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SARS COV-2 Variants and Blood Group Susceptibility: A Review

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Abstract

The newly emerged corona virus is in its highest peak of action and various unseen forms of the same are being identified, which can transmit and spread the disease in a higher pace than the earlier discovered one. There are numerous alternatives of the SARS COV-2 that differ from each other by at a minimum of one alteration. Many of these variants soon gets extinguished while some others remain longer, spread fast, procure further mutations and undergo variation to a new alternant form. This paper incorporates details about these newly identified variants of SARS COV-2 in different nooks of the world. In addition, the association of blood type with SARS COV-2 and the risk factors related to this has also been addressed. People having blood group 'O' are a bit more resistant and have comparatively a higher degree of tolerance towards the attack of novel corona virus, on the other hand those having 'A' blood type are typically more susceptible to the viral attack.

Keywords: SARS Cov-2 variants; Blood type; Mutations; Diseases

Introduction

The covid-19 pandemic varies substantially among individuals, from mild or even asymptomatic infections to severe disease. Indeed, 4 million covid-19 related deaths have been reported globally. A thorough knowledge on factors that affect susceptibility to infection and disease progression is necessary. Socio-demographic factors, multiple factors like diabetes, hypertension etc. and chronic kidney diseases immensely add death risks related to covid-19. New evidences and reports suggest that the ABO blood group also play an important role in the immunopathogenesis of SARS COV-2 infection. Group "A" is reported to be with increased risk of higher disease susceptibility and worse outcome compared to blood group "O".

SARS Cov-2 Variants

After being exposed to SARS and MARS, it was on 31 December 2019, the WHO China Country Office was informed about pneumonia of unknown cause in Wuhan City, Hubei Province- China. As of 3 January 2020, a total of 44 patients with pneumonia had been reported to the WHO by the national authorities in China. The cluster was initially reported when the Chinese authorities recognized a new coronavirus as the causative agent of SARS-CoV2 which was named as COVID-19 by the World Health Organization [1]. Almost all virus encounter mutation and change overtime to a new form. The recombination frequency will be higher in the S gene which codes for viral spike (S) [2]. These variants either establish or disappear or they remain rooted causing infections in the host organism. Latterly a number of virus varieties were spotted at different parts of the world.

The variants are B.1.1.7 (lineage emerged in the UK in late 2020), B.1.351 (a new variant, named for the N501Y mutation in the Receptor Binding Domain (RBD), in late 2020.), P.1 (501Y.V3 or Brazilian variant) and B.1.427 and B.1.429 (California or West Coast variants emerged in late spring or early summer of 2020). They appeared to spread more easily and quickly, which might eventually lead to more cases of covid-19 throughout the world. Initial studies propose, B.1.1.7 variant of SARS COV-2 are about 50 percent more transmissible than other forms, with 17 defining mutations, while B. 1.351 with 9. Moreover, P.1 has nearly the same three mutations as of B.1.351. An alternative of SARS COV-2 containing a D614G substitution in the gene encoding the spike protein sprout out in the early February 2020. These new forms of the already existing virus spread and replaced the initial one, thereby set up as a paramount body in a short span of time. The D614G mutation replaced the initial SARS COV-2 strain spotted in China and soon became a dominant form of virus circulating globally. Studies revealed that the infecting and transmitting capability of D614G substitutions (variants) outweigh the initial non variant, which is mainly due to the change in its biochemical properties which improve its attachment potential with ACE2 receptor. This mutation helps the virus to spread and is deadly for humans as it increases the rate of infection [3]. Moreover patients infected with D614G associated SARS COV-2 are more likely to have a comparatively higher percent of viral loads in their upper respiratory tract than those who got infected by the strains that lack these mutations. On 14th December 2020, a variant SARS COV-2 VOC 202012/01 has been reported to World Health Organization, which contains 23 nucleotide substitutions and is not phylogenetically related to the SARS COV-2 virus circulating in UK by the time it was uncovered. Preliminary modeling, phylogenetic and laboratory findings suggest, these mutant forms are prone to high transmissibility among individuals. However, VOC-202012/01 has appeared in 31 other countries/territories/areas in five of the six WHO regions. On 18th December, national authorities in South Africa has detected a new SARS COV-2 alternate that is rapidly spreading in the province and named it as 501Y.V2, because of a N501Y mutation. The SARS-COV-2 VOC 202012/01 from the UK also has the N501Y mutation in the spike protein that the virus uses to bind to the human ACE2 receptor. Soon, its presence has been reported in many other parts of the world [4-6]. It has been named VUI-202012/01 (the first "Variant under Investigation" in December 2020) and is defined by a set of 17 changes or mutations. The change in this part of spike protein makes the virus becoming more infectious and spreading more easily between people [7].

