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Article

Blood Groups Genetic Susceptibility Associated with Infectious Disease and Covid-19

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Abstract: This study investigates the relationship between ABO blood group antigens and susceptibility to various infectious diseases, including the recent COVID-19 pandemic. The objective is to understand the genetic variations of blood types and their role in infectious disease susceptibility. The methodology involves a comprehensive review of existing literature, genomic studies, and statistical analysis of single nucleotide polymorphisms (SNPs) associated with blood types. The results indicate significant correlations between blood group antigens and susceptibility to bacterial, parasitic, and viral infections. Notably, blood group O is associated with a lower risk of severe malaria due to decreased rosetting, while blood group A shows a higher incidence of smallpox and Pseudomonas aeruginosa infections. The findings support the importance of early diagnosis and therapeutic development based on blood group genetic variations.

Keywords: Blood Group Susceptibility, COVID-19 Predisposition, Antigens Heredity, Infectious Disease Susceptibility, ABO Gene, Coronavirus 2 (SARS-CoV-2),

1. Introduction

Blood type indicates a particular reaction pattern antigen or antibody (antiserum) in a specified system. Recently more than forty blood group have been discovered which vary according to the antigens attached to various components on erythrocyte blood cells (RBC) surfaces. Blood groups indicate a particular reaction pattern in antigenic determinants in a specified system which is composed of sugar, or proteins expressed on the surfaces of red blood cells. The first human blood group system was published by Karl Landsteiner in his 17th scientific paper in 1901. He identified three main antigen types, called A, B and C (C was later altered to later O for the German “Ohne, meaning “without” or “null” in English)(D FARHUD and Yeganeh, 2013, Laura., 2005).

Independently, in 1907 Jan Jansky categorized human blood groups to four different blood group types using roman numerals I, II, III and IV which correspond to the modern names O, A, B, and AB. Blood group inheritance pattern of multiple alleles was confirmed by Felix Bernstein locus in 1924(Crow, 1993).

Bernstein’s in 1924 "three allele model" determined for the first-time blood alleles. The ABO blood group antigens are encoded by one genetic allele, the ABO locus, which has three substitutes (alleles A, B, and O. A) the child obtains one of them alleles from each parent. Blood types phenotypes are four and six genotypes in human (Hakomori, 1999).

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Table (1) illustration the historical discoveries of antigen and its molecular basis in 20th century. Subsequent studies clarified the enzymatic synthesis of these antigens.

The International Society of Blood Transfusion (ISBT) was initiated in 1935, in Paris as a committee to regulate standardize the terminology of RBC blood group antigens and their expressed alleles. Recently, more than 390 blood group antigens are now recognized, most of which are included in 45 diverse antigens (Cox, 2024), with new discoveries being made all the time(ISBT, 2023). The ISBT organization aids scientific research and practical problems faced in the medical field regarding blood worldwide. Furthermore, ISBT provides detailed information related to alleles associated with blood group antigens by creating the Blood Group Antigen Gene Mutation Database (BGMUT) is a website established(Britannica, 2024, Westhoff et al., 2018). Other types of blood group systems for instance –MNS, P1PK, Kell, Duffy, Kidd,Lewis, Lutheran and others have been identified as demonstrated in table 2 (Regan, 2017).

Since those genetic contents defining ABO phenotype is recognized and this subject is crucial because of the importance of the enzymatic and genetic basis of this carbohydrate structures and the immunological influence antigens in human's health care.

Red blood cell antigens

Erythrocyte blood group antigens are polymorphic, inherited either sugars or proteins, and they are attached to various components in the red blood cell membrane. The ABO system is comprised of two carbohydrate antigens glycosyltransferases that synthesize A and B antigens on RBCs, A and B, and their antibodies (Hakomori, 1999, Cooling, 2015). The four blood types O, A, B, and AB differ only in the terminal sugars on these surface glycoproteins. The cell-surface glycoproteins end in three sugars from attached to free end, N-acetylgalactosamine, galactose, and fucose. A Type O red cell has only these. In type A red cell, the galactose in the middle also has another N-acetygalactosamine attached to it; in type B cells, it also has another galactose attached to it; and type AB red cells have both types of sugar chains (Saladin, 2018).

According to (Regan, 2017) the epitopes of ABO antigens are carbohydrates (sugars) that are linked either to polypeptides (forming glycoproteins) or to lipids (glycolipids). Moreover, genetic, biochemical and biological functions data on erythrocyte antigens have been accumulated. Distinct types of blood group antigens attached to RBC membrane illustrated in (Fig. 1). The figure presented also the aside from the glycan or carbohydrate antigens. Three types of protein that carry blood group antigens on red blood cell membrane comprises: single integral proteins, multi-pass proteins, and proteins glycosylphosphatidylinositol (GPI)-linked proteins. (Westhoff et al., 2018, Laura., 2005). Several discovered red blood cell antigens have been discovered. They were named alphabetically for instance (ABO, MNS, P) scientists used the name of the first patient who produced antibodies against them such as blood system type Duffy and Diago. In 1980 under the regulation of the International Society of Blood Transfusion (ISBT) (Daniels et al., 2004). In addition to its antigens, the human blood content antibodies which are stimulated when the immune system response activate against for several factors the absent blood antigens, in foods or against in microorganisms. Accordingly, blood group O individuals produce anti-A and anti-B antibodies, blood group A individuals have anti-B antibodies, and blood group B individuals have anti-A antibody. In contrast the AB individuals blood circulation is devoid of both anti-A and anti-B antibodies. During transfusion between two persons blood group O is considered as a complete donor, however blood group AB characterizes a receiver from all blood group (Dean L, 2005).

Table 1: The chronological Major blood groups discoveries in the 20th century (Farhud and Zarif Yeganeh, 2013, Regan, 2017)

Blood Group	Year	Reporter (s)	Epitope	Chromosome
ABO – System	1901	Landsteiner K	A, B and H antigens (Carbohydrate (N-Acetyl-D-galactosamine, galactose).) essentially produce IgM antibody reactions,	9
M/ N system	1927	Landsteiner K, Levine P	Main antigens M, N, S, s GPA/GPB (glycophorins A and B).	4
P- system	1927	Landsteiner K, Levine P	Glycolipid. Antigen P1	22
Secretor and not secretor ss	1932	Schiff F, Sasaki H		
Factor Q	1935	Imamuras S		
Rh^+, Rh^-	1940	Landsteiner K, Wiener A	Protein antigens. C, c, D, E,	1
Lutheran (Lu)	1945	Callenders S, Race RR, Paykoc Z	Immunoglobulin Protein. Set of 21 antigens	19
KeL system	1946	Coombs RRA, Mourant AE, Race RR	Antibodies to glycoprotein. Producing lead to haemolytic disease of the baby producing anti K1 can severe	7
Lewis	1946	Mourant AE	Carbohydrate antigen Lewis correlated	19
Duffy	1950	Cutbush et al., 1950)	Protein (chemokine receptor). Main antigens Fya and Fyb .	1
Kidd	JK	Race RR et al.	Protein mostly antigens Jka and Jkb	18
Diego	1953	Levine P. et al	Glycoprotein (band 3, AE1 or anion exchange).	17

