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Editorial

Omicron Variant: Characteristics and Interaction

Simranjeet Kaur Akshita and Amandeep Singh*

Department of Pharmaceutics, ISF College of Pharmacy, Punjab, India

***Corresponding Author:** Amandeep Singh, Department of Pharmaceutics, ISF College of Pharmacy, Punjab, India

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Introduction

On 26 November 2021, WHO designated the variant B.1.1.529 a variant of concern, named Omicron, on the advice of WHO's Technical Advisory Group on Virus Evolution (TAG-VE). This decision was based on the evidence presented to the TAG-VE that Omicron has several mutations that may have an impact on how it behaves, for example, on how easily it spreads or the severity of illness it causes.

Severity of disease

It is not yet clear whether infection with Omicron causes more severe disease compared to infections with other variants, including Delta. Preliminary data suggests that there are increasing rates of hospitalization in South Africa, but this may be due to increasing overall numbers of people becoming infected, rather than a result of specific infection with Omicron. There is currently no information to suggest that symptoms associated with Omicron are different from those from other variants. Initial reported infections were among university students-younger individuals who tend to have more mild disease-but understanding the level of severity of the Omicron variant will take days to several weeks. All variants of COVID-19, including the Delta variant that is dominant worldwide, can cause severe disease or death, in particular for the most vulnerable people, and thus prevention is always key.

Emergence

On November 11, 2021, the primary occurrence of significantly mutated SARCOV-2 was searched out in Botswana, followed by a few counts of instances of this variation in South Africa on November 14, 2021.First and foremost, on November 14, 2021, the contagions identified were 273. However, as the day passed, a precipitous surge was observed, peaking up to five times its original level after 14 days. These new cases of the strain have sparked worldwide concern. The marked increase of omicron instances has been found in multiple other nations as of November 28, 2021, including the Netherlands, France, Germany, Italy, and Australia. The first case was recognized in the United States on December 1, 2021, with a chunk of cases spreading in Europe on December 13, 2021. There have been 958 occurrences of this extremely infectious strain recorded in Europe. Twenty-two of the cases were linked to tourists. In contrast to previous versions, the omicron may be projected to proliferate expeditiously based on all of these scenarios. The sheerly promulgating omicron variant invaded the United States on November 15, 2021, with a paramount peak of 70,000 cases. On the second day, a total of 10,000 people were found to be infected with this variant. In each of these cases, the panic button was clinked among British citizens.

Morphology

Like, corona virus it is also a type of RNA viruses, which are prone to recurrent genomic alterations because of their nature. Protein structure and dynamics, including viral proteins, are changed as a result of the mutation. S-protein, envelope protein, membrane protein, and nucleocapsid protein are the four structural proteins found on its surface. The nucleocapsid protein is a ribonucleoprotein that binds to RNA during viral replication. The viral envelope is made up of two components, E1 and E2. E1 is a transmembrane protein matrix, and E2 is a pathogenic glycoprotein that aids infusion; this envelope is built up of fatty layers, which are broken down when exposed to soap; this is why hand washing is required. Spike glycoprotein is one of the virus's major structural proteins

and it has Receptor Binding Domains (RBD), which are responsible for binding. The Spike protein in the Omicron variation has 37 alterations, including six deletion mutations, one insertion mutation, and 30 substitution mutations. The RBD, which ranges from 333-527 (amino acid residue), has been determined to be the site of the majority of known VOC mutations. When these Spike protein mutations in Omicron are compared to pre-existing concern variations (Alpha, Beta, Gamma, and Delta), 26 mutations are unique to Omicron, whereas 7 mutations overlap between Omicron and Alpha. A unique insertion mutation has been discovered in his severely mutated Spike variation ins214EPE.

Spike protein nucleotide sequences from Omicron and reference Wuhan SARS-CoV-2 sequences suggest that Omicron's ins214EPE can be encoded by two distinct nucleotide sequence insertions. GAGCCAGAA and GCCAGAAGA are the insertion candidates. Using default BLAST settings, an NCBI BLAST search for 'CGTGAGCCAGAAGAT' was run, which contains both probable insertion candidates (GAGCCAGAA, GCCAGAAGA) [1-8].

How it interacts with host cell

The Spike glycoprotein is one of the virus's major structural proteins, with a stalk entrenched in the viral membrane and a huge head that interacts with the host Angiotensin Converting Enzyme 2 (ACE2) receptor (as illustrated in figure 1.) found in the lungs, kidneys, and gut. The Spike protein, which is made up of three peptide chains, includes a unique N-terminal domain called S1 that is responsible for receptor binding and is referred to as the Receptor Binding Domain, as well as a C-terminal domain called S2 that is responsible for fusion. The major function of RBD is to bind to the ACE2 receptor. Although the RBD is the Spike protein's interacting domain, the actual region of contact is known as the Receptor Binding Motif (RBM), which is located between residues 438 and 506. The majority of the mutations occur in the S protein receptor-binding domain (RBD), which might affect infectivity and antibody resistance. This is because the RBD on the S protein aids in the binding of the S protein to the host angiotensin-converting enzyme 2. (ACE2). The omicron is aided in entering the host cell by S-ACE2 binding, which starts the viral infection process.

Figure 1: Shows binding between the omicron variant and ACE-2 receptor.

The binding free energy (BFE) between the S RBD and the ACE2 has been found to be proportional to viral infectivity in several investigations. The energy of binding of omicron with the ACE-2 receptor is different than the other variants (as shown in table.1). As a result, an antibody that binds tightly to the RBD would destroy the virus directly.

Type of energy	Omicron	Other Variant/ Wild Type
Electrostatic energy	-3083.962 +/- 89.676 kJ/mol	-1232.614 +/- 64.543 kJ/mol
SASA energy	42.889 +/- 3.818 kJ/mol	-43.889 +/- 3.469 kJ/mol
van der Waal energy	-335.186 +/- 21.937 kJ/mol	-363.775 +/- 20.446 kJ/mol
Binding energy	-2658.233 +/- 129.686 kJ/mol	-1022.467 +/- 150.703 kJ/mol

Table 1: Total energy of binding of RBD with the human ACE2 receptor.

Alpha	Beta	Gamma	Delta	Omicron
Alpha variants show 4 unique spike mutations: A570D D1118H S982A T7161	Beta variants show 6 unique spike mutations: A701V D215G D80A ΔL241 ΔL242 ΔA243	Gamma variants show 8 unique spike mutations: D138Y K417T L18F P26S R190S T1027I T20N V1176F	Delta variants show 7 unique spike mutation: D950N E156G L452R P681R T19R ΔF157 ΔR158	Omicron show 26 unique spike mutation: A67V D796Y E484A G339D G446S G496S L2121 L981F N440K N679K N764K N856K Ins214EPE N969K Q493R Q498R Q954H S371L S373P S375F S477N T547K T951 Y505H ΔV143 ΔN211

Table a: Mutation difference of variants of COVID-19.

Figure a: Methods of prevention.

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