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## Review

## A comprehensive review on Covid-19 Omicron (B.1.1.529) variant

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## ABSTRACT

The world has been combating different variants of SARS-COV-19 since its first outbreak in Wuhan city. SARS-COV-19 is caused by the coronavirus. The corona virus mutates and becomes more transmissible than earlier variants as the day passes. Till 24 November 2021, SARS-COV-19 has four variants Alpha, Beta, Gamma, and Delta, respectively. Among them, the delta variant caused severe havoc across the world. South Africa registered a new variant with the World Health Organization (WHO) on 24 November 2021, which is much more transmissible than previous variants. The WHO classified it as a variant of concern (VOC) on 26 November 2021 and called it the Greek letter Omicron (B.1.1.529), the fifteenth letter in the alphabet. Here a serious attempt was made to comprehend the omicron variant's origin, nomenclature, characteristics, mutations, the difference between delta and omicron variant, epidemiology, transmission, clinical features, impact on immunity, immune evasion, vaccines efficacy, etc. © 2022 Published by Elsevier B.V. on behalf of King Saud University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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**1. Introduction**

Coronaviruses are a class of viruses that bring about diseases like severe acute respiratory syndrome (SARS-CoV-2), which causes SARS (which produces COVID19). The term "variant of concern" (VOC) mentions viral variations having mutations in their spike protein receptor-binding domain (RBD) that increase attaching power in the RBDhACE2(Receptor-binding domain human angiotensin converting enzyme-2)complex complex while also promoting rapid propagation in human populations (Dudas et al., 2021). COVID-19 pandemic has risen for almost two years, with approximately 400 million confirmed cases and over 5 million casualties, as stated by the World Health Organization(WHO) (WHO Tracking SARS-CoV-2 variants, 2022). The native severe acute SARS-CoV-2 virus, discovered in late 2019, mutated into many variants. WHO has divided these variants into three groups to prioritize monitoring and research: variants of concern (VOCs), variants of interest (VOIs), and variants under monitoring (VUMs), Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1), and Delta (D.1) are the previous four VOCs (B.1.617.2) (WHO Tracking SARS-CoV-2

variants, 2022). WHO identified a novel variant called Omicron (B.1.1.529) as the fifth Variant of concern on 26 November 2021, causing widespread worry. The origins of the Omicron version have yet to be discovered. The examination of Severe acute respiratory syndrome-covid-2 variant sequences demonstrates that Omicron is well defined from the other SARS-CoV-2 types and that identifying its closest neighbor is problematic (Kupferschmidt, 2021b). As claimed by the findings of phylogenetic analyses, the Omicron variant disunited early from other severe acute respiratory syndrome-covid-2 types rather than developing from preceding VOCs (Kupferschmidt, 2021b). Chances are great Omicron variety was bred in immunocompromised persons (e.g., Human immune virus(HIV) patients co-infected with SARS-CoV-2) over a long period; otherwise, if it developed in a nonhuman species and was lately reintroduced into humans (Kumar et al., 2021c).

*1.1. Omicron variant*

SARS-CoV-2, the virus which is the prime reason for COVID-19, has a variant known as Omicron. It was first reported to WHO on

24 November 2021 by South Africa; the WHO declared it a VOC (a variant of concern) on 26 November 2021 and described it as Omicron, the fifteenth character in the Greek alphabet (Wong et al., 2022). The Omicron variant features exceptionally multiple unique mutations (Torjesen, 2021; Haseltine, 2022a), many of which impaired the spike protein aimed by most COVID-19 immunizations at discovery. Concerns about its spread, immune system by-pass, and vaccination defiance have arisen due to this level of heterogeneity.

Consequently, the Variant was quickly labeled as a variant of concern. However, as of 14 January 2022, Omicron had spread to over 139 countries. As of 20 January 2022, the Omicron variant had been discovered in 171 nations throughout the world (DISEASES, 2022). The global prevalence of Omicron is pictorially given in Fig. 1.

1.2. Classification

On 26 November, the World Health Organization’s Technical Advisory Group on SARS-CoV-2 Virus Origin assigned Phylogenetic Assignment of Named Global Outbreak (PANGO) lineage B.1.1.529 as VOC and given the Greek letter Omicron (Wong et al., 2022; Parekh, 2022).

2. Nomenclature

The lineage and component mutations of SARS-CoV-2 variants are classified (Tao et al., 2021). Many institutions, including governments and several news organizations, mentioned relevant

variants in colloquial terms by the country where they were initially discovered (Bejar, 2022; CTV Why The Who Won’t Call It The ‘U.K. Variant’, 2022). The world health organization stated that Nu is readily confused with “new” and that Xi is the familiar rear-most name (News, 2022a). Finally, the world health organization adopts the entire Greek alphabet, and future variations may be named after constellations (News, 2022b).

2.1. Lineages and clades

SARS-CoV-2 has several mutations, and subcategories of the virus could be classified into broader groups called lineages or clades. There have been three main, widely used nomenclatures proposed (WHO SARS-CoV-2, 2021).

The global initiative on sharing all influenza data (GISAID) had identified eight worldwide clades as of January 2021 (GISAID, 2022). Hadfield et al. released the Next strain in 2017 with the goal of “real-time pathogen evolution tracking” (Hadfield et al., 2018). As of June 2021, the Next strain had been used to track SARS-CoV-2, recognizing 13 significant clades (19A–B, 20A–20J, and 21A) (Nextstrain “Nextstrain COVID-19”, 2022). The software squad behind the Phylogenetic Assignment of Named Global Outbreak Lineages (PANGOLIN), advanced by Rambaut et al., gave a dynamic nomenclature for SARS-CoV-2 lineages that aims at enthusiastically circulating virus lineages and those that spread to new places (Rambaut et al., 2020). Every country’s public health entity may establish its naming mechanism to record specific variants. For example, Public Health England assigned a year, month, and number to each tracked Variant in the pattern [YYYY] [MM]/