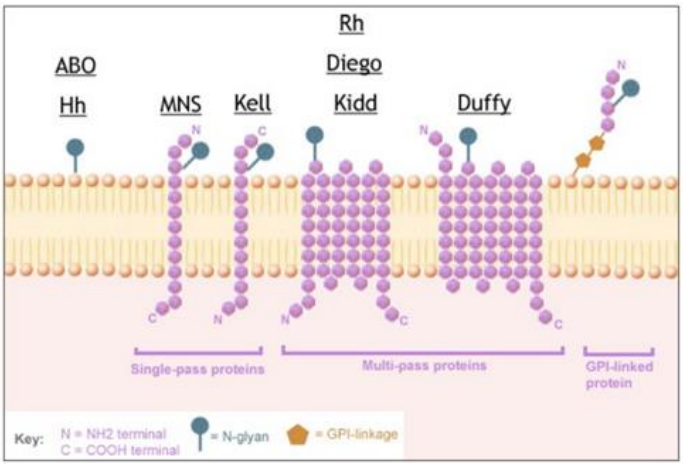

Figure 1; illustrations the Blood group antigens A, B, O and AB chemical structure and other antigens attached with three types of blood group proteins single-integrated proteins, multi-integrated proteins, and glycosylphosphatidylinositol (GPI)-linked proteins (Dean L, 2005).

These antigens are produced by a series of reactions in which enzymes catalyze the transfer of sugar units. While the antigen Rh blood group are large proteins on the red blood cell membrane. (RhD or positive D antigen) which is a large protein. Some people have a type of the gene that does not produce D antigen, thus the RhD protein is lacking from their erythrocytes (Dean L, 2005).

Blood Group Genes Encoded Antigens

The genetic structures of the human ABO blood group system are determined by the presence or absence of specific alleles on the ABO gene on chromosome 9. There are three main alleles that determine the ABO blood group: A, B, and O. Allele A encodes the A antigen on the surface of red blood cells. Allele B encodes the B antigen. Allele O does not encode any antigen (Westhoff et al., 2018, Regan, 2017).

The molecular bases of human blood group are controlled by separate genetic loci. Initially, ABO genes and their alleles were on the identical chromosomal region on chromosome (9) at 9q34.1-q34.2. The genomic structure of ABO genes consists of seven exons which extend almost 19 kb of genomic DNA on chromosome 9, band q34. (Dean L, 2005, Chen et al., 2004).

In the blood cells the H antigen enzyme synthesizes fucosyltransferases required encoded by the H locus (FUT1). Corresponding, the H antigen which secreted in saliva and other bodily tissue, synthesize enzyme encoded by the Se locus (FUT2) gene (Regan, 2017). The two linked genes on chromosome 19, FUT1 (or H) and FUT2 (or Se for secretor). These two genes undergo each locus co-dominants Mendelian inheritance and encodes for a different enzyme (glycosyltransferase), which attaches specific monosaccharides onto precursor disaccharide chains (Shirato, 2011). If the person inherits two identical alleles for defective FUT2 which essential for the common non-secretor phenotype when antigen A, B, and/or H absent. Homozygous individuals didn't inherited alleles at both the FUT1 and FUT2 loci have the Bombay phenotype (Reid et al., 2012, Daniels, 2013).

Modification of oligosaccharides on cell surface glycoproteins determines the ABO blood group of an individual. The A/B variations in the sequence of the protein between individuals determine the type of modification and the blood group (polymorphism) produce from several single nucleotide variations in the ABO gene, which result in A and B transferases that have four amino acid differences between them in the catalytic domain, two of which (Leu266Met and Gly268Ala) are mainly responsible for the substrate specificity. The most common group O allele encodes an inactive glycosyltransferase that leaves the ABO antigen precursor (the H antigen) unmodified. The group O phenotype results from mutations in ABO that cause a loss of glycosyltransferase activity. results from a single nucleotide deletion near the 5′ end of the gene that causes a frameshift and early termination with no active enzyme glycosyltransferase that leaves the ABO antigen precursor (the H antigen) unmodified (Westhoff et al., 2018).

The variation molecular changes associated components carrying antigens that consequently resulting diseases associated. (Westhoff et al., 2018).

It has been found that modifications in blood group antigen expression can rise or reduction host susceptibility to many infectious diseases (Cooling, 2015). Furthermore, genomic studies found over a hundred different single nucleotide polymorphisms (SNPs) as a substitute for blood type for A, B, and AB and in the Leiden Open Variation Database (Yamamoto, 2004, Daniels, 2005, Wang et al., 2021). According to (Wang et al., 2021) genotyping association between ABO blood groups and SNP of 1008 persons. Several

SNPs have been identified (Table 2), however rs8176719, rs635634 and rs7030248 showed significant frequency in patients and potentially sufficient to create a multinomial prognostic model (Wang et al., 2021).

Although genotyping of single nucleotide polymorphisms (SNPs) was carried out for everyone in blood centers and transfusion services but for many reasons, do not depend on the results of genetic assays for ABO typing. One of these the errors presented by the genetic implications comparing to the ABO ideal biochemical blood group detection for the huge amount of database can be obtained from genomic analysis for SNPs analysis (Cooling, 2015, Wang et al., 2021).

Table 2. Classification performance of selected SNPs in China Multi-Ethnic Cohort (CMEC) for ABO blood types.

SNP	SNP	SNP	SNP
O	***A***	***B***	***AB***
rs2039184	*rs2039184*	*rs77843399*	*rs9919007*
rs76321958	*rs7864821*	*rs8176720*	*rs8176746*
rs7864821	*rs9919007*	*rs8176719*	*rs687289*
rs9919007	*rs7857390*	*rs635634*	*rs8176681*
rs8176740	*rs7853989*	*rs7030248*	*rs507666*
rs7853989	*rs8176720*	*rs7025162*	*rs3118662*
rs4962040	*rs8176719*	*rs493014*	full set
rs529565	*rs630014*	*rs3118662*	
rs630014	*rs635634*	*rs7030248 + rs635634*	
rs651007	*rs7030248*	full set	
rs7030248	*rs7025162*		
rs1752337	*rs13289928*		
rs493014	*rs635634 + rs8176719*		

Distribution of Blood Group in The World

The frequency distribution of the four ABO blood groups, A, B, AB, O, and other types of antigens varies in different populations throughout the world. Therefore, several studies compared the phenotype incidences among diverse ethnic groups and populations. The most common blood type is O in the worldwide, followed by group A. Whereas, group B is less frequency, and group AB is the least proportion. In the United States the frequencies of blood type ABO and Rh are recently examined by collecting data from blood donors over a 10-year and the percentage of O blood group is highest rate.

While in the British Caucasian population, the percentage of group A is 42%, B 9%, AB 3%, and O 46%, but there is national variation in these occurrences (Garratty et al., 2004, Regan, 2017) . In Iraq, the most frequencies are for the blood group O, then A, B as blood group and the lower percentage AB (Salih, 2009). According to (Abd Ali Al-Maliki and Haider, 2020, Salih, 2009) distribution of ABO and RhD blood groups in the Al-Najaf province in Iraq presented that blood group O is the predominant 39.7% followed by blood group A 26.5%, blood group B 24.4% and blood group AB 9.4%. Additionally, the percentage of Rh+ (92.6%) while Rh- is (7.4%).

