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Original article

The Role of Blood Group and Demographic Factors in Dengue Infection: Implication of Public Health in Bangladesh

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Abstract

Background: Dengue fever, caused by the Dengue virus, has become a global health concern, with its prevalence expanding significantly over the decades. ***Objective:*** This study aimed to investigate the relationship between ABO blood groups and susceptibility to dengue infection. ***Methodology:*** A cross-sectional study was conducted in Dhaka city, Bangladesh, from March to September 2023, involving 1200 individuals, including Dengue positive and negative cases. ***Result:*** The results showed that the blood group had a significant association ($p<0.05$*) with the frequency of Dengue virus infection. While blood type A had the lowest susceptibility to dengue infection, those with blood groups O and AB had a much higher risk. Age group and living in an urban area were found to be significant factors related to dengue infection ($p<0.05$*). ***Conclusion:*** These results underscore the importance of considering demographic characteristics and blood groups in understanding Dengue transmission dynamics and devising effective public health strategies for its control.

Keywords: Dengue virus, Dhaka, ABO blood types

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Introduction:

Before 1970, only nine countries experienced significant dengue epidemics. Now, dengue is endemic in over 100 countries across Africa, the Americas, the Eastern Mediterranean, South-East Asia, and the Western Pacific. The Americas, Southeast Asia, and the Western Pacific bear approximately 70% of the burden, with Asia being the most affected region.[1] Dengue virus is a RNA virus (Flaviviridae family) with four distinct serotypes (DENV 1-4) that are common in tropical climates.[2] Between January 1st and August 7th, 2023, Bangladesh reported 69,483 confirmed dengue cases and 327 deaths, with a higher than usual case fatality rate (0.47%). Notably, 63% of cases and 62% of deaths occurred in July 2023. This surge, starting earlier than usual, deviates from past patterns and indicates an unusual seasonality.[3] The transmission of these viruses occurs through the bite of an infected mosquito. Female mosquitoes, in particular, feed on the blood of various hosts, such as birds or mammals. During this feeding process, mosquitoes release saliva before and during the bite. Once the virus is transmitted, the newly infected host may experience symptoms.[4] Genetic factors are also

involved, along with environmental factors, incases of illness susceptibility. Despite exposure, not everyone gets infected, as individuals may have varying levels of susceptibility or resistance. Therefore, factors like genetics, i.e. blood group, and environmental conditions can affect disease development.[5] Various research studies speculate that the human leukocyte antigen (HLA) haplotype determines the propensity to dengue infection, but they have not identified any clear or precise polymorphisms. The ABO blood type is a component of innate immunity, and people with various ABO blood groups have varied susceptibility to or resistance to viral and bacterial infections and illnesses. Kaipainen and Vuorinen proposed a correlation between blood groupings and disease in 1960. The ABO blood group plays a considerable role in making a person susceptible or resistant to different bacterial or vector-borne diseases.[6] There are four major blood groups (blood types): A, B, AB, and O. Each blood group have RhD positive or RhD negative, for a total of eight blood groups and few specific blood groups are the most prevalent for vector-borne diseases i.e, dengue and chikungunya.[7] A person's susceptibility or resistance to dengue infections might be determined by testing their blood type. The primary objective of this study was to identify blood groups that may be correlated with an individual's resistance to or susceptibility to dengue infection.

Materials and Methods:

This was a retrospective observational study conducted in Dhaka city during the period from March to September 2023. Data regarding 600 dengue NS1 antigen/dengue immunoglobulin M (IgM) antibodies or both (IgM & IgG) positive serum samples as well as 600 dengue negative serum samples as a control group were collected by Simple Random Sampling method irrespective of age and sex from the clinical laboratory of Bashundhara Ad-din Medical College and Rushmono Specialized Hospital, Dhaka.