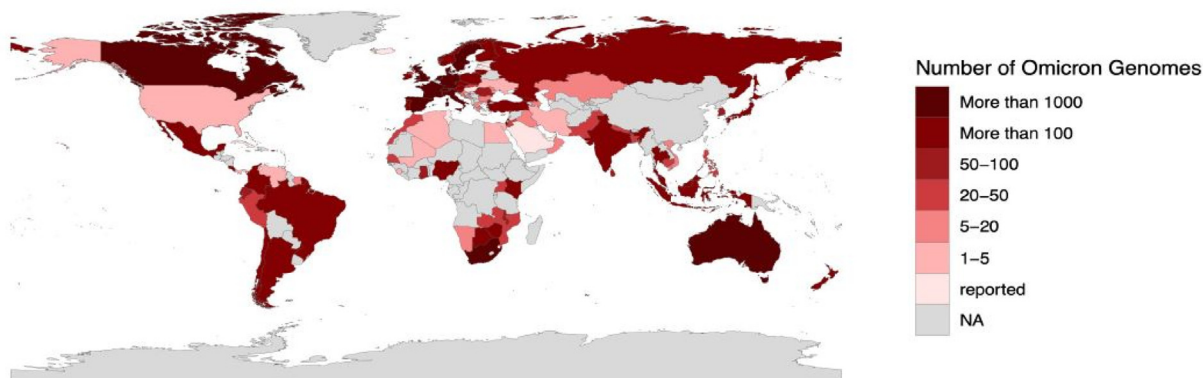


Fig. 1. Omicron global prevalence. Source of Fig. 1: Network for Genomic Surveillance in South Africa (NGS-SA). [https://www.nicd.ac.za/wp-content/uploads/2022/01/Update-of-SA-sequencing-data-from-GISAID-14-Jan-2022\\_dash\\_v2-Read-Only.pdf](https://www.nicd.ac.za/wp-content/uploads/2022/01/Update-of-SA-sequencing-data-from-GISAID-14-Jan-2022_dash_v2-Read-Only.pdf).

Table 1

Variants of concern (VOC) tracking. Source of Table 1: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/accessed> 14 January 2022.

WHO label	Pango lineage	GISAID clade	Next strain clade	Additional amino acid changes monitored	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	+S:484 K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20 J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/478 K.V1	21A	+S:417 N +S:E484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GRA	21 K, 21L,21 M	+S:R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

Table 2

Variant of interest (VOI) tracking. Source of Table 2: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/accessed> 14 January 2022.

WHO label	Pango lineage*	GISAID clade	Next strain clade	Earliest documented samples	Date of designation
Lambda	C.37	C.37 GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021
Mu	B.1.631	GH	21H	Colombia, Jan-2021	30-Aug-2021

[NN], with the prefixes 'VUI' or 'VOC' suggesting a variety that is being investigated or that is causing concern. A three-letter code represents the month in this system, which has been changed to use the format [YY] [MMM]-[NN] (UKSHA, 2021) (see Table 1 and Table 2).

2.2. Variants of concern (VOC)

2.3. Variants of interest that are currently labeled (VOI)

3. Differences between Delta and Omicron variants

The Omicron variant has added alteration power over the Delta variant. Nevertheless, this does not mean it is extra threatening. No novel symptoms have been found because of the omicron variant; it may spread faster than other variants due to its mutations. SARS-CoV-2, the virus that sources COVID-19, has the highest mutation rate of any virus (Ettaboina et al., 2021b).

3.1. Delta variant

There are nine different versions of the spike protein, a projection on the virus's exterior that helps the virus's adhesion to human tissues. The "Receptor-Binding Domain"(RBD), a molecular hook, contains two. This makes it cling to cells more effectively. Thus according to Penn State University's Suresh V. Kuchipudi, who inquiries viral advancement (Ettaboina et al., 2021b).

3.2. Omicron variant

It's a mutation beast, including at least 30 mutations in the spike protein, out of which half changes are at the RBD (Kumar et al., 2022). Typically, the initial SARS-CoV-2 virus was transmit-

ted to 2or 3 people by infecting only 6 people. Delta had a significant influence. Delta has a four-day incubation period compared to the original virus's six-day incubation period, making people vulnerable sooner. The communication rate and reproduction time of the Omicron are unknown. More information on the omicron variant growth rates in other geographies will be available in the coming days (Ettaboina et al., 2021a).

3.3. Cell entry mechanism

According to new findings, Omicron has a new strategy for entering the host and can achieve cell access without the help of the transmembrane serine protease 2 (TMPRSS2) (Zhao et al., 2022). In contrast to Delta variation, Omicron uses the endocytic pathway for entrance and viral replication rather than the TMPRSS2 pathway, which may have led to the discrepancies in disease presentation after exposure to Delta and Omicron variants (Zhao et al., 2022). Because TMPRSS2 is widely expressed in alveolar lung cells, lung involvement following exposure may be absent or limited due to Omicron's lack of reliance on the TMPRSS2 pathway for reproduction. (Zhao et al., 2022; Saito et al., 2022). In addition, when compared to the Delta variant, Omicron's fusion capacities are diminished, making it more difficult to construct syncytia (a structure formed by the fusion of several cells). Following an Omicron infection, the syncytia generation potential diminishes, resulting in milder clinical symptoms and tissue tropism. (Zhao et al., 2022; Saito et al., 2022; Youk et al., 2020).

4. Existing methods for the detection of COVID variants

4.1. Diagnosis

A reverse transcriptase-polymerase screening test was used to diagnose SARS-COVID-2 infection (RT-PCR),high-throughput genome sequencing, anti-viral immunoglobulin M (IgM), and G (IgG) antibody serology, and a lung X-ray (Ozdemir, 2020).