Both studies finding is in agreement with (Ayit et al., 2022) findings in the population of Babylon city in Iraq which showed bloods group O was the most common in both sexes, followed by blood groups B and A, with the B group higher among females and less high among men. The AB blood group was the least common of the four. Blood type B was prevalent in females (26.97%) compared to males (24.41%). Whereas blood type A was more prevalent in males (24.59%) compared to females (24.12%) (Ayit et al., 2022).

ABO Antigens and Infectious Disease

Blood types of antigens have a significant role in infection disease acting as receptors or coreceptors for microbes such as bacteria, parasites, and viruses. In addition, many blood group antigens are involved in intercellular signal transduction pathways. In the other hand antigen can adherence the microorganism membrane. Moreover, several blood groups can be involved in immune responses against pathogens agents through modifying the innate immune response to infection (Cooling, 2015).

Previous studies have verified that phenotypes blood group types associated with variation response against diverse infections agents for instance bacteria, parasite, viruses (Cheng et al., 2005, Kim et al., 2021). Furthermore, many scholars have reported that the susceptibility to various diseases, like malignancy, cardiac, hematologic disorders, cognitive disorders, diseases, metabolic diseases (Shen et al., 2020, Abegaz, 2021, Franchini et al., 2012, Kominato et al., 2020)

Blood Group Predisposition Association with Bacterial Infection

Preliminary etiological studies have examined the relationship between blood type and bacterial infection resistance against an infectious disease. It has been identified the contribution of group O with increased incidence of cholera, plague, tuberculosis infections, and mumps. However, blood type A is related to increased incidence of smallpox and Pseudomonas aeruginosa infection. Whereas blood type B is found to be contributed with increased frequency of gonorrhea, tuberculosis, and Streptococcus pneumoniae, E. coli, and salmonella infections. Individuals with blood type AB is related with increased rate of smallpox and E. coli and salmonella infections (Harris et al., 2005, Cooling, 2015). Other studies have concluded that Group A individuals rarely may obtain a B antigen from a bacterial infection that results in the release of a deacetylase enzyme. This converts N-Acetyl-D-galactosamine into a-galactosamine, which is similar to galactose, the immunodominant sugar of group B, thereby sometimes causing the red cells to appear to be group AB (Cheng et al., 2005, Kim et al., 2021).

Research conducted by Rowe in 2007 study the association between ABO blood groups and Plasmodium falciparum infection severity the bacteria which causing malaria showed that participants blood group O, low probability to develop severe malaria because of decreased resetting. Resetting is a process where red cells infected attach themselves onto healthy red blood cells, as a result this increases the severity of the disease. Authors of this study carried out a case-control study where patient from malaria endemic regions were selected and included in this study. Next step involved blood group typing and measuring the degree of resetting, this was done using flow cytometry. The results of the study showed a significantly lower rate of resetting in blood group O compared to groups A, B and AB. This suggests that the absence of A and B antigens on surface of red blood cells decreases the cells susceptibility from forming rosetts when infected by Plasmodium falciparum. As a result, this lowers the severity of malaria in blood group O individuals (Rowe et al., 2007).

Another research study investigated the relationship between blood group O and Helicobacter pylori (H. pylori) infection, which emphasises the association of increased risk of gastric carcinoma in these individuals. The study included patients that were diagnosed with atrophic gastritis and underwent endoscopic biopsy and serological testing for H. pylori infection. Standard agglutination methods were conducted for blood group typing. Furthermore, the study discovered that individuals with blood group I had a higher prevalence of H. pylori infection and were at higher risk of developing gastric carcinoma. These results imply the interaction between H. Pylori and blood group antigens may play a role to gastric disease pathogenesis (Kitamura et al., 2015).

Staphylococcus Aureus

An old Russian investigation (Veselov and Malyshkina, 1988), found a correlation between group A and a greater carriage rate of Staphylococcus aureus (S. aureus). A

subsequent prospective German investigation looked at 227 healthy volunteers' pharyngeal and nasal carriage of S. aureus according to their ABO, Lewis, and Secretor status. 156 people with chronic nasal carriage and 77 people with pharyngeal carriage were study participants. Upon univariate analysis, there was no significant link between Secretor status and ABO group when comparing carriers and non-carriers. But when data were examined using Secretor status as a variable in a multivariate analysis, other patterns emerged. Group O patients had a higher prevalence of pharyngeal colonization among non-secretors 60% while 40% of other blood groups) whereas group A individuals had the lowest rate (3/16; 20%). On the other hand, regardless of ABO type, pharyngeal carriage was rare among secretors (Se+) (65 – 73. Nurjadi et al., 2012 concluded that no association was found between nasal carriage and blood groupings. Nasal keratinocytes are ectodermal in origin and are unlikely to express either FUT3 or FUT2, as the authors of that study stated (Nurjadi et al., 2012).

Group A and Group B Streptococcus

Group A Streptococcus (GAS) and Group B Streptococcus (GBS) are bacteria responsible for various infections in humans. However, their main targets and modes of transmission are different. GAS can cause infections mainly affecting the skin and throat. This can lead to cellulitis, impetigo, scarlet fever, pharyngitis (strep throat), necrotizing fasciitis, and rheumatic fever in severe instances. Direct contact with infected wounds and respiratory droplets is a major form of transmission. GBS, or Streptococcus agalactiae, on the other hand, poses a serious risk to newborn children and pregnant women. It can lead to serious infections in infants, such as pneumonia meningitis in infants, and sepsis; these illnesses are frequently passed from mother to child during delivery(Hon et al., 2020, Gergova et al., 2024). GBS can result in amnionitis and urinary tract infections in pregnant women. For management of this infection in pregnant women antibiotics are prescribed with penicillin being first line choice for both types of bacteria. Pregnant women are therefore should be screened for GBS in particular, if they test positive, they should be given antibiotics throughout labor (Morcos Hanna and Noor., 2023).

Studies and Historical Context

After World War II interest in the relationship of ABO blood group types and susceptibility to GAS infections grew, with multiple studies between 1932-1968 investigating blood types in patients and various streptococcal infections. This included rheumatic disease, scarlet fever and pharyngitis. The studies revealed a trend linking between non-group O status and increased prevalence of streptococcal illness (Haverkorn and Goslings, 1969).

For patients with rheumatic fever and rheumatic disease patients that didn't display blood group O had an increased risk of disease. The range of the relative risk was 1.02 to 1.55. However, when data from sixteen different studies investigating this combined, they looked at 203,454 participants showed that the incidence of non-group O blood types in patients (58% versus 55%) was almost the same as in controls (Haverkorn, 1969). This suggests that non-O blood types do not substantially increase the risk of these conditions.

Group B streptococcus

Regan and colleagues' (1978) conducted a retrospective observational paper which revealed that women of blood type B and their babies had a higher prevalence of GBS. Of the 1,062 mothers, 11% had a positive GBS culture. According to ABO type, colonized mothers 28% against 16%, while colonized newborns (30%), and infected infants (30%) had nearly twice as high rates of GBS colonization (Regan, 1978).

