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Review RRJoPC

Description and Prevention of Omicron

Suhail M.[1,*], Blessy Jacob[2], Visaga Perumal[3], Vineeth Chandy[4]

Abstract

November 9, 2021, Botswana becomes the first country to recognise it (Nov 11 2021). The new variant (B.1.529) has been represented in 77 countries. Omicron presents 32 changes in spike protein Scribd, restricting the point of interaction with the ACE2 receptor protein. Computational shows and components' recreation has been applied to investigate the collaboration between the SARS-CoV-2 RBD and the ACE2 receptor. The receptor-binding domain (RBD), which more barely joins the ACE2 receptor in the omicron variety; this uncovered that the ACE2 receptor displays an improved restricting profile towards the S protein of the omicron variation when contrasted with the Delta variation. We initiated the changes either by cancellation, modification, or expansion to explain the all-around expected plan of S-protein for the Omicron variety, utilising the Alpha fold with 1268 amino acids, where the Omicron variation showed more than 30 transformations at various locals of S protein. We played out the phylogenetic investigation of all SARS-COV-2 variations, given that spike S protein introduced the longest transformative distance compared to other variants. The non-identical cluster arrangements shown by the omicron (VOC) and omicron S proteins contain 34 amino acid corrosive (AA) changes. AlphaFold2 is an open-source computational methodology created to assist us with obtaining exact protein structures given hereditary information. The progressions in the S, M, and N proteins of the as of late recognized SARS-CoV-2 Omicron assortment were contemplated, and various amino acids on RBD were adjusted, which might influence the collaboration between the RBD and ACE2, while the S309 immunizer may in any case be viable in killing Omicron RBD. The SARS-CoV-2 is classified as VOI (a variant of interest) and VOC (a variant of concern). The Omicron will come under the VOC because of its omicron-containing mutation gene. A SARS-CoV-2 VOI is a SARS-CoV-2 variation with innate changes that are expected or alluded to impact contamination characteristics like getting ailment reality and immune take off, suggestive or helpful break. The SARS-CoV-2 VOC (a variant of concern) is a SARS-CoV-2 variety that meets the importance of a VOI (a variant of interest) and is estimated through a similar estimation. The omicron cases in India are increasing every day in every state of India, especially Maharashtra, Karnataka, Kerala, Delhi, etc. Immunization with BNT162b2 has been shown to prompt killing sum neutralizer against the familial infection of 2.4-overlay of the mean gaining strength sum. It compromises the ability of the counter-acting agent to guarantee against contamination. In any case, much lower balance levels are adequate for insurance against serious infection. The Pfizer-Biotech immunisation could be essentially diminished against omicron with a 41-overlay lower level of killing neutralizer when contrasted with a variation of infection when compared with the previous variant characterised by spike protein substitution D614G. The third doses of the Pfizer immunization give a comparative degree of killing neutralizer against omicron as seen after two dosages against the first infection. When compared to wild types, individuals who received two doses of vaccine demonstrated a more than a 25-point decrease in balance titres against omicron suggesting that two dosages of the

***Author for Correspondence**
Suhail M.

[1]Student, Department of Pharmaceutical Chemistry, T. John College of Pharmacy, Gottigere, Bengaluru, Karnataka, India
[2]Lecturer, Department of Pharmaceutical Chemistry, T. John College of Pharmacy, Gottigere, Bengaluru, Karnataka, India
[3]H.O.D, Department of Pharmaceutical Chemistry, T. John College of Pharmacy, Gottigere, Bengaluru, Karnataka, India
[4]Principal, Department of Pharmacy, T. John College of Pharmacy, Gottigere, Bengaluru, Karnataka, India

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Pfizer vaccine may not be adequate to safeguard against illness with the omicron variety. The support piece of the ongoing vaccination grows the counter acting agent focus by 25-cross-over.

Keywords: Omicron, SARS-CoV-2, mutations, binding, RBD, ACE2, classification, VOI, VOC, characterization, statistics, diagnosis, vaccines, neutralization, Pfizer, prevention

INTRODUCTION

As one more improvement in the SARS-CoV-2 pandemic, the Omicron variety, heredity B1.1.529, was first perceived in South Africa on November 10th, 2021. The spike protein contains 32 mutations in the omicron variant and a receptor-binding domain (RBD) containing 15 changes. Epidemiological information gathered throughout the long stretch of November in South Africa recommends that the contagiousness of Omicron is higher than Delta's, the most contagious variation to date [1].

It covers practically every one of the critical changes of the past VOCs (Alpha, Beta, Gamma, and Delta), including K417N, E484A, and N501Y, and other known transformations that are demonstrated to change the awareness of the infection to balance by defensive antibodies [2].

The spike protein of the omicron shows 32 changes, and the receptor-binding domain (RBD) exhibits 15 changes. These progressions were not recognised in any of them as late definite varieties. Further, we likewise distinguished nine extra transformations in different qualities that were >85% common in all Omicron (n=70) groupings. These transformations are ORF1a: K856R, ORF1a: L2084I, ORF1a: A2710T, ORF1a: T3255I, ORF1a: P3395H, ORF1a: I3758V, ORF1b: P314L, ORF1b: I1566V, and ORF9b: P10S. Of these, the main two transformations (ORF1a: T3255I or nsp4: T492I and ORF1b: P314L or nsp12: P323L) were seen in Delta and Delta Plus variations that were available with a huge predominance (>40%). P323L mutation in nsp12 has co-advanced with D614G [10, 11]. Our outcomes showed 46 outstanding changes in ORF1a, ORF1b, and S attributes of the SARS-CoV-2 Omicron variety transcendent at over half repeat. Moreover, we recognised E: T9I, M: D3G, M: Q19E, M: A63T, N: P13L, N: R203K, and N: G204R changes in practically all groupings broken down (i.e., 100% prevalent) [3].

