Genetic Heterogeneity and Ethno-historical Considerations of Burusho and Balti Tribes with Regard to ABO and Rh Blood Group Alleles

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Abstract

Background: To study comparative genetic data with regard to ABO and Rh group alleles of Burusho and Balti tribes of northern Pakistan in order to determine origin of these populations.

Methods: A prospective study was conducted from November 2006 to January 2007 at Combined Military Hospital Gilgit in which a total of 4318 blood samples were taken for ABO and Rh D blood grouping. They comprised of 3210 samples taken from the Burusho and 1008 samples of the Balti population. The method of sampling was random. Genetic affinities and gene diversity of the two populations was determined in terms of genetic distancing analysis with regards to ABO and Rh loci.

Results: The average ABO allele frequencies in the Burusho population were ABO*A (0.37) ABO*B (0.32) ABO*AB (0.02) and ABO*O (0.29). Similarly the average allele frequencies of Balti population were ABO*A (0.23) ABO*B (0.31) ABO*AB (0.09) and ABO*O (0.37). In Brusho alleles frequencies for D and d of the Rh group system were 0.942 and 0.0580, for Balti 0.950 and 0.500 respectively for the total data. There is a marked increase in the frequency of blood group gene A in Burusho population and a corresponding decrease in blood group gene O as we proceed from older to younger age groups. Also there is significant divergence (p <0.05) in Burusho population for the distribution of ABO alleles from the general South Asiatic trend (O greater than B greater than A). Probably because of the relatively small starting value of r < 0.5 a selection took place against group O resulting in an increase of the blood group gene A in Burusho population.

Conclusion: The genetic distance analysis reveals that the two tribes included in this study are genetically distant from one another and the genetic clustering pattern correlates with linguistic/ethnic affiliation and geographical proximity of these tribal populations to a certain extent.

Introduction

Palaeolithic humans inhabited the present day areas of Pakistan. Evidence for the presence of archaic homo-sapiens also exists. The area of present day Pakistan may have been inhabited by modern humans as early as 60,000 – 70,000 years back. Indus Valley civilization flourished in 3d and 2d millennia BC.¹ The present day Pakistani population is estimated to be more than 150 million. It is roughly inhabited by more than eighteen ethnic groups speaking more than sixty different languages².

Few comparative genetic and historical studies are available for Northern Pakistan population and generally the results of most studies have been compared with oral tradition about origin of these ethnic groups³.

Alternative forms of genes any one of which may occupy a single locus on homologous chromosomes are called alleles. The major alleles of ABO system are A, B and O. Alleles arise by mutations and may result in phenotypic diversity. Mutations may occur at the DNA level and may also result in the creation of new polymorphisms associated with altered gene⁴.

The frequency of an allele is the proportion it contributes to the total pool of alleles at that locus in a given population. It can be calculated from phenotype frequencies. The sum of allele frequencies at a given locus must be equal to 1.00^{5} .

This study included a large cohort of ethnic Burusho comprising of 3210 individuals and Balti population comprising of 1008 individuals. The major tribes of both the populations were studied in regards to their ABO system allele frequencies to determine what light they can shed on the origins and genetic history of these subgroups that make up the Pakistani population.

Patients and Methods

A total of 4318 blood samples were collected for ABO and Rh grouping by Elder's card method. The sample comprised of 3210 samples from Burusho population and 1008 blood samples from the Balti clan. Informed consent was obtained from all the participants of the study. The method of selection was random.

ABO and Rh-group phenotype frequencies were calculated for the Burusho and Balti population with the help of Hardy Weinberg equation as under:

Allele frequency = $(P^2+2PQ+Q^2 = 1)$.

Genetic distance between the two cohorts was calculated. Student t-test was used to compare the gene frequencies. Finally, a comparative analyses of ABO allele frequency of the Burusho population was done with that of the Greek and Pakistani populations. Similarly the Balti population was compared with the Pakistani and Sino-Tibetan population.

Results

The minimum age of the cohort was 03-years while the maximum was 93 years. The average ABO allele frequencies in the Burusho population were ABO*A (0.37) ABO*B (0.32) ABO*AB (0.02) and ABO*O (0.29) (Table 1). Similarly the average Balti population were allele frequencies of ABO*A (0.23) ABO*B (0.31) ABO*AB (0.09) and ABO*O (0.37) (Table 2). In Brusho alleles frequencies for D and d of the Rh group system were 0.942 and 0.0580, for Balti 0.950 and 0.500 respectively for the total data (Table 3).

