Frontiers in Health InformaticsISSN-Online: 2676-7104 www.healthinformaticsjournal.com
2024; Vol 13: Issue 3 Open Access

In the Territory of Omicron

Aljin.V[1], Krishna Prasanth Baalann[2]*, Nikhil Athithya[3] and Srini CM[4]
[1]Assistant Professor, Department of Community Medicine, Sree Balaji Medical College and Hospital, Bharath Institute of Higher Education & Research, Chennai
[2]Epidemiologist &Assistant Professor, Department of Community Medicine, Sree Balaji Medical College Andhospital
[3&4]House Surgeon, Department of Community Medicine, Sree Balaji Medical College and Hospital, Bharath Institute of Higher Education & Research, Chennai

---

Cite this paper as:
Aljin.V, Krishna Prasanth Baalann, Nikhil Athithya and Srini CM (2024). In the Territory of Omicron. *Frontiers in Health Informatics,* 13(3), 4945-4947

ABSTRACT

The SARSCoV2 virus causes COVID19 disease, a new virus thatcauses a pandemic and affects countries in all aspects. The pandemic is existing for more than 2 years affecting the population psychologically and economically. Presently, it has undergone enormous mutations and The World Health Organisation(WHO) categorized as fifth mutant of significance, Omicron, designated by World Health Organisation (WHO). Omicron has been reported in more than half of the nations worldwide. As it is high number of mutations, it has a high transmission rates when compared to previously prevailed variants and original strain. Additionally, this has a high rates of reinfection especially with its sub-lineage. Some of the vaccines are effective against this variant while some others are minimal effect. Furthermore, every vaccine produces antibodies that neutralises the viral load. This article concerned on Omicron, its genetics , vaccine efficacy against omicron and its lineage.

Keywords: *COVID19, Omicron variant, vaccine and omicron*

INTRODUCTION:

SARS-CoV-2 virus causespneumonia cases worldwide namely COVID19. The first case of this new pandemic causing virus was reported on 31st December 2019 in Wuhan after which it spread across the globe leading to morbidity and mortality among the global population(1). More than 450 million population has been affected by this virus with mild symptoms such as pyrexia, cough, malaise and ageusia or loss of smell to more critical symptoms such as shortness of breath or difficulty in breathing, confusion, chest pain, hyper coagulable states making it a life-threatening disease accounting to nearly 6 million deaths worldwide. In order to reduce the transmission among communities, some of the general measures like washing hands frequently, maintaining atleast 1 metre distance from a person in public places, wearing masks when going out, being in well ventilated or open spaces, getting vaccination, were asked to be implemented and followed on a daily basis by WHO.

Changing Nature of SARS CoV-19:

As like all viruses, this virus changed over time affecting virus properties of how fast it spreads, vaccine and medicines efficacy, how severe it affects if there's associated comorbidities or other public health and social measures. After emergence of variants during late 2020,to prioritise global surveillance and inform ongoing response to the pandemic, the characterisation of Specific VOIs and VOCs - Variant of Interest and Variant of Concern has been undertaken. Alpha variant, Beta variant, Gammavariant, Deltavariant and Omicron variant are presently classified VOCs while Lambda mutant strain and Mu mutant strain are currently designated VOIs(2).Variants of interest are those whose genetic changes are predicted to have an impact on virus properties such as infectivity, immunity, severity of the disease, and avoidance of diagnosis. or treatment and is known to cause multiple clusters of COVID19 cases in many countries with growing prevalence and quantity of cases throughout time or to produce epidemiological consequences suggesting an emergingglobal public health threat. The Variant of concern is an VOI that are linked to at least one of the following changes at the level of importance to public health: increased pathogenicity or virulence, or altered clinical disease symptoms; or reduced benefits of social and preventive medicine interventions, available diagnostics, vaccines, and treatments(2).

A New Variant in Late 2021:

In South Africa, B.1.1.529 strain was first publicized on November 24,after identifying a steep increase in infection occurring simultaneously with the detection of this variant. WHO initially designated this variant as Variant Under Monitoring(VUM). After two days, Technical Advisory Group on SARS-CoV2 Virus Evolution (TAG-VE)which monitor as well as analyses SARS-CoV2 virus evolution on a regular basis, convened to assess variant B.1.1.529(3). It was recommended by the TAG-VE that it should be classified as just a VOC. The WHO classified this variant as VOC and named it Omicron on the very same day.

Omicron is a strain with the most mutations so far, facilitating its rapid transmission among communities globally. It has more than 50 mutations in its genome, some of which are worrisome as they are associated with escaping tendency from humoral immunity. About 30 mutations has been identified on spike surface protein of the virus that is responsible for binding ACE2 receptors to infection. Strain B.1.1.529, Strain BA.1,Strain BA.2and Strain BA.3 are four Omicron lineages(3).More than 150 countries has reported with atleast one case of omicron variant as of now.

How Different is Omicron?

This virus is composed of structural proteins (spike protein (S), matrix protein (M), envelope protein (E), and nucleo-capsid protein (NC)) and non-structural proteins (NSP1-NSP16)(3). Spike glycoprotein has two subunits S_1 acting as main receptor binding domain and S2 with fusion mechanism. The virus cell entry is facilitated by specific proteases (furin, thrypsin, Catherin or serino-protease 2 [TMPRSS2]) while the main target receptor for viral attack is Angiotensin converting enzyme 2 (hACE2). There are many point mutations including mis-sense mutation, synonymous and non synonymous deletions and single amino acid mutations(4).