In contrast a prospective case-control in an Ohio study with 50% African Americans showed no association. ABO blood group types and GBS bacteria colonization or infection were not shown to be significantly correlated in these trials (Iams and Sprague, 1981. , Ancona et al., 1980.).

Parasite Infection and ABO Groups

The relationship between blood group and Schistosoma has been widely investigated. A relationship exists between blood group A and increased susceptibility to Schistosoma infections, particularly S. mansoni (Ndamba J et al., 1997., Haseeb et al., 2008, Camus D et al., 1977). Ndamba with other researchers in (1997) identified the highest blood group percentage is group A30.7% to get S. mansoni infection while the percentage patients with group O is 10.1%. Additionally, blood group A individuals have more predisposition to have periportal fibrosis (Symmers fibrosis) 50.2%, while 20.45% of group O individuals. Similar results were reported in two older Brazilian studies, which also found an association between hepatosplenic infection and group A (59%) and the percentage of group O individuals is 28% (Camus D et al., 1977, Pereira FEL et al., 1979.). Colley and other scientists in 2014 suggested that the absence of anti-A antibody in circulation of blood group A individual might cause increasing risk infection with S. mansoni susceptibility more than other blood groups. (Colley et al., 2014).

Blood Group and Risk Infection with viruses

It has been investigated the relationship between ABO blood groups and likelihood of norovirus infection, this showed that participants with blood group O are more susceptible to norovirus infection. The results indicate that histo-blood group antigens play the role of receptors for the virus. The study conducted analysis of serum samples from norovirus infected individuals to determine their ABO blood group and secretor status. The study discovered that patients with blood group O presented with increasing rate of norovirus infection versus other blood groups. To conclude the study determined that specific blood group antigens show a role in viral binding entry, which in return increases the likelihood of contracting an infection. (Hutson et al., 2005).

Secretor Status and HIV Production and Infection

Sector status refers to specific blood group antigens (ABH antigens) in bodily fluids, expressed by the FUT2 gene. Patients who are referred to as "secretors" (Se+) produce saliva and other bodily fluids containing these antigens while "non-secretors" (Se-) do not.

The role of Secretor status in HIV infection development is a topic of great interest, especially in heterosexual transmission. The Secret or statuses of heterosexual partners of HIV-positive patients were compared by Blackwell et al. (1991). According to this study, spouses who contracted HIV had considerably higher rates of Se+ persons is (88%) contrasted with HIV rate (54%) who were HIV negative. On the other hand, those who acquired HIV through intravenous drug use or homosexual transmission did not vary in their secretor status (Blackwell (Blackwell et al., 1991).

A larger investigation of HIV transmission among female commercial sex workers in Senegal discovered that HIV-1-positive women were more likely to be Se+ (86%) versus (72%), even after accounting for co-infection with other sexually diffused infections. Combining data from both investigations revealed that a nonsecretor phenotype may offer some protection against heterosexual HIV transmission (OR 0.39 [95% CI 0.21 to 0.72]; P = 0.0022) (Ali et al., 2000).

Small European research evaluated HIV progression rates among 31 HIV-infected males based on Secretor status. According to Kindberg et al. (2006), males with long-term

asymptomatic illness were overrepresented in the nonsecretor phenotype (66.7% vs. 21%; $P < 0.001$).

Lewis Antigens and HIV

Lewis's antigens are a different group of blood group antigens, which are glycolipids present on the surface of red blood cells as well as in secretions. They are likewise determined by the FUT2 gene, much like Secretor status.

One researcher hypothesized that the Le(b+) phenotype would protect opposed to HIV infection. Puissant with his colleagues in (2005) found a moderate in the dominance of Le(a−b−) red cells (16% versus 12%; P = 0.007) among 968 HIV-infected individuals. When corrected for ABO type, only individuals in groups A and AB showed an increase in the prevalence of the Le(b−) phenotype. The authors hypothesized that Le(b)-active glycans may operate as a competitive inhibitor of DC-SIGN on mucosal dendritic cells. If this theory is true, a Le(b+) maternal phenotype may protect against perinatal HIV transmission in breast-fed babies (Puissant, 2005).

ABO blood groups and HIV

Studies have proven that HIV can be neutralized by blood group-active antibodies. Antibodies against blood type A have been shown by Hansen et al. (1990) to impede HIV infection in a dose-dependent manner. Furthermore, the study achieved 80% viral suppression at micromolar concentrations by preincubating HIV with a panel of 20 distinct antibodies targeting carbohydrate epitopes prior to infection of MT4 cells(Hansen et al., 1990).

Further studies have demonstrated that ABO-specific monoclonal antibodies could possibly neutralize HIV passaged in human lymphocytes of a known ABO type. for instance, HIV in blood group A-positive cell lines were shown to be partly neutralized by ABO-incompatible serum (O and B groups), however, this was not achieved when group A or heat-inactivated serums were used. According to these findings, there may be some protection against HIV infection provided by ABO incompatibility during the initial viral exposure period (Arendrup et al., 1991, Neil et al., 2005).

A 16-year retrospective study on 271,000 Brazilian blood donors found that group B donors had a slightly increased prevalence of HIV. 14% of group B individuals were among the 389 HIV-positive donors (0.01%) identified during screening; this proportion is slightly greater than the overall population's (9%) or (1.5) with [95% CI (1.13 -2) (Onsten et al., 2013).

According to a study has been accomplished in Saudia Arabia (Ahmad A. Shaikh et al 2024) to verify relationship of microbial infection among individual donors during blood transfusion and ABO group type besides Kell blood system. The scientist observed donors blood group O higher risk to infection. followed by those with group A, B, and lastly AB. Significant connotations were detected between HIV and blood group A, hepatitis (B) antibodies occurrence and group AB, and malaria and group A. Regarding the association of the Kell blood group system with several microbial infections, doners person with the Kell-positive hepatitis (B) were the most prevalent, and significant associations, HIV, and syphilis

SARS-CoV

A comprehensive review done by Cooling 2005 displays a detailed analysis looking at the impact of human blood group antigens on host susceptibility to different diseases. The analysis found that participants with blood groups A, B and AB are more vulnerable to SARS-CoV infection that those with blood group O. A possible protective factor for group O individuals is having anti-A and anti-B antibodies. These antibodies may be able to reduce the risk of infection by blocking the virus's ability to bind to host cells.

In addition to this another study conducted by Guillon (Guillon et al., 2008) investigated the relationship between spike proteins of SARS-CoV virus and angiotensin-converting enzyme 2 cellular receptor (ACE2). Results showed that anti-A antibody may be able to prevent this interaction; this suggests a possible explanation for the protective effect observed in blood group O individuals. This work emphasises the potential importance of endogenous antiA antibody in providing SARS-CoV resistance in group O patients. (Guillon et al., 2008).

A study achieved by Cheng et al. in 2005 examined the blood type distribution of SARS-CoV patients in Hong Kong. They discovered a far lower percentage of blood group O. This study further supports the hypothesis that blood type O provides protection against SARS-CoV infection (Cheng et al., 2005).

The role of CD147 was investigated, also known as Basigin or EMMPRIN. SARS-CoV virus uses the CD147 receptor to invade host cells. Blood type antigens may regulate the interaction between CD147 and spike proteins, which is an alternative pathway in which the virus enters the body. This CD147 mediated entrance is not entirely proven, more research is required to further prove this (Cheng et al., 2005).