	Burusho Population	
(ABO) *A	:	0.37
(ABO) *B	:	0.32
(ABO) *AB	:	0.02
(ABO) *O	:	0.29

Table 1: ABO Genotype Frequencies for

(ABO) *A	:	0.23
(ABO) *B	:	0.31
(ABO) *AB	:	0.09
(ABO) *O	:	0.37

Table 2: ABO Genotype Frequencies forBalti Population

Table 3: Allele Frequencies for Rh D

Burusho	:	0.942
Balti	:	0.950

Statistical analysis showed a significant difference (p < 0.05) between the frequencies of blood group A for the two populations. Furthermore there was also a significant difference (p < 0.05) for the frequencies of blood group A between the Burusho and the Pakistani population. The overall difference between the frequencies of ABO blood groups of Burusho and Balti population was insignificant (p = 0.25).

Secondly Burusho population showed a divergence for the distribution of ABO alleles from the general Asiatic trend of (0 > B > A). There was a decrease in percentage of blood group A from the older age group (Age > 70yrs = 81.0%) compared to the younger age group (Age < 20 yrs = 36.0%).

Discussion

The Hardy Weinberg equation is employed to calculate the allele frequencies for ABO and Rh systems. However Hardy Weinberg equation relies on certain basic conditions. These include no mutations, no migrations of the population, lack of selected advantages or disadvantages of a particular trait which should be large enough for a population so that chance alone cannot alter its allele frequencies⁶. In fact it is not possible to meet all of these conditions in their entirety. The resulting changes in ABO and Rh allele frequencies may not be obvious in human population over a few generations but can accumulate and can explain many of the differences in allele frequencies between populations⁷. Y-chromosomal DNA variation pattern of Pakistani population has broken the myth that Burusho or Balti population has any possible origin from the armies of Alexander the great^{8, 9}. The common haplotypes found in Greek population were neither detected in Burusho or Balti population. No over all support for a Greek origin by Y-chromosomal analysis was found but this finding does require the important assumption that modern Greeks are representatives of Alexander's Army¹⁰.

The Balti are thought to have migrated from Tibet where predominant haplotype groups are of 4 and 26. Neither is present in the Balti population¹¹.

In our study a comparative analysis of Burusho population with ABO allele frequencies of Pakistani and Greek population was also revealing (Table 4) as was the comparison of ABO allele frequencies of Balti population with Pakistani and Sino-Tibetan population (Table 5).

Table 4: ABO Comparative Analysis ofBurusho Population

		Burusho	Pakistani	Greek
ABO	(A)	0.37	0.20	0.42
ABO	(B)	0.32	0.32	0.14
ABO	(AB)	0.02	0.06	0.04
ABO	(O)	0.29	0.42	0.40

Our analysis showed a significant divergence of ABO allele frequencies of Burusho and general Pakistani population. The general South – Asiatic trend of (0 > B > A) was absent in the Burusho population¹².

Comparing the ABO allele of Burusho and Balti population we observed a significant difference in ABO (A) and ABO (O) allele frequencies (p < 0.05). The probable explanation is that the two groups might have a totally separate different ethnic origin. However over a period of time the ABO allele frequencies might have changed due to effect of gene flow¹³.

The Balti population is closer to general Asiatic ABO frequencies. Also its ABO frequencies

are much nearer to Sino-Tibetan ABO frequencies¹⁴. An interesting observation is the corresponding decrease in group O frequencies as we proceed from older to younger age groups in the Burusho population. Probably because of relating small starting value of r < 0.5 a selection took place against group O resulting in an increase of blood group A in Burusho population¹⁵. Mother-Child incompatibility and natural disasters rampant in these areas might have also contributed to this trend¹⁶.

Table 5: ABO Comparative Analysis ofBalti Population

		Balti	Pakistani	Sino-Tibetan
ABO	(A)	0.23	0.20	0.23
ABO	(B)	0.31	0.32	0.25
ABO	(AB)	0.09	0.06	0.06
ABO	(0)	0.37	0.42	0.46

The genetics distance analysis gave a value of (> 1) which reveals that the two tribes i.e. Burusho and Balti are genetically distant entities in terms of ABO frequencies. The general Rh frequencies are similar for the total data¹⁷. However the general genetic clustering pattern correlates well with the genetic affiliation and geographical proximity of these tribal populations to a certain extent¹⁸.

It may be emphasized that there exists a marked phenotypical difference of Burusho and Balti population from the rest of the population of Pakistan. This sharp contrast of the phenotype from the typical Pakistani population may still suggest a heretical association of Burusho and Balti population in having its roots distant to those who dwell in South East Asia^{19, 20}.

Conclusion

The genetic distance analysis reveals that the two tribes included in this study are genetically distant from one another and the genetic clustering pattern correlates with linguistic/ethnic affiliation and geographical proximity of these tribal populations to a certain extent.

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