

Distribution of A1A2BO and Rh Blood Groups Among the Rajputs of Uttaranchal

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ABSTRACT The present paper is the result of a study of distribution of A1A2BO and Rh(D) blood group carried out among the Rajputs of Mussoorie, Uttaranchal. The frequency of A1 is highest with a percentage frequency of 38.54% and that of Rh+ is 94.63%. It has been observed that when the allele frequency of the present population is compared, it falls close to other populations of the Himalayan region.

INTRODUCTION

Human population genetics is the study of the nature and source of the inherited differences and involve predicting the changes that may take place in relative frequencies of different genes that may be found in a population, and with determining the conditions under which equilibrium between forces affecting their frequencies may be obtained. It is implied here that this discipline of human genetics incorporates within itself the study of genetic and environmental factors, as well as the forces of micro-evolution leading to macro-evolution, which influences the genetic structure of a human population.

In the present state of our knowledge, human population genetics is not only the static study of 'Gene-geography', but also involves the dynamics of it, and the etiology of hereditary similarity and diversity of various morphological and genetic characters among various population groups. Since most of the morphological characters are subjected to many intricate factors such as environment, nutrition and cumulative effect of various genes, these traditional traits which were used to characterize typological units, are becoming more and more confined to the elucidation of specific problems to which their use is immediately applicable. Genetic characters are, therefore, the obvious choice for understanding variations between and within populations.

Human blood, considered as vital fluid for centuries, has come to occupy a vital place in the study of human genetics as it is the most readily

available tissue, which provides an array of discontinuous polymorphic, serological and biochemical characters. It is an established fact that most of the serological and biochemical characters have a distinct hereditary mechanism and so it is desirable that the biological variability be measured in terms of traits whose precise mode of inheritance is known. Moreover, they are generally determined at the time of conception and are least affected by external environment after their determination. It is this that explains the importance of serological and biochemical markers in understanding the genetic structure of human populations, as well as variations among them.

The significance of this study lies in the fact that it describes the population variation among humans living within a limited area and time frame of an ecological zone. It is hoped that once the variation and their patterns are recognized, these can further help in explaining the present day genetic structure of these populations. The study may also help in isolating micro-evolutionary mechanisms operating at breeding population level within an ecosystem assuming of course, that observations are the result of genetic and environmental interaction and genetic consequences of such factors as population size, migration and mating pattern in that population.

MATERIALS AND METHODS

For the present study, the data were collected from Rajputs of Mussoorie, Uttaranchal. The other population groups of the area comprised of Brahmins, Scheduled Castes and Scheduled

Tribes. 205 samples were collected and analyzed for ABO and Rh(D) blood group systems. All the necessary precautions were taken for random sampling. Individual data of each subject- name, age, sex, caste, sub-caste, maternal uncle's caste, place of birth etc. were also collected using a brief questionnaire. The samples were analyzed for blood groups ABO and Rh(D); the test was done using Anti-A, Anti-A1, Anti-B, Anti-H and Anti-D. for ABO blood grouping, cell suspension technique was used. Samples were collected in normal saline solution, washed and analyzed in 3-5% suspension of red cells in saline. For Rh(D) blood grouping, slide method was used (Bhasin and Chahal, 1996).

RESULTS AND DISCUSSION

ABO System: Among 205 Rajputs tested for A1A2BO blood groups, it was observed that A1 has the highest frequency (38.54), followed by group B (25.85), group O (23.91), A1B (10.24) and least being A2 (0.98) and A2B (0.48). The allele frequency of O is highest, about 0.4899 followed by A1 (0.2976), B (0.2165) and the least allele frequency is found to be of A2 (0.0099).

The chi-square test to test the goodness of fit between the observed and expected frequencies is 0.2201, which is non-significant with 2 degrees of freedom at 5% probability level ($.30 > p > .20$). Hence, the result indicates a good agreement between the observed and expected frequencies and that the population is in genetic equilibrium.

The value of D/σ is -0.8633, which is quite low and less than 2, thereby indicating that the population obeys Hardy-Weinberg Law and no

Table 1: Frequency distribution of phenotype and allele frequencies of ABO blood group among Rajputs of Uttaranchal

Pheno-type	Observed no.	%	Allele	Allele frequency
A1	79	38.54	ABO*A1	29.36
A2	2	0.98	ABO*A2	0.97
B	53	25.85	ABO*B	21.35
O	49	23.91	ABO*O	48.32
A1B	21	10.24		
A2B	1	0.48		
Total	205	100.00	Total	100.00

sampling error has been committed.

Rh System: Out of 205 samples tested with Rh(D), it is concluded that 194 (94.63%) are Rh positive and only 11 (5.37%) are Rh negative. The

Table 2: Frequency distribution on phenotype and allele frequencies of Rhesus blood group among Rajputs of Uttaranchal

Phenotype	Observed No.	%	Allele	Allele frequency
Rh < %	194	94.63	D	77.0
Rh %	11	5.37	d	23.0
Total	205	100.00		100.0

incidence of homozygous Rh positive individuals (DD) is 0.9471 and that of heterozygous Rh positive individuals (Dd) is 0.0529.

In the present study, carried out among the Rajputs of Mussoorie, it has been observed that the population under study falls close to the populations of the neighbouring areas of Uttaranchal and Himachal Pradesh. When the allele frequency of the present population was compared with some populations of the Western, Easter and Central Himalayas, it showed non-significant variation with most of the population groups. (Tiwari and Bhasin, 1968; Mourant et al., 1976; Bhasin et al., 1992; Bhasin and Walter, 2001)

On the whole, it has been observed that the present population is falling close to the population groups of the Himalaya, particularly with the Western and Central Himalayan regions.

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