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Association between ABO blood groups and susceptibility to COVID-19

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ABSTRACT:
Growing evidence suggests that ABO blood group may play a role in theimmunopathogenesis of SARS-CoV-2 infection, with group O individuals lesslikely to test positive and group A conferring a higher susceptibility to infectionand propensity to severe disease. The level of evidence supporting an associationbetween ABO type and SARS-CoV-2/COVID-19 ranges from small observationalstudies, to genome-wide-association-analyses and country-level meta-regressionanalyses. ABO blood group antigens are oligosaccharides expressed on red cellsand other tissues (notably endothelium). There are several hypotheses to explainthe differences in SARS-CoV-2 infection by ABO type. For example, anti-A andor anti-B antibodies (e.g. present in group O individuals) could bind to corre-sponding antigens on the viral envelope and contribute to viral neutralization,thereby preventing target cell infection. The SARS-CoV-2 virus and SARS-CoVspike (S) proteins may be bound by anti-A isoagglutinins (e.g. present in group Oand group B individuals), which may block interactions between virus and angio-tensin-converting-enzyme-2-receptor, thereby preventing entry into lung epithe-lial cells. ABO type-associated variations in angiotensin-converting enzyme-1activity and levels of von Willebrand factor (VWF) and factor VIII could alsoinfluence adverse outcomes, notably in group A individuals who express highVWF levels. In conclusion, group O may be associated with a lower risk ofSARS-CoV-2 infection and group A may be associated with a higher risk ofSARS-CoV-2 infection along with severe disease. However, prospective andmechanistic studies are needed to verify several of the proposed associations.Based on the strength of available studies, there are insufficient data for guidingpolicy in this regard.
Keywords: Covid-19, ABO blood group

I. INTRODUCTION:

This new CoV infection called as COVID-19 originated in Wuhan, Hubei Province, China in December 2019 (Zhu et al.,2020). The causative agent for this respiratory illness is severe acute respiratory syndrome coronavirus 2 (SARS-COV-2). These epidemics have a high infection transmission rate and in general, the direct cause of death is severe atypical pneumonia (Yin and Wunderink ,2018).The disease spread rapidly from the initial epicenter, Wuhan to rest of the world and has become a pandemic (Isam et al., 2021). The main risk factors include pneumonia, acute kidney failure, acute heart failure. People with underlying health conditions such as cardiovascular disease, diabetes, chronic respiratory disease and the elderly above 60 years are most susceptible to COVID-19. Hospitals announced a cluster of cases of unknown cause pneumonia in Wuhan, Hubei, China on 31 December 2019, attracting great national and worldwide attention. Coronavirus (CoV) is a wide family of single-stranded, positive-sense RNA viruses belonging to the Nidovirales order. The order includes families of the Roniviridae, Arteriviridae, and Coronaviridae. The family Coronaviridae is subdivided into subfamilies Torovirinae and Coronavirinae. Coronavirinae is further subclassified into alpha, beta, gamma and delta COVs(Fehr and Perlman.,2015)Phylogenetic clustering accounts for certain virus subtypes being named. The viral RNA genome varies in length from 26 to 32 kilobases. They can be separated from various species of animals. Those include birds, cattle and mammals such as camels, bats and masks Civets of leaves, rats, pigs, cats …. The widespread COV distribution and infectivity make it a major pathogen. The moderate clinical signs are associated with human pathogenic subtypes of CoV. Yet extreme coronavirus-related acute respiratory syndrome (SARS-CoV) and the Middle East The two notable exceptions are respiratory coronavirus syndrome (MERS-CoV). In Saudi Arabia MERS-CoV was first observed in 2012. It has been responsible for 2,494 confirmed cases which have resulted in 858 deaths. In 2002, a Beta-COV subtype spread rapidly in Guangdong, China. In 37 countries this epidemic resulted in 8,000

infections and 774 deaths(Lauet al.,2020)The COVID-19 pandemic spurred a crisis that is unprece-dented in modern times (Zhu et al.,2019). The disease course variessubstantially among individuals, from mild or even sub-clinical infection to severe disease. Indeed, more than1 million COVID-19-related deaths have been reportedglobally. There is interest in potential risk factors thataffect susceptibility to infection and disease progression.Multiple medical (e.g. diabetes, hypertension) andsociodemographic (e.g. sex, age and race/ethnicity) riskfactors for severe outcomes were already established (Wiersingaet al.,2019). Growing evidence suggests that the ABO blood groupmay also play a role in the immune pathogenesis ofSARS-CoV-2 infection, with group O being protective andgroup A conferring risks of higher disease susceptibility and severity (Barnkobet al.,2020). An international group of experts in transfusion medicine and haematology were assembled by the International Society of Blood Transfusion (ISBT). Tothis end, we provide an overview of the ABO blood groupsystem, ABO population frequencies and distributions, itsrole as a histo-blood group antigen, not just a bloodgroup antigen, and the known associations between ABOtype and various infectious and non-infectious diseases.