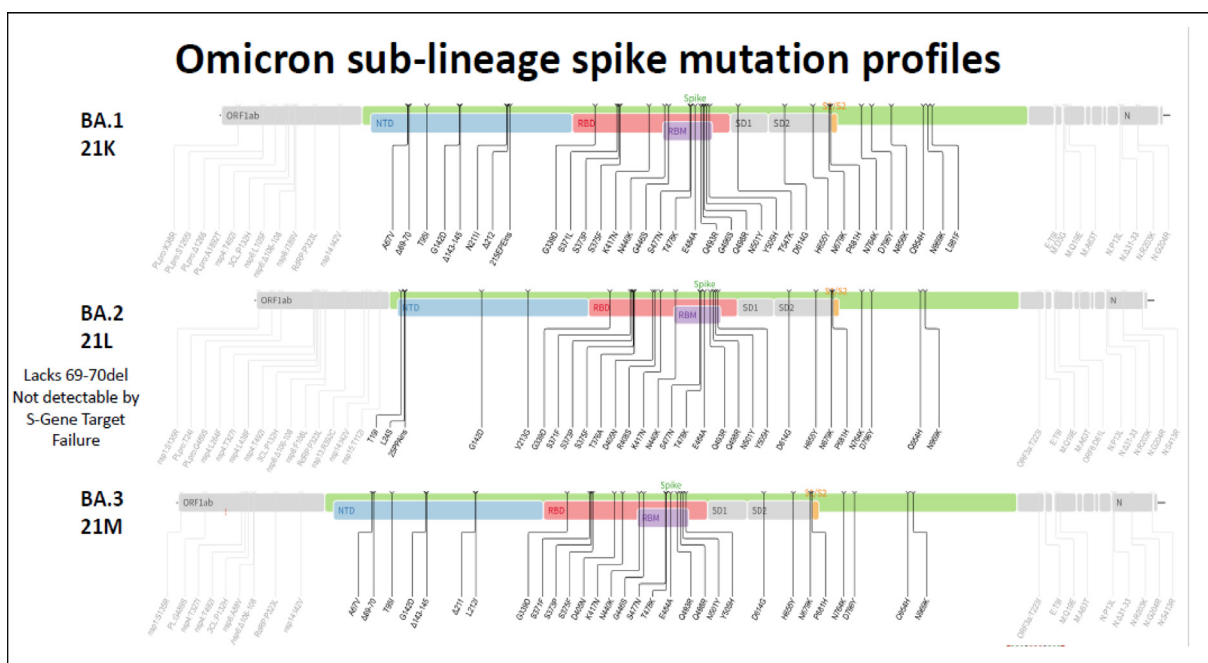


Fig. 2. Omicron sub-lineage spike mutation profiles. Source of Fig. 2, 1) Lineage definitions based on https://github.com/cov-lineages/pango-designation/issues/367. 2) Images from https://covdb.stanford.edu/page/mutation-viewer/ (NICD SARS CoV 2 Sequencing Update 7 January 2022).

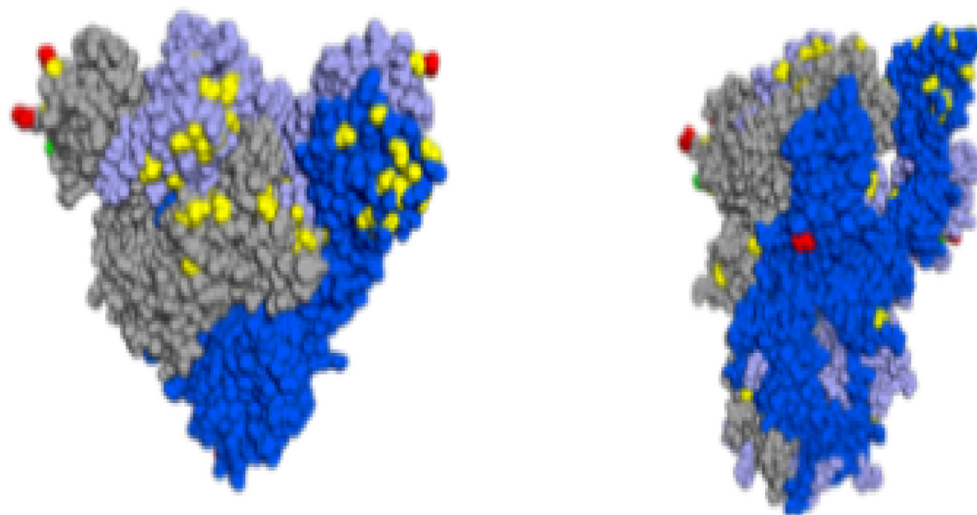


Fig. 3. Amino acid changes of omicron variant.

#### 4.2. Polymerase chain reaction test or molecular test

To detect the virus's genetic material, the COVID-19 test engages a laboratory skill known as polymerase chain reaction (PCR). A nasal or throat swab could be used to obtain a fluid specimen from an infected person, or saliva can be recovered by expectorating to a tube. If handled on-site or over a few days, the findings could be generated in less time. If the tests are moved to an independent lab, the processing delays can be investigated off-site. When performed by a trained professional, the test yields the most precise results, but the quick results may miss a few cases (Ettaboina et al., 2021b).

#### 4.3. Antigen test

The COVID-19 test searches for proteins produced by the virus. The fluid sample was taken with a nose swab, which cut down on time to get the results. Others might be sent to a laboratory for testing. When procedures are followed appropriately, a positive antigen test result is deemed accurate. Even yet, false-negative findings are more likely, which means you could be infected but not show symptoms. Depending on the circumstances, a doctor may order a PCR test to confirm whether a person is positive or negative for an antigen test (Ettaboina et al., 2021b).

#### 4.4. Lateral flow analysis

Although fast lateral flow tests (LFTs) can't tell which variety you have, they can tell you whether you're positive or negative. Separate yourself immediately if you get a positive lateral flow test (Ettaboina et al., 2021a).

### 5. SARS-COVID-19 symptoms in general, notably Omicron variant

Fever, cough, runny nose, and bodily pains are some of the most significant symptoms. Deprivation of sensation (smell and taste) and breathing difficulties are common signs. Severe body cramps, cold, confusion, and a mild temperature (Ettaboina et al., 2021b).

### 6. Mutations

Numerous variations are present in the Variant, some of which have scientists concerned (AFP, 2022a). Compared with the origi-

nal Wuhan variety, the Omicron variant comprises 60 mutations: 50 non-synonymous mutations, eight synonymous mutations, and two non-coding mutants (Haseltine, 2022b). The spike protein, the principal antigenic aim of antibodies produced by infections and more commonly used in vaccinations, has 30 mutations. Most of those modifications haven't been observed before in any other species (Times, 2022; Callaway, 2021). In collation with the earlier virus, the spike protein has 30 amino acid modifications, 15 from the receptor-binding domain (Kumar et al., 2022). Additional genomic areas have many deletions and alterations and three alterations at the furin break site in this Variant (UKSHA, 2021). The furin braking area enlarges SARS-CoV-2 infection (Zhang et al., 2021a) (see Fig. 2).