A few of these variations of concern (VOC) have been recognised all through the pandemic and have been associated with huge scope floods of disease. Until now, while a few of these VOC have displayed differing levels of neutralizer opposition in vitro, inoculation, just as past contamination by SARS-CoV-2, has been displayed to keep a critical degree of assurance against leap forward or re-diseases, especially to the extent discourage actual disorder and mortality. Be that as it may, the new representation of the B.1.1.529 variation, which was subsequently assigned as Omicron, contains a more noteworthy number of changes than the past VOC. Most of the transformations related to the Omicron VOC are situated in the spike protein of the infection, apparently because of determination for the avoidance of neutralizer reactions, and could have an impotent effect on the capacity of previous antibodies to kill the infection. Even though how much this is, the case presently cannot seem to be entirely settled. A past examination of CD8+ T cell reactions to the first SARS-CoV-2 variation in healing people observed an expansive and shifted resistant reaction in practically all patients inspected, even in people with the generally low enemy of SARS-CoV-2 neutralizer responses.

An ensuing examination of this information observed that transformations related to the Alpha, Beta, and Gamma VOCs had exceptionally negligible cross-over with the epitopes distinguished in this previous review, recommending that the CD8+ T cell reaction from prior contamination would likely be viable against the new variants [4].

BINDING PROPERTIES OF OMICRON VARIANT

The Omicron variation has aggregated countless transformations, especially in spike protein that is liable for the starting of disease through cell passage. There are 15 transformations on the receptor

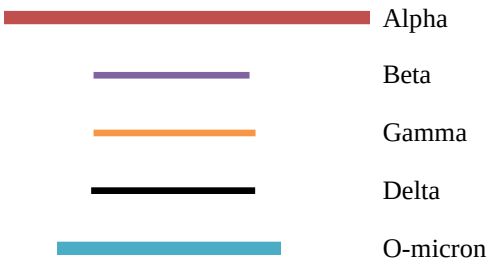

Figure 1. Mutations of SARS-COV-2 variants.

restricting space (RBD) of the spike protein, which has more than 30 changes altogether (Figure 1). Such a huge number of totaled changes are incredible. Since the spike protein is not just the receptor ACE2 (Angiotensin changing over chemical 2) binding partner [5, 6]. In addition, the significant antigenicity site, thusly the target of various antibodies, it is great impotent to research the effects on the viability of killing antibodies, under the worries of insusceptible breaks. Moreover, around 10 changes happen at the RBD restricting point of interaction to the ACE2 receptor protein.

Computational exhibiting and components diversions have been applied to investigate the attachment between the SARS-CoV-2 RBD and the ACE2 receptor [7, 8]. Before the plans of the RBDACE2 complex were settled probably, homology showing and entertainment have adequately expected the model and assessed the joint efforts [8, 9]. Programmatic experiences were likewise used to concentrate on the communications among RBD and ACE2 from different vertebrates, and the outcomes give hints on the sub-atomic systems to SARS-CoV-2 contamination to different creatures [10, 11]. Here, we followed a practically identical philosophy, fostered the development of human ACE2 and the RBD of Omicron variety (in the future connoted as ACE2-RBDO, where the superscript shows Omicron). Then, at that point, the complicated construction was exposed to atomistic sub-atomic elements recreations to refine the model and to test the dynamical cooperations among ACE2 and RBD. In the wake of contrasting with the wild kind ACE2-RBD complex framework, we observed that the RBDO displays more grounded restricting to human ACE2, recommending that the Omicron variation contaminates cells using a similar system and the infectivity may be improved because of the more grounded restricting communications. We completed a quantitative examination on the dependability of the ACE2-RBD complex for the Omicron variation and contrasted it with that of the wild sort framework. The connections were surveyed utilizing a few amounts, including hydrogen bonds, van der Waals contacts, covered surface regions, and the limiting free energies components recovery results and the quantitative relationship show that the restricting interchanges among ACE2 and RBD are to some degree more grounded for the Omicron variety than for the wild sort. This data gives atomic premise to improved infectivity of the Omicron variation. The greater part of balance antibodies are found to tie to RBD epitopes, a significant number of them contend with ACE2 communications, past investigation has discovered that a considerable lot of the balance antibodies are as yet viable to an enormous reach out against the SARS CoV2 variations before Omicron variation. Nonetheless, the most recent outcomes have shown that 85% of recently depicted balance antibodies lost their adequacy against the new variation Omicron [12].

CHARECTERIZATION OF SARS-COV-2 OMICRON

The drawn out and broad spread of SARS-CoV-2 has initiated a few surprising transformations that can increase infection transmission and sickness seriousness. Another SARS-CoV-2 variety of B.1.1.529 was perceived in South Africa on 24 November 2021, and the World Health Organization (WHO) hence presented it, B.1.1.529 is a variation of concern (VOC) and it is named as Omicron. The most recent SARS-CoV-2 variation is especially concerning a direct result of the huge number of transformations present in its genome, and in what way little is had some significant awareness of the variation. To recognize the transformative connection among Omicron and the remainder of the SARS-CoV-2 variations, we played out the phylogenetic investigation of all SARS-CoV-2 variations in view of the spike (S) protein arrangement.