Blood Type and the SARS Cov-2

ABO blood groups which are genetically inherited and a correlation is suggested between ABO blood type, cardiovascular disease and cancers, as well as typing and susceptibility to certain infections, including SARS coronavirus [8,9]. Examining individuals affected by SARS Cov-2 advocated, the blood group ABO, play a role in the immune-pathogenic of SARS Cov-2, where group 'O' individuals to encounter a lowest affect from this viral attack and group 'A' on the other hand mount at the peak of being infected by the virus [10].

Furthermore major proportion of victims having A or AB type blood shows a high need for mechanical ventilation and CRRT than one with group O or B group, similarly biomarkers of renal and hepatic dysfunction was higher in patients with A or AB blood type. Those in severe condition of covid-19 and with A or AB group are in high need of mechanical ventilation, CRRT and prolonged ICU dependence compared to those having an O or B type [11]. The cause for this phenomenon could reside in the presence in O blood group subjects of IgG anti-A isoagglutinins which would prevent the binding of SARS cov-2, thereby inhibiting its entry into targeted cells [12]. Moreover, people with blood group O can recognize certain foreign proteins and that extend to proteins or viral surfaces so less likely to get a disease. SARS-CoV-2's spike (S) protein is 1273 amino acids long and uses ACE2 receptors for its binding on the host cell membrane thereby facilitating its entry into the cell after the proteolytic cleavage of 's' protein by trans-membrane protease serine-2. This exposes a fusogenic peptide which promotes the fusion of viral envelop with host cell membrane as a result of which the virus gain entry into the host by endocytosis, proceed with viral replication and thereby the release of multiple off-springs [9]. Hence the mutations in the S gene, particularly those that affect portions of the protein that are critical for pathogenesis and normal function (such as the Receptor Binding Domain (RBD) or furin cleavage site) or those that cause conformational changes to the S protein, are very important. If these changes are not identified or recognized by "first-wave" antibodies, these mutations may provide an opportunity for the virus to escape from immunity to the original SARS-CoV-2 strain. The anti-A antibodies inhibit binding of glycosylated SARS COV-2 protein expressing cells to Angiotensin Converting Enzyme 2 (ACE-2) on the cell surface, so these antibodies might block the interaction of virus and its receptors thereby providing protection to the concerned individual [10].

Evidence suggests that, at biochemical and physiological levels, there may be a contribution of ABO blood type to disease biology along with host factors contributing to COVID-19 severity [10]. Association between the ABO blood group and COVID-19 susceptibility and severity was shown in recent studies and it is reported that those with blood group A have a higher susceptibility and severity whereas people with blood group O have a lower one [13]. The data from New York-Presbyterian/Columbia University Irving Medical Center (NYP/CUIMC) hospital in New York City, USA showed moderately increased infection prevalence among non-O blood types and among Rh-positive individuals. It was also reported that the intubation risk was increased among AB and B types and decreased among A and Rh-negative types and risk of the death was slightly increased among type AB individuals and was decreased among types A, B, and Rh-negative types [14].

Discussion and Conclusion

Apart from all the physical out-turns; this resurgence of corona virus has in many ways lead to social crisis as well as affected the mental well-being of life in this world. Newly detected alternatives of SARS COV-2 are having an increased power for transmission thereby affecting a large number of people belonging to different age group inhabiting in different parts of the world, accelerating the severity of the disease. All of the known viruses including this recently emerged one undergo a noticeable alterations in them overtime and arising with an increased capability to infect host organisms in which it get accommodated and replicate to produce an enormous number of progeny viruses, which in turn stress on the high need for becoming more vigilant and remain protected to reduce the outbreak and minimize fatality of this viral disease to some extent. Moreover looking forward, there is a high chance for the detection of several other varieties of SARS Cov-2 as the cases are rapidly increasing and virus might undergo more number of alterations and modifications in them thereby transforming to a never seen before type of microbe with a further higher degree of transmittance as well power to cause infection. As always, it's important to remember that notably, B.1.1.7, B.1.351 and P.1 have now all been identified in multiple countries and since mutation is regularly occurring, new variants will continue to emerge. This ongoing mutation threat emphasizes the importance of genomic surveillance programs to track SARS-CoV-2 evolution, which in turn helps to restrict the spread of disease and improve public health practices, including diagnostics and vaccine development and distribution. Also additional research is required to identify the role of ABO blood group in SARS-CoV-2 infectivity and COVID-19 disease severity.

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