According to Fig. 3. The top image (left) and side view (right) of the Omicron mutations in the spike protein show amino acid changes (yellow), removals (red), and additions (green). Two monomers (grey and light blue) carry their receptor-binding

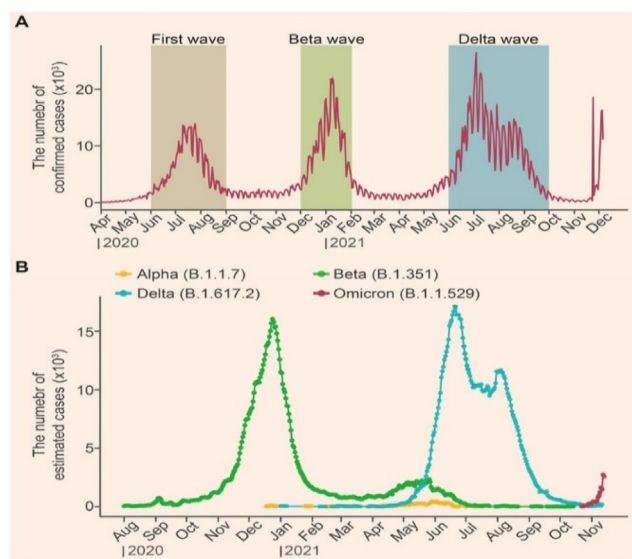


Fig. 4. (A and B) Spread of Omicron variant in south Africa. **Figure source.** MedComm, Volume. 2, Issue. 4, Pages. 838–845, First published. December/13/2021, DOI. (<https://doi.org/10.1002/mco2.110>) (He et al., 2021c). (C). Epidemiological data of Omicron variant in south Africa. **Figure source;** MedComm, Volume. 2, Issue. 4, Pages. 838–845, First published. December/13/2021, DOI. (<https://doi.org/10.1002/mco2.110>) (He et al., 2021c).

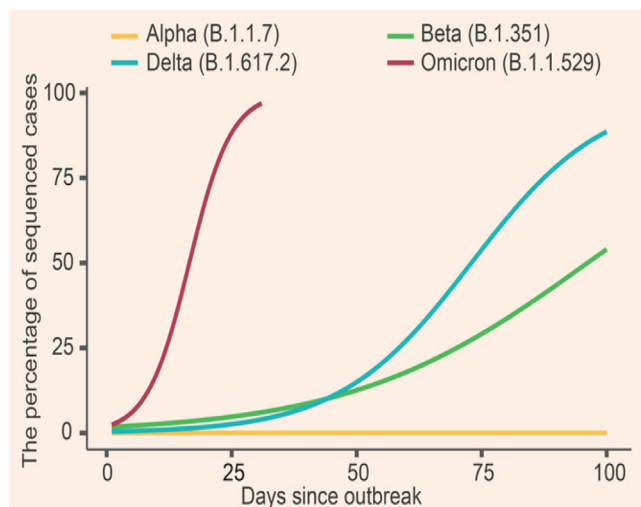


Fig. 4 (continued)

domains in the “down” conformation, while one (dark blue) is in the “up” or “open” conformation in this trimeric structure. (Fig. 3). (WHO Classification of Omicron, 2022). Structure from PDB: 6VYB and WHO mutation data (Walls et al., 2020).

At least each new mutation might be acquired from one of the coronaviruses that creates the prevalent cold, for example, Human Coronavirus 229E(HCoV-229E) or the human immunodeficiency virus (HIV); South Africa does have the world’s most extensive occurrence of HIV infection, generating a greater possibility of simultaneous infection; a connection to Human immunodeficiency virus might explain the massive number of mutations discovered inside the omicron variant’s segregation (Lang, 2022). Indeed, the virus must be competent to progress for a lengthy period unaccompanied by killing or eliminating its host to be influenced by any such changes. People with a weaker immune system who have adequate medical care are one example. This is the case in South Africa, where people with HIV account for an additional 20% of the inhabitants (AVERT HIV AND AIDS IN SOUTH AFRICA, 2022).

6.1. Stealth variant

Omicron has 2 types. As per researchers, the ‘standard’ one is now known as BA.1 /B.1.1.529.1, whereas BA.2 /B.1.1.529.2 is Omicron’s second Variant. BA.2 is characterized as ‘Camouflage Omicron’ because it excludes the ‘S’ Gene Target Failure (SGTF)-causing deletion seen within the ‘standard’ form. (69–70) that allowed several PCR tests to identify it as an Alpha or omicron variant (GUARDIAN Scientists, 2022).

7. The origin of the variant is uncertain; however, various theories have been proposed

7.1. Simultaneous infection or Co-Infected

Originated as a result of an intermittent coronavirus co-infection (e.g., HCoV-229E). According to a preprint study that

Table 3  
Omicron mutations.

A67V	S371L	G446S	G496S	D614G	D796Y
T95I	S373P	S477N	Q498R	H655Y	N856K
Y145D	S375F	T478K	N501Y	N679K	Q954H
L212I	K417N	E484A	Y505H	P681H	N969K
G339D	N440K	Q493R	T547K	N764K	L981F

looked at the mutations, an insert (ins214EPE) was only detected in the Omicron form (Venkatakrisnan et al., 2021).

7.2. Persistently infected patient

This theory is supported by sequencing studies that show changes in the virus in chronically infected patients (COUZIN-FRANKEL, 2022). According to selection analysis, the Spike protein exhibits three distinct modifications, having 13 amino acids that were earlier heavily preserved among SARS-CoV-2 and other Sarbecoviruses(the viral subgenus having SARS-COV and SARS-CoV-2). The spike protein tolerated considerable sequence switch, possibly in retaliation to choosy factors favoring improved communication, immunological by-pass, or virus reproduction. According to the theory, this could have developed in a population, an individual, or a small class of persistently infested people (Martin et al., 2021).

7.3. Natural choice

SARS-CoV-2 has evolved in response to selective pressures favoring mutations that boost viral infection. Vaccine-advance or antibody-aversion mutations, such as those reported in Omicron, can set off a dominant mechanism of SARS-CoV-2 advancement once the lion’s share of the globe’s population has been inoculated or affected (Wang et al., 2021).