Coronavirus-2 (SARS-CoV-2) and Blood Groups

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) infection is the most important recent pandemic infectious disease threaten the worldwide (Zhou et al., 2020, Yan et al., 2021). The first case was reported in 2019 in Douhan then the infections quickly spread around the world. The virus SARS-COV-2 infects respiratory system of human with similar medical examination symptoms with MERS-COV and SARS-COV(Chan et al., 2020). According to estimates obtained from WHO recent epidemiological report for COVID-19 more than seven million deaths have been reported globally(WHO, 2024). The infection severity presented ranges from asymptomatic infection to mild disease. The most essential symptom of COVID-19 categorized by dry cough, fever, dyspnea, and fatigue, to aggressive infection may cause severe respiratory failure and patients' mortality (Schmiedel et al., 2021, Joseph et al., 2020).

When COVID-19 infection invasive the lower respiratory tract and therefore inflammation of lung alveoli patients need for admission intensive care and a ventilator to supply oxygen that might be led to mild and moderate COVID-19. The severe COVID-19 infection can lead to acute respiratory distress syndrome (ARDS), with several organs' failure, consequently, causes patients death (Zhu et al., 2020).

Coronaviruses are positive-strand RNA viruses ~30 kb (Grellet et al., 2022). Different genetic variation SNPs in Covid-19 genome as similar to other viruses change during multiple replications some of these modification increase its pathogenesis, transmission and vaccine efficiency that have been rapidly spreading worldwide over the pandemic time (Malone et al., 2022). Initially, COVID-19 type Alpha was considered as the one of virus concern variant by the World Health Organization. It was first identified in Kent in the United Kingdom in September 2020 and drove the UK's second wave. It is considered 30-40% more transmissible than the original (wild-type) SARS-CoV-2 coronavirus(Oxford., 23 Jul 2021.). Alpha has since been outpaced by newer variants whose mutations spur even more aggressive transmission. Other variants Delta and Omicron diffuse subsequently Alpha, each having mutations in two of the three regions. It has been suggesting that they may have similar effects on the innate immune system(Jennifer Michalowsi and Marks., 2022).

Blood group Predisposition and COVID-19

Several studies aiming to associate genetic variation at the chromosome several gene cluster and the blood system type with complement activation and sever infection of COVID-19 (Ellinghaus et al., 2020, Eatz et al., 2023, Razaq and Alkufi, 2022). The role of

blood type is complicated in the overall process of infection (Cooling, 2015). It has been reported that human blood phenotype can play a role in varying a patient's predisposition to coronavirus infection. This view is supported by Alhassani in (2022) with his colleagues that blood group A+ is the prevalent proportion comparing with other blood groups and the lowest was in the AB+ blood group for both genders.(Alhassani et al., 2022). Similarly, Eatz (2023) demonstrated the COVID-19 severity and mortality participants related with ABO group. The study analysed of 669 out of 2741 COVID-19-positive, collected patients since January 2020 until 31 March 2021 at the University of Miami Emergency Department (ED). They found that blood type A is linked to increased risk of respiratory failure while blood type O offers some protective effects and less risk of COVID-19 mortality. Finally, patients with O- blood type displayed lowest threat of developing COVID-19 pneumonia and lowest biomarkers of severe infection than did other blood types (Eatz et al., 2023).

The study Abegaz (2021) provide in-depth analysis of the viral infections showing that the antigen glycoproteins preform as a receptors located on the cell membrane of red blood that allow viral to access into the human cell (Abegaz, 2021). The findings of Abegaz (2021) are consistent with Goel with other researchers in 2021 results who found that persons with ABO blood group have antigens expressed on red cells and other tissues, particularly endothelium. The researchers suggested an explanation hypothesis due to the differences in SARS-CoV-2 infection by ABO type. For instance, anti-A and or anti-B antibodies occur in group O individuals may bind to corresponding antigens on the viral envelope causing viral neutralization. Consequently, preventing target cell infection. The SARS-CoV-2 virus and SARS-CoV spike (S) proteins could be bound by anti-A is agglutinins which present in group O and group B individuals, which may inhibit interfaces between virus and angiotensin-converting-enzyme-2-receptor and that may lead to avoiding viral accessing inside lung epithelial cells (Goel et al., 2021).

Recent research has support the previous findings (Ferous et al., 2024) that the A blood group may be associated with increased susceptibility to SARS-CoV-2 infection, also perhaps with increased disease severity and overall mortality.

Analysis of the genetic predisposition to determine analyzed single (SNP) involved in COVID-19 infection was carried out by several studies (Ellinghaus et al., 2020, Abegaz, 2021, Razaq and Alkufi, 2022).

The respiratory failure genome-wide association study (GWAS) set out to determine single relationship study collecting 1980 patients with severe Covid-19 and severe respiratory infection from seven hospitals in the Italian and Spanish in main European SARS-CoV-2 medical center. The researchers identified two significant loci from patients with severe COVID-19 infection, one in chromosome three (3p21.31) and another with chromosome 9 (9q34.2.) Further results revealed the association signal located genes locus 3p21.31, are SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1. The association signal at locus 9q34.2 related to the ABO blood group locus. The key gene was ABO. At locus 3p21.31. SNP at rs11385942 the high frequent for insertion–deletion GA or G variant and the rs657152 A or C SNP at locus 9q34.2. Ultimate results for this study a blood-group–specific analysis showed patients' blood group A are significantly in risk with severe infection. Corresponding to patients with blood group O are more protective than other blood groups (Ellinghaus et al., 2020).

It has been identified specific gene cluster loci at a 3p21.31 polymorphism that associated ABO with susceptibility to infect with SARS-CoV-1 in patients with COVID-19 (Chen et al., 2022, Valenti et al., 2021).

This finding confirms the association between a modified SNPs at loci (rs11385942) that predisposes to severe COVID-19 and is associated with stimulate complement production in circulation blood in particular C5a and sC5-C9 and C5a only in the non-O blood group (Valenti et al., 2021). However, this genetic variation in polymorphism is not

directly affect complement gene expression loci, but it might have related with assistance complement activation indirectly by elevated infection severity during systemic inflammation and organ failure (Bianco et al., 2021).

According to the study which established to determine single allele polymorphism positions in genome sequence individual of severe COVID-19 infection of Iraqi patients. The researchers tried to clarify the genetic variation behind the variance between individuals to get severe infection with COVID-19 more than others. They detected a single nucleotide two mutants type SNPs for mostly A/C and C/C associated sever infection corresponding the sequence, ABO locus rs657152 at the 9q34.2c associate with severe infection comparing with the control A/A nucleotide sequence of blood cells in the same loci of mild infection patients and with the normal control sequence individuals (Razaq and Alkufi, 2022).

In another study conducted by (Valenti et al., 2021) find out variant at the rs11385949 G>GA, located on the chromosome 3 gene cluster related with severe COVID-19 susceptibility. Furthermore, the study showed that complement pathway activation at rs11385949, which affected especially C5a and SC5b-9 in all blood groups except O blood group stimulate C5a levels. Also, the rs11385949 risk variant associated with complement activation and blood ferritin titer during viral replication. Finally, the study concludes that linking genetic susceptibility to increase COVID-19 pathogenesis with a heavy inflammatory response (Valenti et al., 2021).