Susceptibility ABO blood group to Covid

During the severe acute respiratory syndrome coronavirus (SARS-CoV-1) epidemic, several observations suggested that ABO type may contribute to disease, with less susceptibility in group O individuals (Chenget al.,2005).

Most studies identified a higher proportion of group A, and a lower proportion of group O, among COVID-19 patients, as compared to healthy controls (Zhaoet al.,2020).

Some study described a higher rate of infection in group AB patients and a lower rate in group Opatients . In contrast, an additional study did not find any correlation between group A status and COVID-19; nonetheless, group O individuals had a lower risk of COVID-19 and group B and AB individuals had a higher risk (Latzet al.,2020). One potential reason for these varying results is that many such studies did not account for various confounders (e.g.age), including comorbidities. Another potential confounder for some of the studies could be the use of randomly selected volunteer blood donors as controls, because of the risk of group O epidemiological predominance due to blood collectors selectively recruiting group O donors. Importantly, volunteer blood donors are not necessarily representative of general populations; although convenient, their use as a control group is notIt has also been hypothesized that anti-A and anti-Bantibodies could interfere with virus–cell interactions. In a secondary analysis of data from ~1900 patients with COVID-19, subjects with circulating anti-A were significantly less represented in the disease group as compared to those lacking anti-A. In addition, anti-A in group Oindividuals was more protective than anti-A in group B individuals; this may relate to the increased presence of IgG anti-A,B in group O plasma (Stussiet al.,2005).One study attempted a meta-regression analysis of 101 nations using their known blood group distributions, including ~9-million COVID-19 cases and ~450 000 deaths in a total population of ~7 billion. Although therewas no association of group A or B with overall mortality, group O significantly correlated with lower mortality (p = 0_02). The authors proposed that COVID-19 mortality was lower in nations with higher group O prevalence because overall population ABO blood group prevalencewasanalysed as the control .Studies have also examined the relationship between the Rhesus blood group (e.g. Rh(D) type) and COVID-19. One study suggested that Rh(D)-positive individuals were more likely to test positive for SARS-CoV-2 (Latzet al.,2020).

Mechanisms for associations between ABO blood group and COVID-19

Several pathophysiological mechanisms were proposed toexplain the association between ABO type and SARS-CoV-2 infection .Anti-A and/or anti-B antibodiesmight bind to A and/or B antigens expressed on theviral envelope, thereby preventing infection of target cells;that is, these naturally occurring antibodies could functionas viral neutralizing antibodies. If true, this would helpexplain differences in initial susceptibility for SARS-CoV-2infection. For example, an anti-A viral neutralizing antibodyin a potentially susceptible group O host would bindthe A antigen on virus produced by, and inhaled from, aninfected group A (or group AB) host (Breiman et al.,2020). Why this mechanismwould be relevant to disease severity per se is lessobvious, because subsequent rounds of viral proliferationin a group O host would produce virus expressing the Hantigen on its envelope. However, assuming that diseaseseverity relates to the size of the infecting inoculum andyielding the subsequent viral load, a neutralizing isoagglutinin(e.g. anti-A) could attenuate infection, if not preventinginfection altogether. Finally, the entry barrier for thisvirus is the epithelium of the respiratory tract and,

possibly,the digestive tract. Thus, to prevent infection, circulatingantibodies may need to reach these cell surfaces; although,presumably, the most effective antibodies for this purposeare of the secretory IgA isotype, to date, no data are availableabout the IgA isotype for either anti-A and/or anti-Bin this regard.Glycan structures at various N-glycosylation sites ofthe SARS-CoV S protein were previously described (Liet al.,2005).

In addition, N-glycans of recombinant SARS-CoV-2S protein were recently characterized ; although ABHantigen structures were not described, this may be due tothe cell line used to produce the recombinant protein.Interestingly, the receptor-binding domains of the SARSCoV-2 and SARS-CoV S proteins are structurally nearlyidentical ; in addition, glycosylation yields S trimersin which the receptor-binding domains are covered by Nglycans.Thus, it is conceivable that SARS-CoV-2 S proteincould be specifically bound by human anti-A antibodies,which could then block the interaction betweenthe virus and the angiotensin-converting enzyme 2 receptor(ACE2R), thereby preventing entry into the lungepithelium. Relevant to this hypothesis, monoclonal ornaturally occurring anti-A antibodies dose-dependentlyinhibited interaction between SARS-CoV S protein andACE2R, in a model where the A antigen was associatedwith S protein (Guillonet al.,2008).

