83% of the people are Hindu, India also is the home of more than 120 million Muslims – one of the world's largest Muslim populations. The Indian population also includes Christians, Sikhs, Jains, Buddhists, and Parsis. The caste system reflects the occupationally and religiously defined Indian hierarchies (Hutton 1961). Traditionally, there are four broad categories of castes (*varnas*), including a category of outcastes, earlier called "untouchables" but now commonly referred to as "dalits." Within these broad categories there are thousands of castes and subcastes, whose relative status varies from region to region.

The Indian population is divided into a large number of groups with different languages, religions, castes, and tribes. Throughout the ages many population groups have migrated toward India along northeastern and northwestern 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 group (with mixed groups known as the Mussulmans).

Although Islam does not distinguish 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 (Afzal 2004). The study of the gene pools can throw some light on the origin, ancestry, health, and morbidity status of the groups; for example, there might be either unknown rare mutations or else genetic polymorphism for particular markers (Kirk 1985). It was with this aim that the present research was designed to study the genetic structure and the microdifferentiation of Muslim populations as well as Hindus, including their ge-

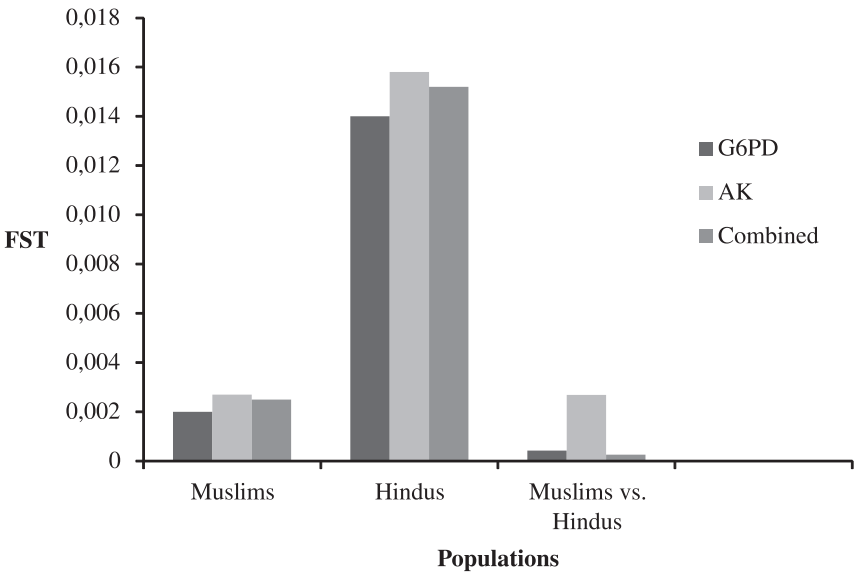

Fig. 2: The values of F_{ST} to compare the genetic divergence between and within Muslims and Hindus on the basis of enzyme marker loci.

netic distances and isolation. We reported the genetic composition of the population of Aligarh.

In the present study, we have investigated the patterns of gene differentiation 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 (Basu et al. 2003). The Muslims have a higher heterozygosity than Hindus, for both markers, G6PD as well as AK; this may be due to the practice of inbreeding among Muslims.

Despite G6PD being an X-linked trait, phenotypically males and females do not show any difference, perhaps because mainly due to female being regarded as a mosaic with respect to traits controlled by genes on X-chromosome. Thus, the enzyme activity remains the same for both males and females.[3] The genetic distances between the populations are very low. By using the UPGMA method, a dendrogram was constructed and it shows that Bania and Rajput are closer and making one cluster which joins to the Jatav and/or joins to Sheikhs. This group joins to another cluster, in which Pathan and Ansari are combined. Syed and Brahmin are close to each other and are older populations.

In the present study, it may be suggested that for the Aligarh population of North India, Hindus and Muslims are very similar to each other, and these populations are not yet genetically differentiated. This may be because both populations have the same ancestors and most of the Muslims of North India have converted from Hindus, though these conversions have been made very recently. On the other hand, differences within the populations seem to be high; especially among Hindus (Fig. 1), perhaps because the marriages between different castes is not allowed in the Indian society, so the castes among Hindus are pure. However, for better results, more marker loci should be taken and Muslim *biradaris* with older history may be compared with the present Aligarh Muslims populations, which appear to be rather new and neo-settlers.

3 Marks (1958); Lyon (1961); Bhasin and Chahal (1996).

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Ein Außerirdischer mit einer Frauen-Tätowierung

Zu einer nicht gendergerechten Rezeption einer Maori-Tätowierung in der populärkulturellen Science-Fiction-Serie "Star Trek"

Georg Schifko

Bei der Produktion der weltweit bekannten Serie "Star Trek" hat man sich öfter "Anregungen aus den unterschiedlichsten Kulturen" (Heilmann und Wenskus 2006: 794; Schifko 2013b: 173) geholt.[1]

1 Dies gilt auch für andere bekannte Science-Fiction-Filme wie z. B. "Star Wars" (Schifko 2015). Es sind hier keineswegs allgemeine Anthropomorphismen angesprochen, durch die sich selbst die fremdartigsten Aliens im Science-Fiction auszeichnen (Raabe 2003: 117), sondern vielmehr spezifische Entlehnungen aus ganz konkreten Kulturen gemeint.