The Omicron S protein is containing the longest transformative changes than other variants of the COVID-19 (Table 1). The different gathering plan of present VOC varieties showed that the Omicron S protein contains 34 amino destructive changes including A67V, H69-, V70-, T95I, G142-, V143-, Y144-, Y145D, N211-, L212I, G339D, S371L, S373P, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K and L981F (Figure 2). These results obviously show that the Omicron S protein is by and large changed, appeared differently in relation to past SARS-CoV-2 varieties. The SARS-CoV-2 S protein is critical for mediating entry into have cells and is the central target of killing antibodies [13, 14]. The construction of the S protein is a fundamental. Normal for any variation and acquiring this construction assists us with better understanding the Omicron variation. Alpha fold2 is an open-source computational methodology created to assist us with obtaining exact protein structures in view of hereditary information [15]. The developments of S, M, and N proteins of the as of late perceived SARS-CoV-2 Omicron variety and analyzed the movements of S protein and its parts, S1 NTD and RBD, observed numerous amino acids on RBD, were transformed, which might influence the relation between the RBD and ACE2, while the S309 immunizer could in any case be successful in killing Omicron RBD. The Omicron S1 NTD structures which is showing contrasts from the first strain, which could prompt diminished acknowledgment by antibodies bringing about likely immune escape and diminished viability of the current immunizations. Taken S together, the changes on S protein may build the insusceptible departure and contagiousness of the Omicron variation [16].

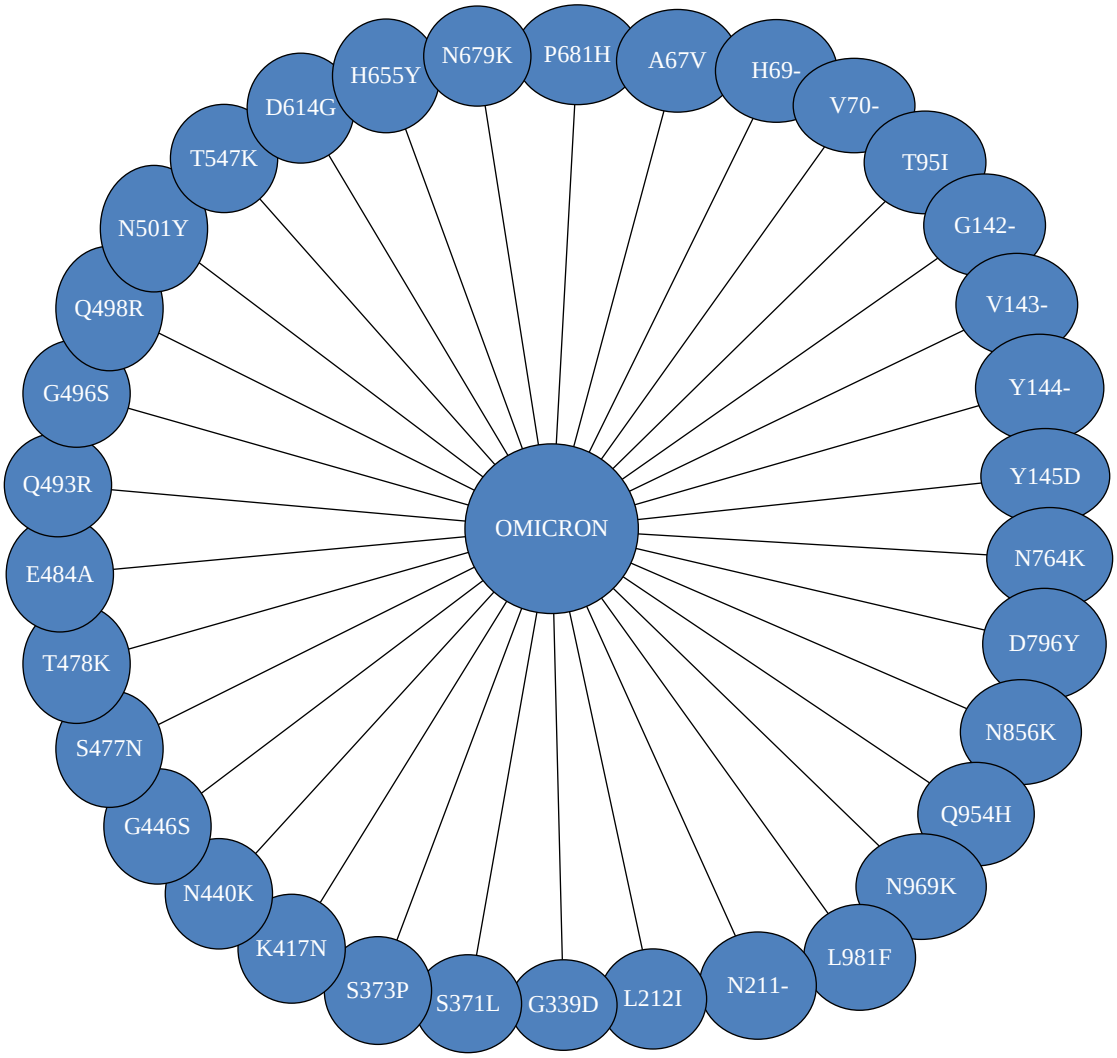

Figure 2. Omicron S protien containing thirty four amino acid mutation.