7.4. Mammal pool

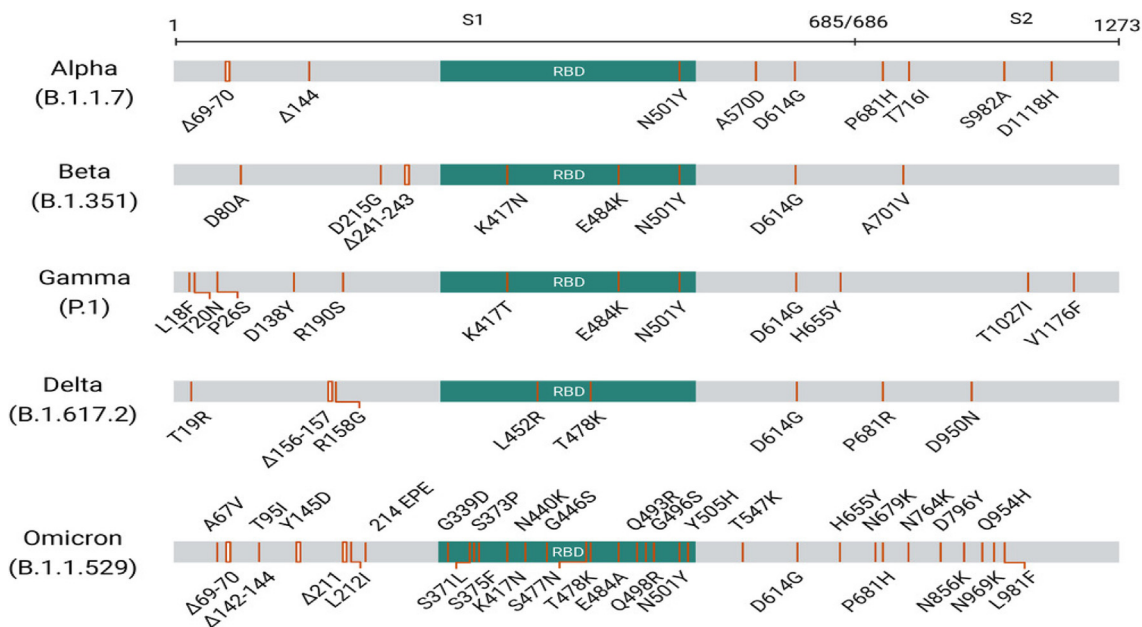
Omicron may have developed in a nonhuman species before being the latest reintroduced into humans. According to evidence, nonhumans have large viral reservoirs (e.g., Between December 2020 and January 2021, SARS-CoV-2 was found in 80 percent of white-tailed deer samples collected in various areas across Iowa) (LaJeunesse, 2022).

7.5. Inadequate Scrutiny

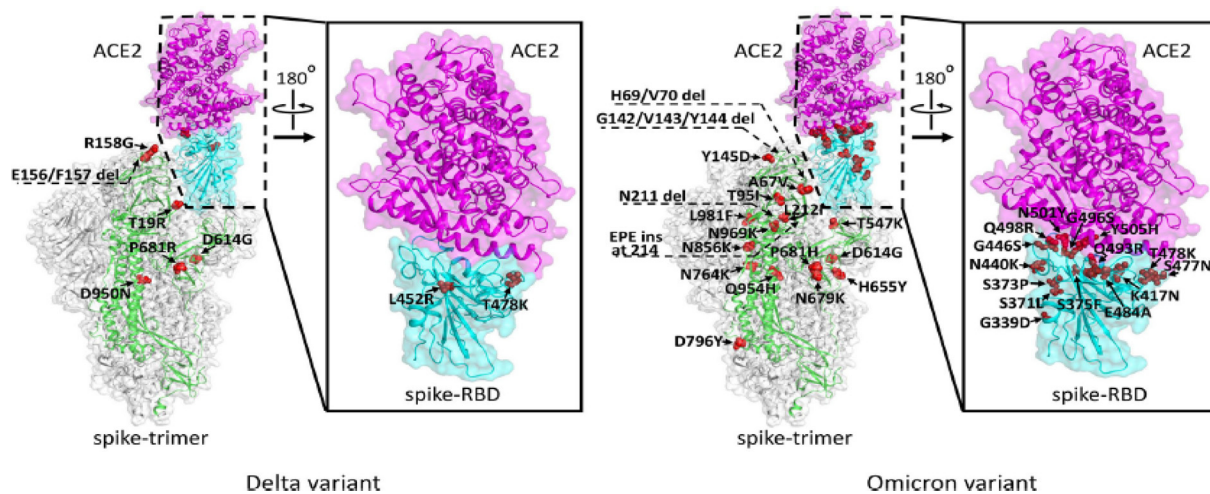
Omicron could have spread and developed in areas where surveillance and sequencing were weak. On 22 November 2021, the Special Administrative Region of Hong Kong uploaded the first sequence of the Variant to GISAID Epi COV, followed on 23 November 2021 by 10 more sequences from South Africa and Botswana (Control, 2022b). The WHO designated Variant B.1.1.529 as the variation of concern. On 26 November 2021, it will be known as Omicron (WHO Update on Omicron, 2022a).

8. Characteristics of Omicron variant

Three major COVID-19 upsurges have been detailed in South Africa since early 2020. (Fig. 4-A). The Beta and Delta variant, respectively, are responsible for two (Fig. 4-B). Within 100 days of the outbreak, the proportion of infections connected with the Beta variant grew to 50% of whole day-to-day infections, according to epidemiological data (Fig. 4C). However, during the same time frame, the delta variant’s infection rate increased to 80%, which indicates the Delta version is highly transmissible among people as matched to the Beta variant. Besides, in South Africa, the % of



**Fig. 5.** The spike mutations of five worrisome variants are depicted in this graphic (VOCs). **Figure source:** Med Comm, Volume: 2, Issue: 4, Pages: 838–845, First published: 13 December 2021, (<https://doi.org/10.1002/mco2.110>).



**Fig. 6.** Protomer of the spike trimer is emphasized in green, its RBD in cyan, and the ACE2 receptor-bound is magenta (He et al., 2021c). **Figure source:** Med Comm, Volume: 2, Issue: 4, Pages: 838–845, First published: 13 December 2021, (<https://doi.org/10.1002/mco2.110>).

omicron infection neared 90% within 25 days (Fig. 4C). The Beta, Delta, and Omicron types' early doubling times were calculated to be 1.7, 1.5, and 1.2 days (Karim and Karim, 2021). According to these findings, the Omicron variant has added infectiousness compared to Delta and Beta types. From a population-based epidemiological data retrospective study, it is also worth noting that a recent retrospective study found a link between Omicron and serious sars-cov-2 re-infection (Pulliam et al., 2021a).

The Omicron variant's genomic sequences found the highest non-synonymous mutations, with some in a spike linked to the disease severity, immune evasion, and transmission. To the greatest extent, higher than 60 substitutions, removals, and additions were found in the Omicron variant (GISAID, 2021), creating the Variant with the most mutation places of all the SARS-CoV-2 variations studied thus far. The Omicron variant of ORF1a contains six changes (K856R, L2084I, A2710T, T3255I, P3395H, and I3758V) and

two removals totaling four amino acids. (Amino acid 2083 and 3674–3676). The Variant has two additions within ORF1b (P314L and I1566V). ORF9b also has a P10S replacement and a 3-residue removal between 27 and 29. The envelope (E) protein has one substitution (T9I), the membrane (M) protein has three additions (D3G, Q19E, and A63T), and the nucleocapsid (N) protein has three additions and a three-residue removal. While the changes mentioned above appear across the viral genome, the other mutations are aggregated in the spike, and the bulk of all Omicron mutations have been discovered. These comprise 30 exchanges which are given in Table 3.