4. Conclusion

Blood provides an ideal opportunity for the study of human variation different responses and genetically inherited variation with blood typing systems associated with increasing or drop microbial infection. Also significant is the fact that the Human blood group system thus contains several different antigenic determinants associations with infectious diseases that play a significant role in infection pathogenesis. Finally, the number of human genomic variations associated with COVID-19 infection that increase susceptibility and severity of infection has been widely investigated in different populations. Several putative risk loci have been identified in ABO blood system associated with patients infected with SARS-2 viral infection.

REFERENCES

1. ABD ALI AL-MALIKI, A. & HAIDER, S. 2020. Normal distribution of ABO blood group and Rhesus factor in Al-Najaf province. European Journal of Experimental Biology, 5, 18-21.
2. ABEGAZ, S. B. 2021. Human ABO Blood Groups and Their Associations with Different Diseases. Biomed Res Int, 2021, 6629060.
3. ALHASSANI, A. A., AL KUFI, S. G. J. & KADHUM, H. A. 2022. Statistical analysis for COVID-19 infections including several association factors: Age, gender and blood parameters. AIP Conference Proceedings, 2547.
4. ALI, S., NIANG, M. A. F., N'DOYE, I., CRITCHLOW, C. W., HAWES, S. E., HILL, A. V. S. & KIVIAT, N. B. 2000. Secretor Polymorphism and Human Immunodeficiency Virus Infection in Senegalese Women. The Journal of Infectious Diseases, 181, 737-739.
5. ANCONA, R. J., FERRIERI, P. & AND WILLIAMS, P. P. 1980. . Maternal factors that enhance the acquisition of group B streptococci by newborn infants. Journal of Medical Microbiology, , 13, pp.273-280.
6. ARENDRUP, M., HANSEN, J. E., CLAUSEN, H., NIELSEN, C., MATHIESEN, L. R. & NIELSEN, J. O. 1991. Antibody to histo-blood group A antigen neutralizes HIV produced by lymphocytes from blood group A donors but not from blood group B or O donors. Aids, 5, 441-4.
7. AYIT, A., AL-KHIKANI, F. & ABADI, R. 2022. Prevalence of ABO Blood Group System in Southern Babylon, Iraq. Journal of Preventive, Diagnostic and Treatment Strategies in Medicine, 1.

8. BLACKWELL, C. C., JAMES, V. S., DAVIDSON, S., WYLD, R., BRETTLE, R. P., ROBERTSON, R. J. & WEIR, D. M. 1991. Secretor status and heterosexual transmission of HIV. Bmj, 303, 825-6.
9. BRITANNICA, T. 2024. International Society of Blood Transfusion . . In: BRITANNICA, T. (ed.) International Society of Blood Transfusion . Encyclopedia Britannica.
10. CAMUS D, BINA JC, CARLIER Y, F., S., & 340. 1977. ABO blood groups and clinical forms of schistosomiasis mansoni. Trans R Soc Trop Med Hyg 71:182. Crossref. PubMed.
11. CHAN, J. F., KOK, K. H., ZHU, Z., CHU, H., TO, K. K., YUAN, S. & YUEN, K. Y. 2020. Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. Emerg Microbes Infect, 9, 221-236.
12. CHEN, D. P., TSENG, C. P., WANG, W. T., WANG, M. C., TSAO, K. C., WU, T. L. & SUN, C. F. 2004. A novel cis-AB allele derived from the A transferase gene by nucleotide substitution C796A. Ann Clin Lab Sci, 34, 437-42.
13. CHEN, P., WANG, J., XU, X., LI, Y., ZHU, Y., LI, X., LI, M. & HAO, P. 2022. Molecular dynamic simulation analysis of SARS-CoV-2 spike mutations and evaluation of ACE2 from pets and wild animals for infection risk. Comput Biol Chem, 96, 107613.
14. CHENG, Y., CHENG, G., CHUI, C. H., LAU, F. Y., CHAN, P. K., NG, M. H., SUNG, J. J. & WONG, R. S. 2005. ABO blood group and susceptibility to severe acute respiratory syndrome. Jama, 293, 1450-1.
15. COLLEY, D. G., BUSTINDUY, A. L., SECOR, W. E. & KING, C. H. 2014. Human schistosomiasis. Lancet, 383, 2253-64.
16. COOLING, L. 2015. Blood Groups in Infection and Host Susceptibility. Clin Microbiol Rev, 28, 801-70.
17. COX, D. 2024. A new understanding of how your blood type influences your health. New Scientist (https://www.newscientist.com/article/mg26134751-500-a-new-understanding-of-how-your-blood-type-influences-your-health/).
18. CROW, J. F. 1993. Felix Bernstein and the first human marker locus. Genetics, 133, 4-7.
19. D FARHUD, D. & YEGANEH, M. Z. 2013. A brief history of human blood groups. Iranian journal of public health, 42, 1.
20. DANIELS, G. 2005. The molecular genetics of blood group polymorphism. Transplant immunology, 14, 143-153.
21. DANIELS, G. 2013. Human Blood Groups, 3rd Edition, Wiley
22. DANIELS, G. L., FLETCHER, A., GARRATTY, G., HENRY, S., JøRGENSEN, J., JUDD, W. J., LEVENE, C., LOMAS-FRANCIS, C., MOULDS, J. J., MOULDS, J. M., MOULDS, M., OVERBEEKE, M., REID, M. E., ROUGER, P., SCOTT, M., SISTONEN, P., SMART, E., TANI, Y., WENDEL, S. & ZELINSKI, T. 2004. Blood group terminology 2004: from the International Society of Blood Transfusion committee on terminology for red cell surface antigens. Vox Sang, 87, 304-16.
23. DEAN L 2005. Blood Groups and Red Cell Antigens. In: GROESBECK., B. B. G. D. T. (ed.) Blood Groups and Red Cell Antigens. USA: National Center for Biotechnology Information (US).
24. EATZ, T., MANTERO, A. M. A., WILLIAMS, E., CASH, C. J., PEREZ, N., CROMAR, Z. J., HERNANDEZ, A., CORDOVA, M., GODBOLE, N., LE, A., LIN, R., LUO, S., PATEL, A., ABU, Y., PALLIKKUTH, S. & PAHWA, S. 2023. Association of ABO Blood Type with Infection and Severity of COVID-19 in Inpatient and Longitudinal Cohorts. COVID, 3, 1429-1439.
25. ELLINGHAUS, D., DEGENHARDT, F., BUJANDA, L., BUTI, M., ALBILLOS, A., INVERNIZZI, P., FERNáNDEZ, J., PRATI, D., BASELLI, G., ASSELTA, R., GRIMSRUD, M. M., MILANI, C., AZIZ, F., KäSSENS, J., MAY, S., WENDORFF, M., WIENBRANDT, L., UELLENDAHL-WERTH, F., ZHENG, T., YI, X., DE PABLO, R., et all. Genomewide Association Study of Severe Covid-19 with Respiratory Failure. N Engl J Med, 383, 1522-1534.
26. FARHUD, D. D. & ZARIF YEGANEH, M. 2013. A brief history of human blood groups. Iran J Public Health, 42, 1-6.