CLASSIFICATION OF OMICRON

In 2021, this variety has multiple changes, some of which are disturbing. Essential proof proposes a lengthy danger of reinfection with this variety when wandering from other VOCs. Considering the proof introduced, The B.1.1.529 variety was first offered with all due appreciation to WHO from South Africa on November 24, definitive of a negative change in COVID-19, the examination of ailment transmission. The TAG-VE has incited WHO that this variety should be named as a VOC and the WHO has permitted B.1.1.529 as a VOC and named as an Omicron.

A SARS-CoV-2 VOI is A SARS-CoV-2 Variation

Second, anticipated or referred to hereditary changes influence infection qualities such as catching, illness seriousness, insusceptible departure, symptomatic or restorative break; it has been distinguished as causing critical local area transmission or different COVID-19 groups, in numerous nations with expanding relative predominance, either by expanding the number of cases after some time, or other evident epidemiological effects on recommending an arising hazard to worldwide general well-being.

A SARS-CoV-2 VOC is A SARS-CoV-2 Infection

The variety that meets the significance of a VOI and through a comparable assessment has been demonstrated to be connected with something like one of the going with changes at a degree of overall general prosperity significance:

- Development in infectiousness or negative change in COVID-19, the investigation of illness transmission; OR
- The extension of hurtfulness or change in clinical disease illustrates; a decrease in the reasonability of general prosperity and social measures or open diagnostics, cimmunizations, and therapeutics [17].

OMICRON CASES IN INDIA

The country's Omicron count has increased to 8209, with Maharashtra (1738) and Rajasthan (1276) contributing the biggest number of instances of the new variation. In the interim, Delhi has 549 cases, Kerala has 536, Karnataka 548, West Bengal 1672, and UP 275. The new variation of SARS-CoV-2 was initially distinguished in South Africa on November 24. In India, the first instances of omicron were affirmed on December 2nd in Karnataka. And every day, revealing cases are expanding in India (Figure 3) [18].

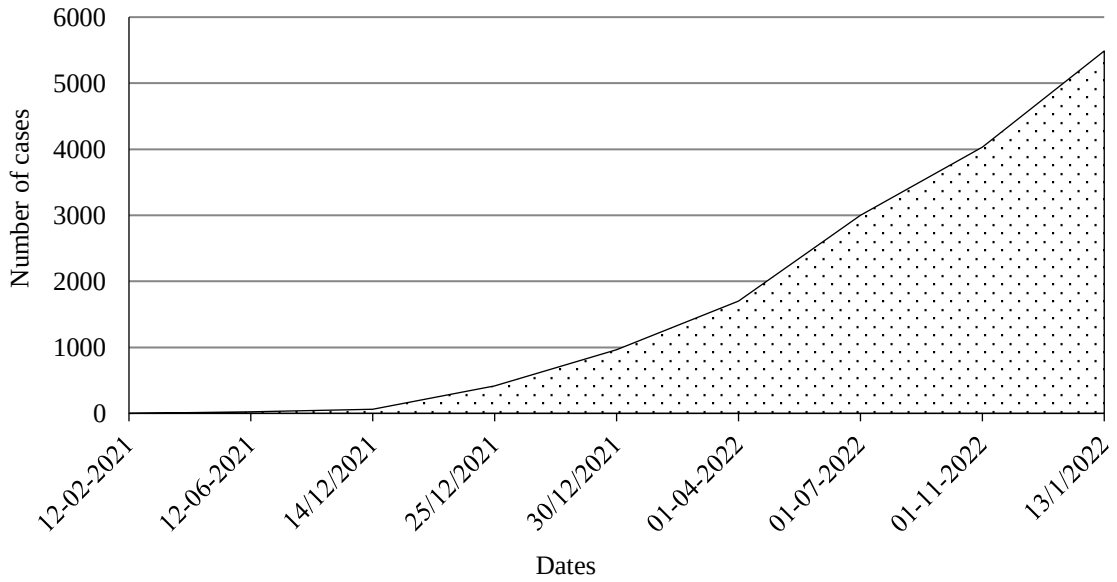

Figure 3. Statistical information about Omicron cases in India.

Table 1. Omicron vs. delta and other variants.

Parameter	Omicron	Delta	Delta AY. 4.2* (offshoot)	Beta or B.1.351	Alpha or B.1.1.7
Transmission rate	More transmissible than Delta.	2X more transmissible than other AY.4.2*, Alpha and Beta.	May be 10–20% more transmissible than Delta.	50% more transmissible than Alpha.	30–50% more transmissible than the original SARS-CoV-2 strain.
Detected by RT-PCR	Yes, 2 out of three genes detected.	Yes	Yes	Yes	Yes
Infection severity	Not clear.	More severe infections in unvaccinated people.	Similar to Delta.	More severe than other variants. Causes hospitalizations and death.	More severe than the original SARS-COV-2 strain. Causes hospitalizations and death.
Prevention through vaccination	Vaccinated people may contract and spread the virus.	Effective against severe illness, hospitalizations, and death. Vaccinated people may contract and spread the virus, but only for a short time.	Vaccinations may be effective	Vaccination does not provide strong protection from mild and moderate disease.	Effective against severe disease and hospitalizations.