Three deletions of H69/V70, G142/V143/Y144, and N211, and one addition of three amino acids (EPE) at place 214 (from rough statements, the fluctuations are narrated as the V143/Y144/Y145 removal in union with G142D and the L212 removal in union with N211I). The spike mutations found in Omicron outnumber those

seen in the other four VOC by nearly-three to four times (Fig. 5) (He et al., 2021a).

It's worth noting that the amino acid alteration D614G is present in all five VOCs. D614G was linked to more tremendous viral heaps in the higher respiratory region and affected younger people (Korber et al., 2020; Plante et al., 2021; Volz et al., 2021). The Omicron version and the Gamma, Beta, and Alpha variants all-share N501Y. This alteration is considered to boost the spike's attachment to angiotensin-converting enzyme 2 (ACE2) and its communication (Yang et al., 2021). The communication may be extended even higher when added with the H69/V70 removal (Leung et al., 2021). Besides, near the furin braking site, Omicron has changes N679K and P681H. Essential amino acids on the furin breaking site may help the spike cleave into S1 and S2, leading to better amalgamation and virus contamination.

Alpha-version also has a P681H mutation (Fig. 5). This mutation is thought to increase SARS-CoV-2 infectivity (Zuckerman et al., 2021). The Omicron variant's RBD contains 15 mutations, whereas the RBD of the contemporary major Delta variant only has the L452R and T478K alterations (Fig. 6). Among these alterations, a cluster of residues around the bound ACE2 receptor has been identified (Fig. 6). Another difficulty is that the change may be undetected by immunologists. It's worth mentioning that neutralizing antibodies most commonly target the spike RBD, and Omicron has 15 RBD mutations (Yuan et al., 2021).

All 15 mutations discovered in Omicron spike RBD may be linked back to further of these antigenic locations, implying that Omicron is resistant to monoclonal antibodies directed at these sites. The LY-CoV555 and LY-CoV016 antibody combination were approved for exigency usage in clinical trials (Zimmerman et al., 2021b).

The previous study has discovered that immune evasion is connected to mutations at the spike's 484 and 417 positions (Zimmerman et al., 2021a) and that both Gamma and Beta variants can avoid nullification by LY-CoV016 (due to K417N/T) and LY-CoV555 (due to E484K) (Starr et al., 2021). Omicron is likely to resist these two antibodies because it carries the E484A and K417N mutations. Other VOC variations have been reported to

exhibit Omicron spike mutations, like N501Y, D614G, P681H, E484, and K417N residue substitutions (Starr et al., 2021).

These changes have been linked to enhanced ACE2 binding affinity, increased transmissibility and pathogenicity, decreased ability to neutralize monoclonal antibodies, and immunological by-pass. However, the effects of other mutations and whether or not combinations of mutations occur are unknown, creating a great deal of mystery regarding how viral behavior and susceptibility may evolve (He et al., 2021c).

The spike protein of the **Receptor binding domain** is currently under the most extraordinary investigations (Fig. 7). However, recent research suggests that the Spike N terminal domain (NTD) might aid virus entry by interacting with sialic-acid receptors. According to a recent investigation of the Omicron variant, it appears to have higher sialic acid-binding energy than prior versions, leading to more extraordinary transmission (Lam et al., 2021). While many Omicron genomes have been posted to foreign sites, some may not contain the complete set of identifying mutations and have their unique mutations (Kupferschmidt, 2021a). A suggestion has been made to broaden the scope of the B.1.1.529 (Omicron) lineage to incorporate variations related to Omicron (BA.1.). A cousin lineage to Omicron (BA.2) has been proposed; this is simply a change in taxonomy to embrace the entire phylogeny. Although both sub-lineages have nearly identical mutations, BA.2 lacks the spike:69/70del removal would not be detected by S-gene target fall down (Rambaut, 2022).

### 8.1. Furin cleavage site in Omicron

Near the furin braking site, Omicron has N679K and P681H changes. Essential amino acids on the furin breaking site may help the spike cleave into S1 and S2, leading to better amalgamation and virus contamination. Alpha-version also has a P681H mutation. This mutation is thought to increase SARS-CoV-2 infectivity (Zuckerman et al., 2021).

A recent study published on the bioRxiv preprint service by Bailey Lubinski et al. tested the host cell furin-mediated cleavability of the spike (S) protein of the Omicron (B.1.529) variant. In conclu-

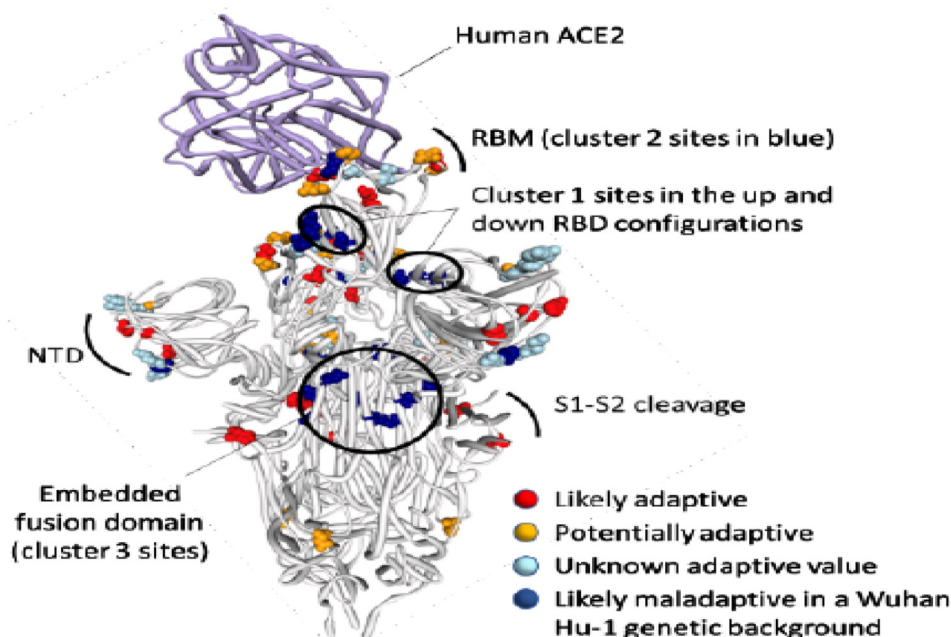


Fig. 7. Distribution of Omicron amino acid replacements on the three-dimensional SARS-CoV-2 Spike trimer. **Figure source:** <https://virological.org/t/selection-analysis-identifies-significant-mutational-changes-in-omicron-that-are-likely-to-influence-both-antibody-neutralization-and-spike-function-part-1-of-2/771>.



sion, they compared the contribution of two S gene alterations, P681H and N679K, to the furin cleavage site activity in Omicron S to other SARS-CoV-2 variants and other coronaviruses and found Furin has a higher affinity for cleaving Omicron S than the Wuhan-Hu-1, Alpha, and Delta strains. This increased furin-mediated cleavage was caused by the N679K mutation in Omicron S, located outside the furin binding pocket (Lubinski et al., 2022).