Omicron variant demonstrates two main mutations – combinations of three deletions and one insertion in S1/RBD subunit and an increased mutational landscapein S2 subunit. Among the mutational landscape, G142D, T478K, N501Y and D614G substantiates penetration of Omicron into the cell. K417N mutation improves evasion of immune system(5).The absence of leucine to arginine substitution at position 452 that increases the affinity for ACE2 receptors in lungs explains limitation of variant to the upper respiratory tract(5). These impact on the transmissibility, morbidity or mortality but remains unclear.

Vaccine Efficacy and the Variant:

Four types of COVID19 vaccines are available, namely nucleic acids (mRNA and DNA), viral vectors, protein subunits, and inactivated viruses.(6) BNT162b2 from Pfizer and mRNA-1273 from Moderna are the two nucleic acid vaccines encoding perfusion spike protein of SARS-CoVx2; the vaccines targeting viral vectors are ChAdOx1 nCoV-19 and Ad26.COV2.S from AstraZeneca and Johnson & Johnson/ Janssen respectively.

In a study by Accorsi EK *et al,* suggested that three doses of mRNA vaccination were associated with protection against Omicron in spite of high odds ratios for Omicron suggesting reduced protection against Omicron, on comparison with unvaccinated and recipient of 2 doses in USA(7).

The pre-print paper revealed that when compared to the D614G mutant serum, the BNT162b2 double immunisation serum had a 27-fold lower neutralisation titre against Omicron at 3 months (8).

Results from a cohort study by Planas *et al* , revealed that vaccinated individuals' sera are deficient or not neutralizing Omicron five months after vaccination. A detectable cross neutralisation activity against Omicron was noted to be triggered by booster dose. In spite of administering the booster dose, it showed an eighteen fold and six fold decrease in ED_{50} when compared with D614G and Delta variant respectively(9).

Omicron Variant Sub-lineage BA.2

The Omicron-variant remains the dominant variant disseminating world wide. In recent weeks, the genomic sequences designated BA.2 has been progressively reported when compared to BA.1 lineage and other Omicron lineage in spite of declining spread of infection across the globe. BA.2 is easier to transmit than BA.1 and found to have growth advantage but reason for this growth advantage is undiscovered for which there are ongoing studies, states in latest news of WHO. On evaluating risk of reinfection with BA.2 compared to BA.1 from initial statistics obtained from a population level reinfection studies, good protection is provided by infection with BA.1 against re-infection with BA.2(10). Vaccine efficacy of the existing vaccines against this lineage is yet to be analysed.

REFERENCES

1. World Health Organisation. Coronavirus disease (COVID-19). http://www.who.int/health-topics/coronavirus#tab=tab_1
2. World Health Organisation. Tracking SARS-CoV-2 variants. https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/
3. World Health Organisation. Classification of Omicron(B.1.1.529): SARS-CoV-2 Variant of Concern. https://www.who.int/news/item/26-11-2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern doi:26/11/2021
4. Vasileios Papanikolaou, Aris Chrysovergis, Vasileios Ragos, Evangelos Tsiambas, Spyros Katsinis, Arezina Manoli, Sotirios Papouliakos, Dimitrios Roukas, Stylianos Mastronikolis, Dimitrios Peschos, Anna Batistatou, Efthimios Kyrodimos, Nicholas Mastronikolis. From delta to Omicron: S1-RBD/S2 mutation/deletion equilibrium in SARS-CoV-2 defined variants, Gene, Volume 814, 2022, 146134, ISSN 0378-1119, https://doi.org/10.1016/j.gene.2021.146134 (https://www.sciencedirect.com/science/article/pii/S0378111921007290)
5. Araf, Y, Akter, F, Tang, Y-d, et al. Omicron variant of SARS-CoV-2: Genomics, transmissibility, and responses to current COVID-19 vaccines. *J Med Virol*. 2022; 1- 8. doi:10.1002/jmv.27588
6. Noh, J.Y., Jeong, H.W. & Shin, EC. SARS-CoV-2 mutations, vaccines, and immunity: implication of variants of concern. Sig Transduct Target Ther 6, 203 (2021). https://doi.org/10.1038/s41392-021-00623-2
7. Accorsi EK, Britton A, Fleming-Dutra KE, et al. Association Between 3 Doses of mRNA COVID-19 Vaccine and Symptomatic Infection Caused by the SARS-CoV-2 Omicron and Delta Variants. JAMA. 2022;327(7):639–651. doi:10.1001/jama.2022.0470 https://doi.org/10.1001/jama.2022.0470
8. Ikemura N, Hoshino A, Higuchi Y, Taminishi S, Inaba T, Matoba S. SARS-CoV-2 Omicron variant escapes neutralization by vaccinated and convalescent sera and therapeutic monoclonal antibodies. medRxiv. 2021 Jan 1. https://www.medrxiv.org/content/10.1101/2021.12.13.21267761v1.full.pdf
9. Planas, D., Saunders, N., Maes, P. *et al.* Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. *Nature* **602,** 671–675 (2022). https://doi.org/10.1038/s41586-021-04389-z
10. World Health Organisation. Statement on Omicron sublineage BA.2. https://www.who.int/news/item/22-02-2022-statement-on-omicron-sublineage-ba.2 doi: 22/02/2022.