27. FEROUS, S., SIAFAKAS, N., BOUFIDOU, F., PATRINOS, G. P., TSAKRIS, A. & ANASTASSOPOULOU, C. 2024. Investigating ABO Blood Groups and Secretor Status in Relation to SARS-CoV-2 Infection and COVID-19 Severity. Journal of Personalized Medicine, 14, 346.
28. FRANCHINI, M., FAVALORO, E. J., TARGHER, G. & LIPPI, G. 2012. ABO blood group, hypercoagulability, and cardiovascular and cancer risk. Crit Rev Clin Lab Sci, 49, 137-49.
29. GARRATTY, G., GLYNN, S. A. & MCENTIRE, R. 2004. ABO and Rh(D) phenotype frequencies of different racial/ethnic groups in the United States. Transfusion, 44, 703-6.
30. GERGOVA, R., BOYANOV, V., MUHTAROVA, A. & ALEXANDROVA, A. 2024. A Review of the Impact of Streptococcal Infections and Antimicrobial Resistance on Human Health. Antibiotics (Basel), 13.
31. GOEL, R., BLOCH, E. M., PIRENNE, F., AL-RIYAMI, A. Z., CROWE, E., DAU, L., LAND, K., TOWNSEND, M., JECKO, T., RAHIMI-LEVENE, N., PATIDAR, G., JOSEPHSON, C. D., ARORA, S., VERMEULEN, M., VRIELINK, H., MONTEMAYOR, C., OREH, A., HINDAWI, S., VAN DEN BERG, K., SERRANO, K., SO-OSMAN, C., WOOD, E., DEVINE, D. V. & SPITALNIK, S. L. 2021. ABO blood group and COVID-19: a review on behalf of the ISBT COVID-19 Working Group. Vox Sang, 116, 849-861.
32. GRELLET, E., L'HOTE, I., GOULET, A. & IMBERT, I. 2022. Replication of the coronavirus genome: A paradox among positive-strand RNA viruses. J Biol Chem, 298, 101923.
33. GUILLON, P., CLEMENT, M., SEBILLE, V., RIVAIN, J. G., CHOU, C. F., RUVOEN-CLOUET, N. & LE PENDU, J. 2008. Inhibition of the interaction between the SARS-CoV spike protein and its cellular receptor by anti-histo-blood group antibodies. Glycobiology, 18, 1085-93.
34. HAKOMORI, S.-I. 1999. Antigen structure and genetic basis of histo-blood groups. Biochimica et Biophysica Acta (BBA) - General Subjects, 1473, 247-266.
35. HANSEN, J.E.S., CLAUSEN, H., N., C., T. & G., H., L.L., NIELSEN, C.M., DABELSTEEN, E., MATHIESEN, L., HAKOMORI, S.I., AND NIELSEN, J.O., 1990. Inhibition of human immunodeficiency virus (HIV) infection in vitro by anticarbohydrate monoclonal antibodies: peripheral glycosylation of HIV envelope glycoprotein gp120 may be a target for virus neutralization. . Journal of Virology, 64, pp.2833-2840.
36. HARRIS, J. B., KHAN, A. I., LAROCQUE, R. C., DORER, D. J., CHOWDHURY, F., FARUQUE, A. S., SACK, D. A., RYAN, E. T., QADRI, F. & CALDERWOOD, S. B. 2005. Blood group, immunity, and risk of infection with Vibrio cholerae in an area of endemicity. Infect Immun, 73, 7422-7.
37. HASEEB, M. A., THORS, C., LINDER, E. & EVELAND, L. K. 2008. Schistosoma mansoni: chemoreception through n-acetyl-d-galactosamine-containing receptors in females offers insight into increased severity of schistosomiasis in individuals with blood group A. Exp Parasitol, 119, 67-73.
38. HAVERKORN, M. J., AND GOSLINGS, W.R.O., 1969. Streptococci, ABO blood groups, and secretor status. . American Journal of Human Genetics, 21, pp.360-375.
39. HON, K. L., CHOW, T. C., CHEUNG, T. S., LAM, W. T., HUNG, L. T., SO, K. W., MARGARET, I. P. & QIAN, S. Y. 2020. Severe Group A and Group B Streptococcus Diseases at a Pediatric ICU: Are they Still Sensitive to the Penicillins? Curr Clin Pharmacol, 15, 125-131.
40. HUTSON, A. M., AIRAUD, F., LEPENDU, J., ESTES, M. K. & ATMAR, R. L. 2005. Norwalk virus infection associates with secretor status genotyped from sera. J Med Virol, 77, 116-20.
41. IAMS, J. D., . & SPRAGUE, M. 1981. . Maternal blood group and colonization with the group B Streptococcus. Journal of Obstetrics and Gynecology, . Journal of Obstetrics and Gynecology, , 139, pp.922-924.
42. ISBT, R. C. I. A. B. G. T. 2023. International Society of Blood Transfusion [Online]. https://www.isbtweb.org/isbt-working-parties/rcibgt.html. [Accessed 19/06/2024 2024].
43. JENNIFER MICHALOWSI & MARKS., R. 2022. Alpha Coronavirus Variant Evolved to Evade Immune System. University of California SanFrancisco.
44. JOSEPH, A., ZAFRANI, L., MABROUKI, A., AZOULAY, E. & DARMON, M. 2020. Acute kidney injury in patients with SARS-CoV-2 infection. Annals of Intensive Care, 10, 117.