8.2. WuhanHu1 has several associations with Delta and Omicron variants

The Omicron variant contains 30 alterations in the Spike protein. Mostly in the RBD (Kumar et al., 2021a) (Fig. 8). RBD T470, T478 loop, and Y505 as viral factors for identifying SARS-CoV-2-RBD by ACE2 were discovered in a prior investigation (Xu et al., 2021). In Delta and Omicron variations, T478 is a frequent mutation (Fig. 8). RBD has the power to be built into a practical and guarded subunit vaccine in opposition to SARS COV- 2 owing to its capacity to generate extremely tough neutralizing antibody (nAb) answers. Compared to the Delta variant, Omicron has numerous modifications at the receptor-binding area of the spike protein. (Fig. 9) It's possible that the Omicron variant is immune to antibody-mediated protection (Table 4).

9. Current evidence regarding Omicron's epidemiology of incidence

The Omicron variant got documented in 171 nations around all 6 WHO Regions, namely the African region, region of Americas, South-East Asian region, European region, Eastern Mediterranean region, and Western Pacific region. as of 20 January 2022, Omicron has accumulated a vast expansion benefit more than Delta, and it is quickly surpassing Delta worldwide. Immune evasion appears to be involved in Omicron's rapid spread. Still, more investigation is necessary to understand the importance of inherent enhanced spread and immune escape in understanding rapid transmission. While the BA.1 lineage was once the most prevalent, new analysis in India, the United Kingdom, South Africa, and Denmark imply that BA.2 is becoming more prevalent. The gearbox drivers and other features of BA.2 are being investigated, but the results are still unknown (WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022b).

There was a steep reduction in reported cases and the number of viral incidents instigated by the Omicron variant. A 48 percent reduction in hospitalization indicates that the Omicron epidemic in South Africa may have peaked (WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022b). During week 52, with a

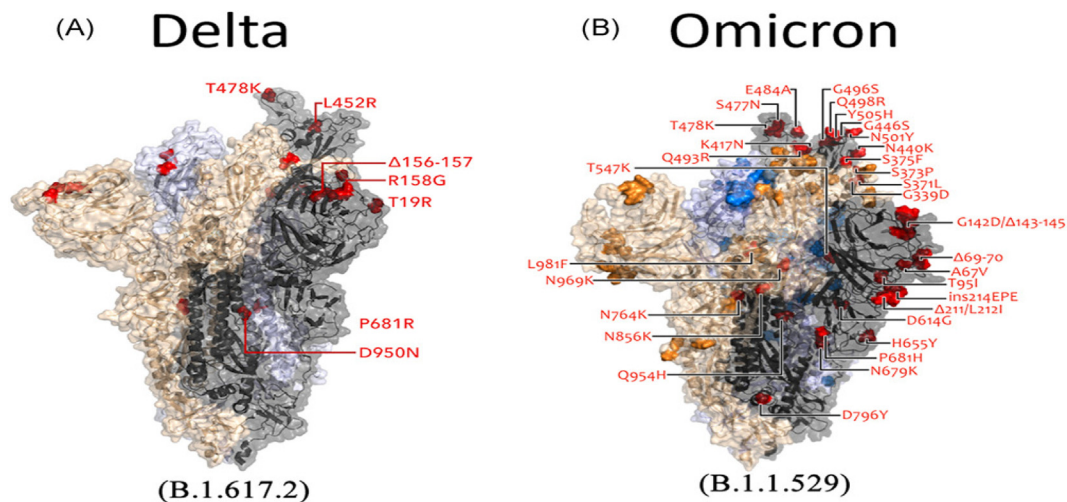


Fig. 8. An examination of variant spike mutations in (A) Delta and (B) Omicron (Kumar et al., 2021b). Figure source: Journal of Medical Virology, First published: 15 December 2021, (<https://doi.org/10.1002/jmv.27526>).

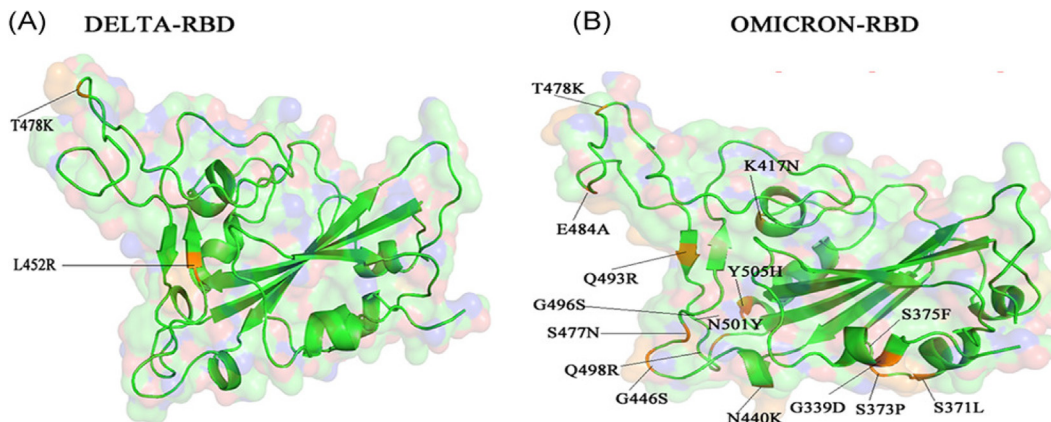


Fig. 9. At RBD, a study of (A) Delta and (B) Omicron variant mutations (RBD). Mutation is highlighted in orange. Omicron RBD possesses 15 mutations. However, Delta RBD has got only two (Kumar et al., 2021b). Figure source: Journal of Medical Virology, First published: 15 December 2021, (<https://doi.org/10.1002/jmv.27526>) (Kumar et al., 2021b).

**Table 4**

In comparison to wild-kind, the Omicron and Delta variants have a spike protein mutation (Wuhan-Hu-1). **Table source:** Journal of Medical Virology, First published: 15 December 2021, (<https://doi.org/10.1002/jmv.27526>).