DIAGNOSIS OF OMICRON

The SARS-CoVID-2 infection was analysed using transcriptase-polymerase assay (RT-PCR), high-throughput genome sequencing, and serological assessment of against viral immunoglobulin M (IgM), G (IgG) antibodies, and lung X-beam [19]. The Food and Drug Administration (FDA) has embraced two tests to investigate SARS-CoV-2 infection. Those include:

- PCR test (also called as molecular test): This COVID-19 test uses a lab strategy called polymerase chain reaction (PCR) to distinguish the infection's hereditary material. A liquid example of contaminated can be gathered with a nasal swab or swab from the throat, or salivation can be gotten by spitting into a cylinder. Results could be significantly quicker when handled nearby or in a couple of days. The test handling delays, whenever assessed off-site or moved to a free lab, give the most exact outcomes when done by a gifted and proficient person; regardless, the quick outcomes might be an inability to distinguish many cases.
- Antigen test: The COVID-19 test searches for the infection's particular proteins. The nasal swab was used to catch a liquid example. The result was a shorter age time. Others might be alluded to by a research centre for assessment. A positive antigen test result is seen as precise when the technique is followed precisely. Indeed, even yet, there is a higher chance of false negative results, and that implies you could be contaminated however you get a negative test. A PCR test might be prescribed by the specialist to affirm whether the individual is positive for an antigen test or negative, contingent upon the conditions.
- Lateral flow tests: Fast or lateral flow tests (LFTs) are presently performed, although the fact that they cannot let you know which variation you have, regardless, they should have the option to let you know whether you are negative or positive. Assume you get a positive LFT result, hole up right away, and get a PCR test to affirm the outcome.

GENERAL SYMPTOMS OF OMICRON AND OTHER VARIANTS

In serious cases, fever, cough, running nose, body aches, loss of sensation (smell and taste) and trouble swallowing are common. Then again, they noticed serious body aches, chills, dizziness, and a gentle fever. According to them, Omicron-positive individuals had no breathing issues to date, and immersion levels remained normal [20].

OUTSPREAD OF OMICRON

Omicron is quickly spreading in South Africa, especially in the Gauteng region, including Johannesburg and Pretoria. The seven-day normal of everyday cases in South Africa expanded fourfold to 2,756. As per the WHO, the COVID omicron variation has been recognised in 57 nations [12] and in light of the primer information, chart was drawn. This diagram showed detailed cases were seen in the top 10 nations and, furthermore, in India, and the information was accounted for in Figure 4. In the Table 2, we detailed revealed omicron cases by day-to-day news chase in South Africa, the United Kingdom, South Korea, the United States, and India, Germany, Denmark, France, Poland, Sweden, and Australia. As per South Africa's administration reports, more youngsters are hospitalised with medium-to-high side effects of omicron variation [21].

Table 2. The Comparision of omicron cases in the top 10 countries and India.

Name of the countries	Cases
South Africa	378,75
United Kingdom	924,002
Germany	111,401
USA	743,994
Denmark	158,020
India	41,208
France	75,758
Poland	30,847
Sweden	30,160
Australia	28,146

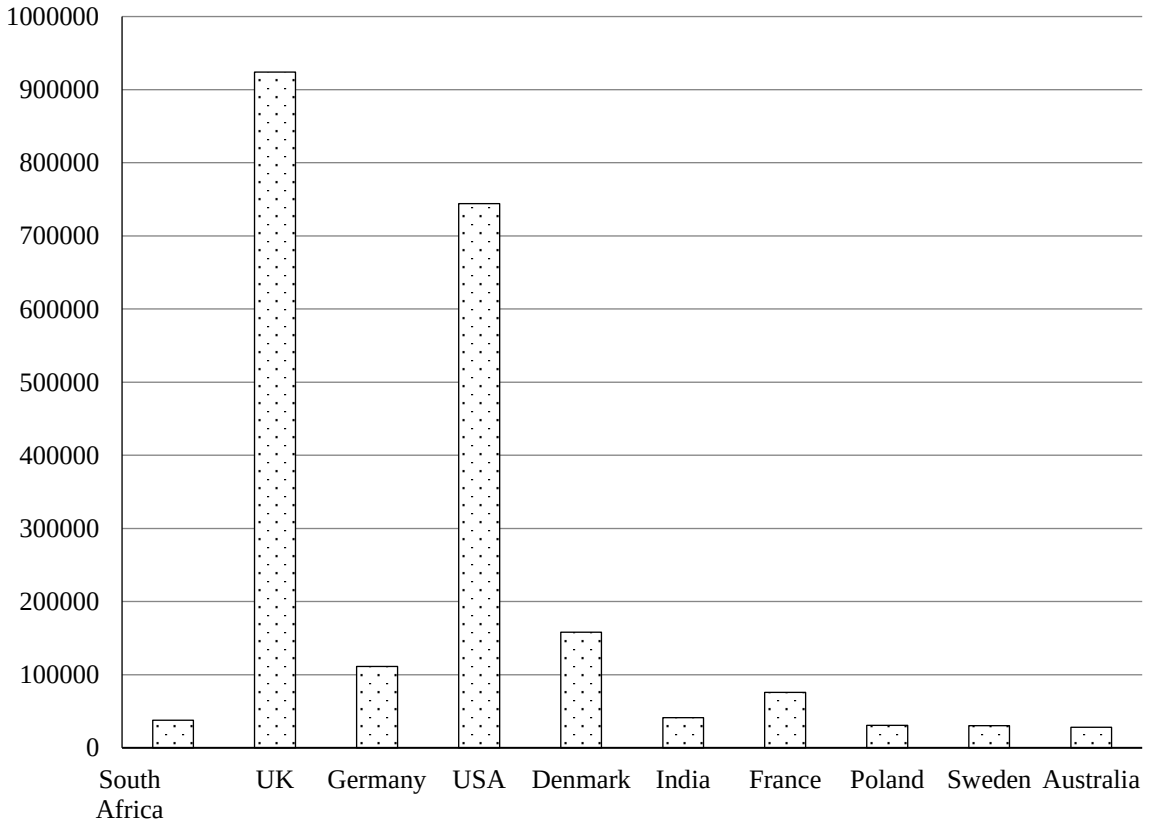

Figure 4. The comparision of omicron cases in the top 10 countries and India (till March 28, 2022).