45. KIM, Y., LATZ, C. A., DECARLO, C. S., LEE, S., PNG, C. Y. M., KIBRIK, P., SUNG, E., ALABI, O. & DUA, A. 2021. Relationship between blood type and outcomes following COVID-19 infection. Semin Vasc Surg, 34, 125-131.
46. KITAMURA, Y., YOSHIHARA, M., ITO, M., BODA, T., MATSUO, T., KOTACHI, T., TANAKA, S. & CHAYAMA, K. 2015. Diagnosis of Helicobacter pylori-induced gastritis by serum pepsinogen levels. J Gastroenterol Hepatol, 30, 1473-7.
47. KOMINATO, Y., SANO, R., TAKAHASHI, Y., HAYAKAWA, A. & OGASAWARA, K. 2020. Human ABO gene transcriptional regulation. Transfusion, 60, 860-869.
48. LAURA., D. 2005. Blood groups and red cell antigens, NCBI Bethesda.
49. MALONE, B., URAKOVA, N., SNIJDER, E. J. & CAMPBELL, E. A. 2022. Structures and functions of coronavirus replication-transcription complexes and their relevance for SARS-CoV-2 drug design. Nat Rev Mol Cell Biol, 23, 21-39.
50. MORCOS HANNA & NOOR., A. 2023. Streptococcus Group B, Treasure Island (FL): StatPearls Publishing.
51. NDAMBA J, GOMO E, NYAZEMA N, MAKAZA N & KC., K. 1997. Schistosomiasis infection in relation to the ABO blood groups among school children in Zimbabwe. Acta Trop Crossref. PubMed., 65:181–190.
52. NEIL, S. J. D., MCKNIGHT, A. I., GUSTAFSSON, K. & WEISS, R. A. 2005. HIV-1 incorporates ABO histo-blood group antigens that sensitize virions to complement-mediated inactivation. Blood, 105, 4693-4699.
53. NURJADI, D., LEPENDU, J., KREMSNER, P. G. & AND ZANGER, P. 2012. Staphylococcus aureus throat carriage is associated with ABO/secretor status. . Journal of Infection,, 65, pp.310-317.
54. ONSTEN, T. G., DE CARVALHO, M. F., ., M., R.C., , AND MENDES-JUNIOR, C. T. & 2013. Distribution of ABO blood group and RHD phenotypes among blood donors and HIV/AIDS patients in the state of Maranhão, northeastern Brazil. Brazilian Journal of Infectious Diseases, 7, pp.267-273.
55. OXFORD., U. O. 23 Jul 2021. Alpha variant spread via " super-seeding" event: warning over covid-19 variants.
56. PEREIRA FEL, BORTOLINI ER, CARNEIRO JLA, DA SILVA CRM & RC., N. 1979. A,B,O blood groups and hepatosplenic form of schistosomiasis mansoni (Symmer's fibrosis). Trans R Soc Trop Med Hyg 73:238. Crossref. PubMed.
57. PUISSANT, B., HORS, J., CARTRON, J.P., AND ROUGER, P. 2005. Increased prevalence of the Lewis(a–b–) phenotype in HIV-1 infected patients. . ,British Journal of Haematology, , 48(1), pp.345-346.
58. RAZAQ, Z. & ALKUFI, S. G. J. 2022. Association between ABO blood groups genotype variation and sever infection of COVID-19 in Iraqi patients. International journal of health sciences, 6, 3330-3344.
59. REGAN, F. A. M. 2017. 21 - Blood Cell Antigens and Antibodies: Erythrocytes, Platelets and Neutrophils. In: BAIN, B. J., BATES, I. & LAFFAN, M. A. (eds.) Dacie and Lewis Practical Haematology (Twelfth Edition). Elsevier.
60. REGAN, J. A., CHAO, S., AND JAMES, S., 1978 Maternal ABO blood group type B: a risk factor in the development of neonatal group B streptococcal disease. Pediatrics, , 62, pp.504-509.
61. REID, M. E., LOMAS-FRANCIS, C. & OLSSON, M. L. 2012. YT - Yt Blood Group System. In: REID, M. E., LOMAS-FRANCIS, C. & OLSSON, M. L. (eds.) The Blood Group Antigen FactsBook (Third Edition). Boston: Academic Press.
62. ROWE, J. A., HANDEL, I. G., THERA, M. A., DEANS, A. M., LYKE, K. E., KONE, A., DIALLO, D. A., RAZA, A., KAI, O., MARSH, K., PLOWE, C. V., DOUMBO, O. K. & MOULDS, J. M. 2007. Blood group O protects against severe Plasmodium falciparum malaria through the mechanism of reduced rosetting. Proc Natl Acad Sci U S A, 104, 17471-6.
63. SALADIN, K. S. 2018. The Unity of Form and Function. Anatomy & Physiology. McGraw-Hill, 2018
64. SALIH, H. A. L. M. Frequency Distribution of ABO Blood Groups and Rh Phenotypes of Blood Donors in babylon Governorate-Iraq. 2009.
65. SCHMIEDEL, B. J., ROCHA, J., GONZALEZ-COLIN, C., BHATTACHARYYA, S., MADRIGAL, A., OTTENSMEIER, C. H., AY, F., CHANDRA, V. & VIJAYANAND, P. 2021. COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types. Nat Commun, 12, 6760.

66. SHAIKH AA, ALQASEM HM, ALSHUBRUQI YA, ALASMARI SZ, MAKKAWI MH. Association of ABO, Rh-D and Kell blood groups with transfusion transmitted infections among blood donors from the Asir Region, Saudi Arabia: A retrospective observational study. Saudi Med J. 2024 Apr;45(4):414-423. doi: 10.15537/smj.2024.45.4.20240007. PMID: 38657987; PMCID: PMC11147570.
67. SHEN, M., PENG, Z., XIAO, Y. & ZHANG, L. 2020. Modelling the epidemic trend of the 2019 novel coronavirus outbreak in China. bioRxiv, 2020.01.23.916726.
68. SHIRATO, H. 2011. Norovirus and histo-blood group antigens. Jpn J Infect Dis, 64, 95-103.
69. VALENTI, L., GRIFFINI, S., LAMORTE, G., GROVETTI, E., UCEDA RENTERIA, S. C., MALVESTITI, F., SCUDELLER, L., BANDERA, A., PEYVANDI, F., PRATI, D., MERONI, P. & CUGNO, M. 2021. Chromosome 3 cluster rs11385942 variant links complement activation with severe COVID-19. J Autoimmun, 117, 102595.
70. WANG, M., GAO, J., LIU, J., ZHAO, X. & LEI, Y. 2021. Genomic Association vs. Serological Determination of ABO Blood Types in a Chinese Cohort, with Application in Mendelian Randomization. Genes (Basel), 12.
71. WESTHOFF, C. M., STORRY, J. R. & SHAZ, B. H. 2018. Chapter 110 - Human Blood Group Antigens and Antibodies. In: HOFFMAN, R., BENZ, E. J., SILBERSTEIN, L. E., HESLOP, H. E., WEITZ, J. I., ANASTASI, J., SALAMA, M. E. & ABUTALIB, S. A. (eds.) Hematology (Seventh Edition). Elsevier.
72. WHO, W. H. O. 2024. WHO. COVID-19 epidemiological update – 17 June 2024 [Online]. WHO. Available: https://www.who.int/publications/m/item/covid-19-epidemiological-update in June 2024 [Accessed 26/06/2024 2024].
73. YAMAMOTO, F. 2004. Review: ABO blood group system--ABH oligosaccharide antigens, anti-A and anti-B, A and B glycosyltransferases, and ABO genes. Immunohematology, 20, 3-22.
74. YAN, T., XIAO, R., WANG, N., SHANG, R. & LIN, G. 2021. Obesity and severe coronavirus disease 2019: molecular mechanisms, paths forward, and therapeutic opportunities. Theranostics, 11, 8234-8253.
75. ZHOU, P., YANG, X.-L., WANG, X.-G., HU, B., ZHANG, L., ZHANG, W., SI, H.-R., ZHU, Y., LI, B., HUANG, C.-L., CHEN, H.-D., CHEN, J., LUO, Y., GUO, H., JIANG, R.-D., LIU, M.-Q., CHEN, Y., SHEN, X.-R., WANG, X., ZHENG, X.-S., ZHAO, K., CHEN, Q.-J., DENG, F., LIU, L.-L., YAN, B., ZHAN, F.-X., WANG, Y.-Y., XIAO, G.-F. & SHI, Z.-L. 2020. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature, 579, 270-273.
76. ZHU, Z., LIAN, X., SU, X., WU, W., MARRARO, G. A. & ZENG, Y. 2020. From SARS and MERS to COVID-19: a brief summary and comparison of severe acute respiratory infections caused by three highly pathogenic human coronaviruses. Respir Res, 21, 224.