All patients with serological confirmation of dengue (NS1, IgM/IgG positivity) were done by immunochromatographic tests (qDetect™ dengue NS1 antigen and qDetect™ dengue IgM/IgG test kit (OMCH, Dhaka, Bangladesh), respectively. ABO and Rh blood grouping reports were collected from dengue patients as well as from dengue-negative persons. General information about dengue fever awareness was recorded through an interview with a semistructured, pre-tested questionnaire from the participants. Proper written consent was obtained from all the participants before data collection. A predesigned questionnaire was used in data collection. All collected data was processed and analyzed using Microsoft Excel version 10. Ethical clearance was obtained from the Ethical Committee of Bashundhara Ad-din Medical College and Hospital, Dhaka.

Results:

The present study investigated the relationship between demographic factors, including age group, sex, residency, ABO blood groups, and dengue infection status among a sample of 1200 individuals. Notably, individuals aged 40-59 years exhibited the highest proportion(42.67%) of dengue-positive cases and age group was significantly ($p<0.05$) associated with dengue infection. Additionally, urban residency was also significantly ($p<0.05$) correlated with a higher incidence of dengue infection. Dengue cases were higher in males (60.83%) compared to females (39.17%). However, there was no significant difference in dengue infection rates according to sex.

Table 1: Socio-demographic status of study participants

	Dengue Negative (n=600)	**Dengue Positive (n=600)**	**P Value**
Age group			
<20 years	173(28.83%)	98(16.33%)	**<0.05**
20-39years	214 (35.67%)	167(27.83%)	
40-59 years	129 (21.5%)	256(42.67%)	
60 years	84 (14%)	79(13.17%)	
Sex			
Male	387(64.5%)	365(60.83%)	0.189
Female	213(35.5%)	235(39.17%)	
Residency			
Urban	487(81.17%)	324(54%)	**<0.05**
Rural	113(18.83%)	276(46%)	

* Chi-square test done
* P value <0.05 is considered as significant

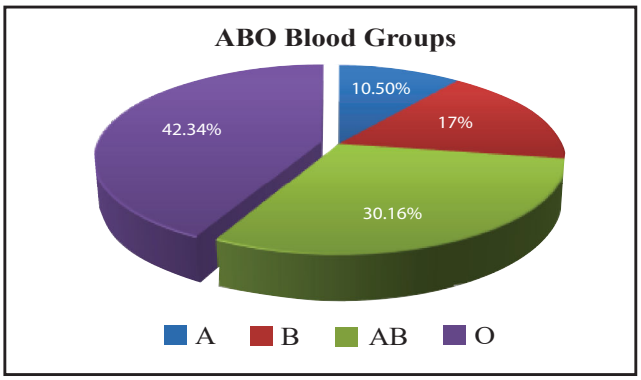

Figure 1: Pie chart showing the frequency distribution of ABO blood groups among dengue-positive cases

Table 2: ABO blood group distribution in dengue positive and negative cases

Blood Group	Dengue Positive (n=600)	Dengue Negative (n=600)	P Value
A	63	125	**<0.05**
B	102	180	
AB	181	138	
O	254	157	

* Chi-square test was used to compare the dengue positive cases and dengue negative controls
* P value <0.05 is considered as significant

About 63 of the 600 dengue-positive cases belonged to blood group A, 181 to blood group AB, and 254 to blood group O (Table 2). Table 2 also shows the distribution of blood types among the Dengue Negative or the control group. A significant association was found between the blood group with dengue positivity (p-value < 0.05).Among the dengue-positive cases, blood type O and AB had the highest rates of dengue infection 42.34% and 30.16% respectively,whereas blood group A had the lowest susceptibility to dengue infection (10.5%).

Discussion:

The emergence and re-emergence of viral diseases transmitted by vectors raise worldwide concerns about the hazard to health and the feasibility of prevention and control. Dengue (DENV) is the most frequent vector-borne viral (*Flaviviridae* family) illness in Asia and the sub-Asian region. It has drawn attention in recent years due to its rising prevalence, extending the geographical range and potential consequences from circulation and unexpected health issues and social burdens.[8] International tourists who visit endemic and epidemic areas have the possibility of acquiring an arbovirus infection. Dengue virus is the most often diagnosed arboviral illness in visitors and locals, whereas the specific arbovirus risk varies with geography.[5] In Bangladesh, there have been several dengue epidemic outbreaks throughout the previous few years. Changing anthropological behaviour, climate change and high mutation frequency are important determinants of arthropod-borne virus emergence. Arthropod-borne viruses adapt readily to new susceptible hosts by alteration of receptor specificity, transmission efficiency, antigenicity, ecological and environmental conditions.[9] Besides all these, there are one of the most important hereditary qualities of an individual is blood. The blood type-disease relationship may be highlighted by the ABO and rhesus (Rh) blood grouping systems. The basis for genetic and evolutionary research and disease may be the blood grouping system.[10] Even though few studies have documented correlations between dengue infections and specific blood groups, relatively very few have related the issue. In Bangladesh the phenotypic frequency of blood group A+ (21.3%), A- (1.6%), B+ (30.1%), B- (1.6%), AB+ (4.4%), AB- (0.7%), O+ (37.3%) and O- (3.0%) whereas Rh positive and Rh negative were 93.1% and 6.9%, respectively.[10] The present study included 1200 subjects among them 600 dengue positive patients (positive for dengue NS1 antigen/dengue immunoglobulin M (IgM) antibodies or both (IgM & IgG) and about 600 were dengue negative people irrespective of age and sex as a control group. Among them aged people (40 to 59 years) were more infected in dengue (Table 1) most probably due to increased prevalence of chronic diseases and other comorbidities in the elderly persons. In modern-day years, epidemiological studies from regions that traditionally demonstrated a classical pattern.[11] A seroprevalence study of adults aged 18–79 years in Singapore comparing the prevalence of anti-dengue IgG antibodies in the population in 2004 and 2010 showed that the age-standardized rates of seroprevalence were significantly lower in 2010 (54.4%) compared to 2004 (63.1%).[12] In this study, males (60.83%) are more infected than female and indicating the heightened risk of transmission in urban environments compared to rural areas (Table 1). It may be influenced by various factors such as sociocultural differences and differences in behavior and activities. Further research is needed to explore these factors and develop targeted prevention strategies. Dengue infection is significantly higher in urban areas ($p > 0.05$) than in rural areas might be due to rural environments based on population size, population density, housing density, infrastructure or surface cover type (impervious surfaces, vegetation), access to urban areas or distance to a road/urban center, environmental changes (including changes to landscapes, rural production systems, climate, land use, and transportation infrastructure) or agricultural practices.[13]

The result of the study demonstrated that individuals with blood group O (42.34%) and AB (30.16%) are more susceptible to dengue infection, while blood group A appeared to be protective against the virus. A research finding of Ravichandran et al.(2019),[6] individuals with blood group O were much less susceptible to dengue fever. In contrast, according to the research by Khode et al.(2013)[14] blood type O is a risk factor for dengue infections and AB blood group is statistically significantly associated with dengue fever as compared to the control group.[15]

Usually host genetic factors and the immune system play a pivotal role in the prevention of viral infections. Two

genetic variables, HLA and ABO blood categories, have been associated with vulnerability or resistance to infectious illnesses. Blood-type antigens are carbohydrate -based, with N-acetyl-d-galactosamine being the immunodominant sugar for A determinants and d-galactose for B determinants.[16] Galactosyltransferases synthesize these sugars. The primary antibody that detects these sugars is natural IgM. DENV patients develop IgM antibodies against glycosylated dengue viral proteins, which may cross-react with host cells. Further research is needed to determine whether an individual's ABO blood type and natural IgM antibody levels impact dengue illness or not.[6] Although previous studies have established a correlation between HLA and dengue disease, no specific polymorphisms have been identified that exhibit an unequivocal association with the severity of the disease. Therefore, it is important to determine whether a correlation exists between the severity of dengue disease and a polymorphism in the galactosyltransferase gene.

The research was constrained by its retrospective case record–based design, which prevented the investigation of several parameters.

Conclusion:

This study concludes that the O and AB blood group is associated with a higher risk of developing dengue fever than those with other blood groups. These results may provide valuable insights into the complex interplay between demographic characteristics and ABO blood groups in dengue infection. Understanding these associations can inform public health interventions aimed at controlling the spread of dengue virus infection.

Conflict of interest:

The authors hereby declare that no conflict of interest exists.

Acknowledgment:

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