WORLD APPROVED VACCINES

Table 3. World approved vaccines.

Manufacturer	Name of Vaccine	Type of vaccine	WHO EUA qualified	Approved schedule 2, 3	Second dose options for completion of series in BC 4
Pfizer-BioNTech	BNT162b2/COMIRNATY/Tozinameran (INN)	mRNA	✓	Two doses, 21–28 days apart	• Moderna • Pfizer-BioNTech
Moderna	mRNA-1273	mRNA	✓	Two doses, 28 days apart	• Moderna • Pfizer-BioNTech
Astra Zeneca	AZD1222 Vaxzevria	Adenovirus (CHAdOx1) Vector	✓	Two doses, 4–12 weeks apart	• AstraZeneca • Moderna • Pfizer-BioNTech
Serum Institute of India	COVISHIELD	Adenovirus (CHAdOx1) Vector	✓	Two doses, 4–12 weeks apart	• AstraZeneca • Moderna • Pfizer-BioNTech
Janssen (Johnson & Johnson)	Ad26.COV2.5	Adenovirus type 26 vector	✓	One dose	• N/A – one dose series
SinoPharm/Beijing Institute of Biological Products (BIBP)	Covilo/BBIBP-CorV	Whole inactivated Coronavirus	✓	Two doses, 21–28 days apart	• Moderna • Pfizer-BioNTech
Sinovac	CoronaVac	Whole inactivated Coronavirus	✓	Two doses, 14–28 days apart	• Moderna • Pfizer-BioNTech
Bharat Biotech, India	COVAXIN	Whole inactivated Coronavirus	✓	Two doses, 14–28 days apart	• Moderna • Pfizer-BioNTech
Novavax	NVX-CoV2373/Nuvaxovid	Protein subunit	✓	Two doses, 21–28 days apart	• Moderna • Pfizer-BioNTech
Serum Institute of India	NVX-CoV2373/Covovax	Protein subunit	✓	Two doses, 21–28 days apart	—

PREVENTION OF OMICRON

Most confirmed Corvid illness 2019 (COVID-19) immunizations depend on the transient articulation of the viral spike (S) glycoprotein (got from the Wu01 strain) to promote extremely intense respiratory conditions. COVID 2 (SARS-CoV-2)-coordinated immunity: (1) Transformations in immune response epitopes on the spike protein can bring about expanded viral protection from killing antibodies and have been related to decreased immunisation effectiveness. (2) Also, they can powerfully impede the movement of monoclonal antibodies utilised for the treatment and avoidance of COVID-19. Not long after its ID in the Gauteng district of South Africa, the balance limit of the D614G infection was a lot higher in tainted and immunized versus inoculated just members, yet the two gatherings had 22-overlay Omicron escape from immunization evoked balance. Recently tainted and inoculated people had leftover balance anticipated to present 73% security from indicative Omicron contamination, while those without past disease were anticipated to hold just around 35%. The two gatherings were anticipated to have significant assurance from serious illness [22].

The Omicron variety of SARS-CoV-2 (B.1.1.529) was named as a variety of concern (VOC) by the World Health Organization (WHO). To decide the powerlessness of the Omicron variation to immunisation-instigated serum action, we dissected examples acquired from 30 people without any proof of earlier disease. Tests were gathered over a period of several months (middle, 4 weeks; territory, 3–6 weeks; “early” time point) after finishing a two-portion course of the BNT162b2

antibody. Focus on individuals had a middle age of 49 years (range, 27–78 years) and a practically identical sex appointment (57% female individuals, 43% male individuals). The killing movement was resolved to utilise a lentivirus-based pseudovirus test. Results acquired in pseudovirus tests ordinarily correspond well with those obtained against real viruses. Sera were endeavored against pseudoviruses granting the spike proteins of the Wu01 vaccination strain, or of the Alpha (B.1.1.7), Delta (B.1.617.2), Beta (B.1.351), or Omicron VOCs (Figure 5). All models showed killing action against the Wu01 strain with a mathematical mean half-inhibitory serum incapacitating (Geomean ID50) of 546.

Serum killing improvement against the Alpha, Delta, and Beta assortments was diminished to Geomean ID50s of 331, 172, and 40, autonomously (tests that did not achieve half counteraction at the most decreased had a go at debilitating of 10 were credited to an ID50 of 5).

Prominently, just nine out of the 30 immunised people (30%) had perceivable serum killing movement against Omicron, bringing about a Geomean ID50 of 8 (F.), Figure 5(a) which was lower than against the Beta variety. To explore the adjustment of serum killing movement against the Omicron variation over a long time and survey the effect of a booster vaccination, we dissected longitudinal examples of the 30 vaccines (Table 3). At 5 months (center, 21 weeks; range, 19–31 weeks; “Late” time point) after the second BNT162b2 inoculation, as well as at multi month (center, 3 weeks; range, 2–12 weeks) after a solitaryBNT162b2 sponsor portion (middle, 41 weeks after the subsequent inoculation; range, 30–44 weeks; “Supporter” time point).