To our knowledge, there areno published studies to date that address this.Other potential mechanisms may explain the epidemiologicalresults. For example, if ABH oligosaccharides areon SARS-CoV-2 S protein, they may modify the affinityof SARS-CoV-2 for ACE2R, its cellular receptor. Thiscould be evaluated formally by producing recombinant Sprotein in otherwise identical host cell lines (e.g. bytransfecting in the relevant glycosyltransferases) and thenquantifying the affinity of the purified proteins for theirreceptor. Analogously, if the virus could be producedin vitro in these ABH-expressing cell lines and purified,the infectivity of a given target cell line could then bequantified. Given the published human population data,one might expect 'group O virions' to be less infectious inthese experiments, thereby correlating with decreasedCOVID-19 disease severity.A different, but not mutually exclusive, mechanism mayinvolve ACE2R, which is also a glycoprotein and mayexpress ABH glycans. It is possible that these glycansnaffect SARS-CoV-2 viral binding to ACE2R, the number ofACE2R proteins on a given cell surface, and/or the efficacyof internalization of the virus: receptor complex. In thiscase, ACE2R expressing H-antigen glycans may not be aseffective at binding and internalizing SARS-CoV-2 producedby any source, irrespective of ABO type. This couldalso underlie COVID-19 disease severity.It is also possible that the ABH glycans themselvescould serve as (alternative) lower-affinity receptors forSARS-CoV-2 S protein or bind other viral envelope structures.Although current evidence suggests that this isunlikely, if it were relevant, then ABH glycan levels oncell surfaces, in plasma, and in secretions would beimportant and could affect initial infection and diseaseseverity. For this purpose, determining the 'secretor phenotype'and Lewis blood group types would be helpful(Cooling,2015).

II. CONCLUSIONS

The role of ABO blood group in SARS-CoV-2 infectivityand COVID-19 disease severity requires additional study;however, accumulating evidence suggests that, at biochemicaland physiological levels, there may be a contributionof ABO blood type to disease biology.

REFERENCE

[1]. -Barnkob MB: Reduced prevalence ofSARS-CoV-2 infection in ABO blood
[2]. -Breiman A, Ruven-Clouet N, Le PenduJ: Harnessing the natural anti-glycan immune response to limit the transmission of enveloped viruses such as SARS-CoV-2. PLoSPathog 2020; 16: e1008556.
[3]. -Cheng Y, Cheng G, Chui CH, et al.:ABO blood group and susceptibility to
[4]. -Cooling L: Blood groups in infection and host susceptibility. Clin Microbiol Rev 2015; 28:801–70.
[5]. diagnosis, and treatment of coronavirusdisease 2019 (COVID-19): a
[6]. -Fehr AR, Perlman S.Coronaviruses: an overview of their replication and pathogenesis.(2015).
[7]. -Group and the COVID-19 Susceptibility.medRxiv 2020.
[8]. -group O. Blood Adv 2020; 4(20):4990–4993.
[9]. -Guillon P, Cl_ement M, S_ebille V, et al.: Inhibition of the interaction between the SARS-CoV spike protein and its cellular receptor by anti-histo-blood group antibodies. Glycobiology 2008;18:1085–93.
[10]. -Isam, J. Z., Kamil, K. Z., &Banoon, S. R. (2021). Review about COVID-19. Research Journal of Biotechnology Vol, 16, 4
[11]. -Latz CA, DeCarlo C, Boitano L, et al.:Blood type and outcomes in patients

[12]. -Lau FH, Majumder R, Torabi R, etal.(2020). Vitamin D insufficiency is
[13]. -Li F, Li W, Farzan M, et al.: Structure of SARS coronavirus spike receptorbinding domain complexed with receptor. Science 2005; 309.
[14]. -Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. (2020).
[15]. pneumonia in China, 2019. N Engl JMed 2020; 382:727–33.
[16]. prevalent in severe COVID-19.
[17]. review. JAMA 2020; 324:782–93.
[18]. severe acute respiratory syndrome.Jama 2005; 293:1450–1.
[19]. -Stussi G, Huggel K, Lutz H, et al.: Isotype-specific detection of ABO bloodgroup antibodies using a novel flowcytometric method. Br J Haematol2005; 130:954–63.
[20]. -Wang C, Horby PW, Hayden FG, Gao GF. A novel coronavirus outbreak of global health concern. Lancet.2020 Jan 14.
[21]. -Wiersinga WJ, Rhodes A, Cheng AC,et al.: Pathophysiology, transmission,with COVID-19. Ann Hematol 2020;1–6.
[22]. -Yin Y, WunderinkRG.MERS, SARSand other coronaviruses as causes ofpneumonia. Respirology (2018);23:130–7.
[23]. -Zhao J, Yang Y, Huang H-P, et alRelationshipbetween the ABO Blood-Zhu N, Zhang D, Wang W, et al.(2020). ANovel Coronavirus from Patients withPneumonia in China, 2019. N Engl JMed.328:727–33.
[24]. -Zhu N, Zhang D, Wang W, et al.: ANovel Coronavirus from patients with