After the two-portion course of the BNT162b2 immunization, the killing movement against Wu01 diminished fourfold during the time span of 5 months from a Geomean ID50 of 546 to 139, and was reached out after publicist inoculation (Geomean ID50 of 6,241). Serum killing activity against the Omicron variety after two vaccination segments remained low, with only 30–37% of the models showing recognizable equilibrium, accomplishing Geomean ID50s of 8 and 9 at the early and late time communities, independently. Nonetheless, killing serum action on the Omicron variant increased by a factor of two. More than 100-overlay after the support piece of BNT162b2, bringing about a Geomean ID50 of 1,195, and was noticeable in every one of the 30 individuals (100%) (Figure 5(b)). The serum killing activity against the Omicron variety following supporter vaccination was fundamentally greater than killing titers against Wu01 after two doses of BNT162b2 [23].

Most confirmed Corvid illness 2019 (COVID-19) immunizations depend on the transient articulation of the viral spike (S) glycoprotein (got from the Wu01 strain) to promote extremely intense respiratory conditions. COVID 2 (SARS-CoV-2)-coordinated immunity: (1) Transformations in immune response epitopes on the spike protein can bring about expanded viral protection from killing antibodies and have been related to decreased immunisation effectiveness. (2) Also, they can powerfully impede the movement of monoclonal antibodies utilised for the treatment and avoidance of COVID-19.

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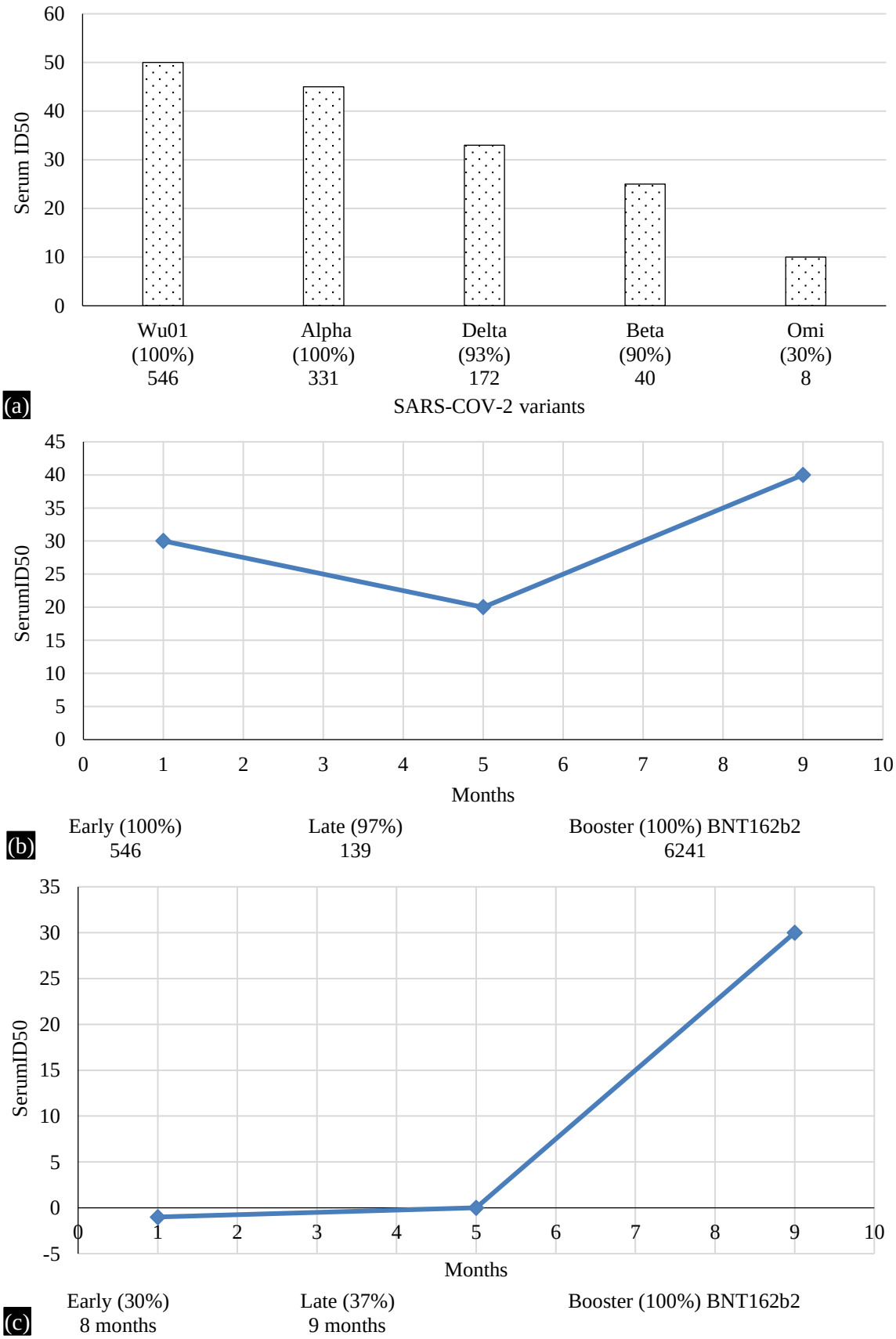

Figure 5. (a) SARS-COV-2 variant, (b) SARS-CoV-2 killing serum movement in immunized people (Wu01), (c) SARS-CoV-2 killing serum movement in immunized people (Omicron).

Serum killing advancement against the Alpha, Delta, and Beta assortments was diminished to Geomean ID50s of 331, 172, and 40, freely (tests that did not achieve half counteraction at the most decreased had a go at debilitating of 10 were credited to an ID50 of 5).

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CONCLUSION

The new variant SARS-CoV-2 omicron is more transmissible than other variants, and the severity of the omicron is less when compared to the previous variant. The booster dose gives more protection or immunity against omicron. Individuals who have taken a booster dose of Pfizer show neutralisation of the omicron virus.

REFERENCES

1. Genovese L, Zaccaria M, Farzan M, Johnson W, Momeni B. Investigating the mutational landscape of the SARS-CoV-2 Omicron variant via ab initio quantum mechanical modeling. BioRxiv. 2021.
2. Zhang L, Li Q, Liang Z, et al. The significant immune escape of pseudotyped SARS-CoV-2 Variant Omicron. Emerg Microbes Infect. 2021; 11(1): 1–5.
3. Kannan SR, Spratt AN, Sharma K, et al. Omicron SARS-CoV-2 variant: Unique features and their impact on pre-existing antibodies. J Autoimmun. 2022; 126: 102779.
4. Karim SS, Karim QA. Omicron SARS-CoV-2 variant: a new chapter in the COVID-19 pandemic. Lancet. 2021; 398(10317): 2126–8.
5. Huang X, Pearce R, Zhang Y. De novo design of protein peptides to block association of the SARS-CoV-2 spike protein with human ACE2. Aging (Albany NY). 2020; 12(12): 11263.
6. Swift T, People M. ACE2: entry receptor for SARS-CoV-2. Science. 2020 Mar 27; 367(6485): 1444–8.
7. Wang Y, Liu M, Gao J. Enhanced receptor binding of SARS-CoV-2 through networks of hydrogen-bonding and hydrophobic interactions. Proc Natl Acad Sci. 2020; 117(25): 13967–74.
8. Lupala CS, Li X, Lei J, et al. Computational simulations reveal the binding dynamics between human ACE2 and the receptor binding domain of SARS-CoV-2 spike protein. bioRxiv. 2020.
9. Xu X, Chen P, Wang J. Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Sci China Life Sci. 2020; 63(3): 457–60.
10. Damas J, Hughes GM, Keough KC, et al. Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. Proc Natl Acad Sci. 2020; 117(36): 22311–22.

11. Vickers NJ. Animal communication: when I'm calling you, will you answer too? Curr Biol. 2017; 27(14): R713–5.
12. Lupala CS, Ye Y, Chen H, Su XD, et al. Mutations on RBD of SARS-CoV-2 Omicron variant result in stronger binding to human ACE2 receptor. Biochem Biophys Res Commun. 2022; 590: 34–41.
13. Sadek A, Zaha D, Ahmed MS. Structural Insights of SARS-CoV-2 Spike Protein from Delta and Omicron Variants. bioRxiv. 2021.
14. Walls AC, Park YJ, Tortorici MA, et al. Structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein. Cell. 2020; 181(2): 281–92.
15. Jumper J, Evans R, Pritzel A, Green T, et al. Highly accurate protein structure prediction with Alpha Fold. Nature. 2021; 596(7873): 583–9.
16. Yang Q, Syed AA, Fahira A, Shi Y. Structural analysis of the SARS-CoV-2 Omicron variant proteins. Research. 2021; 2021: 9769586.
17. Mohapatra Ranjan K, Tiwari Ruchi, Sarangi Ashish K, et al. Omicron (B.1.1.529) variant of SARS-CoV-2: Concerns, challenges, and recent updates. Wiley online library, J Med Virol. 2022; 94(6): 2336–2342.
18. India Today. (2022 Jan 7). Covid cases in India: Nation records 1 lakh daily patients after seven months. [Online]. https://www.indiatoday.in/coronavirus-outbreak/story/covid-in-india-omicron-surge-deaths-new-cases-lockdown-restrictions-1897077-2022-01-07; last updated Jan 2022.
19. Xueying Wang, Yang Zhou, Linlin Ma. Coronavirus Disease 2019 (COVID-19): Diagnosis and prognosis. Blood Genom. 2020; 4(2): 96–107.
20. Ettaboina SK, Nakkala K, Laddha KS. A Mini Review on SARS-COVID-19-2 Omicron Variant (B. 1.1. 529). SciMed J. 2021; 3(4): 399–406.
21. Haldar B. Evaluating the risk factor of novel public health disaster "omicron" variant: an Indian perspective. Model Earth Syst Environ. 2022; 1–6.
22. Cheng SMS, Mok CKP, Leung YWY, et al. Neutralizing antibodies against the SARS-CoV-2 Omicron variant BA.1 following homologous and heterologous CoronaVac or BNT162b2 vaccination. Nat Med. 2022; 28(3): 486–489.
23. Cele S, Jackson L, Khan K, et al. SARS-CoV-2 Omicron has extensive but incomplete escape of Pfizer BNT162b2 elicited neutralization and requires ACE2 for infection. MedRxiv. 2021 Dec 17: 2021.12.08.21267417.