Variant	Sequence ID	Mutation
Wuhan-Hu-1 (Wild-type)	NCBI ID: P0DTC2	-
Delta Variant (B.1.617.2)	NCBI: QWK65230.1	T19R, G142D, Δ156-157, R158G, Δ213-214, <b>L452R, T478K</b> , D614G, P681R, D950N
Omicron (B.1.1.529)	GSAID ID: R40B60_BHP_3321001247/2021	A67V, Δ69-70, T95I, G142D, Δ143-145, N211I, L212V, ins213-214RE, V215P, R216E, <b>G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H</b> , T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F

sum of 60,142 COVID-19 instances uncovered, a 48 percent lower from the earlier week, there was still a marked decline in actual incidents ([WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022b](#)).

Similar results were observed in a few other Southern African countries, which would include Eswatini (1806 incidents vs 4667 incidents linking week 52 to week 51, a 60% lesser); Namibia (4398 incidents versus 7625 incidents, a 42% decline); Lesotho (2161 incidents versus 2862 incidents, a 24% decline); and Zimbabwe (2161 incidents versus 2862 incidents, a 24% decline) (10 468 versus 12 073 incidents, a 13 percent reduction). Nevertheless, total incidents in Mozambique (26860 incidents versus 6751 incidents, a 298 percent growth) and Botswana (26 860 incidents versus 6751 incidents, a 298 percent growth) have risen (10 515 vs 9130 incidents, a 15 percent higher) ([WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022b](#)). In the rest of the nations, where Omicron is fastly dominating, substantial gains in the weekly COVID-19 incidents were documented. In the United Kingdom ([UKHSA Omicron, 2022](#)), In week 52 of 2021, in which the incidence of Omicron was assessed to be > 95 percent on 30 December, over 1.1 million infections were discovered, 51% higher than the earlier week. In Denmark, Omicron was accountable for 90% of events until 28 December 2021, with 116 331 new episodes discovered in week 52, up 47% from the previous week ([Institut., 2022](#)).

South Africa experienced the highest number of Omicron waves, the same as the earlier Delta wave. The prevalence of Omicron in many nations now has significantly beyond the previous pandemic's peak incidence. For instance, in the UK, France, and the United States, incidents of 7-day rolling regularly reached 232 percent, 409 percent, and 306 percent of the previous best-recorded incidence. Large cases were reported weekly in nations like the Philippines (9124 novel cases vs 833 latest infections, a 995 percent growth), Argentina (22912 novel infections versus 58,783 novel infections, a 290 percent growth), Australia (138240 novel infections versus 45,560 novel infections, a 203 percent growth), and India (102330 novel infections versus 46,527 novel infections, a 120% boost) ([WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022b](#)).

## 10. Clinical characteristics

Doctors in South Africa are cautiously confident that Omicron will be less severe than previous versions. The number of confirmed instances, on the other hand, is insufficient to assess whether the disease differs from previously known variants, and there is a time gap between confirmation and hospitalization and death ([Control, 2022a](#)).

On 8 December 2021, the UK's Chief Medical Officer announced that he had communicated with South African health officials and that COVID hospitalizations had increased by 300 percent in a week. At the end of November and the beginning of December,

Tshwane Hospital in Gauteng Province, South Africa, supplied two weeks of data on 166 patients with probable Omicron. After individuals were hospitalized for another cause, COVID infections were usually found. Eighty percent of admitted individuals were under fifty years old ([BBC, 2022](#)). The majority of COVID patients did not require oxygen. SARS-CoV-2 positive patients admitted to the COVID wards stayed 2.8 days in the last two weeks, compared to 8.5 days in the previous 18 months. However, according to the data, 9 of the 166 COVID patients died due to the condition (5 killed out of 33 admissions aged over 60 years) ([SaMRC, 2022](#)). Early research suggests that the number of infections in people of all ages is increasing, particularly in children beneath the five-stage (although early in the wave and instances can rise early on in younger generations) ([Ministry, 2022](#)).

## 11. Immunity effects

### 11.1. Following prior infection or vaccination

The WHO technical briefing dated 23 December 2021 states that immune by-pass following previous disease or immunization has a crucial role in the rapid rise of Omicron cases ([WHO Enhancing readiness for Omicron \(B.1.1.529\), 2022](#)).

A meta-evaluation by Netzl, A. et al. compiled all antibody off-setting experiments in opposition to Omicron datasets up to 22 December 2021. The fold reduction in neutralization related to Omicron was significant with convalescent sera (20x). This is confounded by the fact that most Omicron-associated titers were below the detection limit of their tests. Individuals who were already contacted and then had two doses of vaccination or were thrice vaccinated, on the other hand, showed a 7-time reduction. Moreover, practically all samples from third dose vaccines were collected in less than one month following the final dosage. Decreased antibody titers to Omicron might lead to a higher vulnerability to re-infection ([Netzl et al., 2021a](#)).

For those sick or immunized previously, 70–80 percent of CD4+ and CD8+ reactions have been kept for Omicron virus, according to multiple datasets on cellular immunity ([Ahmed et al., 2021](#); [De Marco et al., 2021](#); [Keeton et al., 2021](#); [Redd et al., 2021](#); [May et al., 2021](#)). The observed lower probability of hospitalization for those with re-infection due to the Omicron variety is likely due to well-maintained cellular immunity to Omicron, which might help guard against serious disease and death ([Ferguson et al., 2021a](#)).

Compared to the Delta variant, the probability of re-infection alongside the Omicron variant remained 5.4 (95 percent CI: 4.87–6.00) times greater in England. For unprotected and vaccinated cases, the comparative dangers were 6.36 (95 percent CI: 5.23–7.74) and 5.02 (95 percent CI: 4.47–5.67) correspondingly, which means the protection for Omicron re-infection after a previous infection could be 19 percent. According to a recent analysis by UKSHA (UK health and security agency), 5.9% of identified inci-

dents between 1 November and 13 December 2021 were due to re-infection, with the relative risk for Omicron re-infection being 3.3 (95 percent CI: 2.8 to 3.8) in comparison to various variants (Ferguson et al., 2021b).

Denmark withstands a growth in the number of re-infection incidents (Institut, 2022). Similarly, the Israeli Ministry of Health observed increased re-infection cases grouped by immunization (Health, 2022). These figures match South African studies that Omicron can elude immunization following a natural infection.

## 11.2. Immune evasion

### 11.2.1. Vaccine efficacy (vaccination-induced immune evasion)

Most studies demonstrate a significant decrease in nullifying titers for Omicron when equated to other VOCs and with an original virus. In contrast to the results of the humoral immune answer, an early *in-silico* figure from 16 people who took the Pfizer shot anticipates that 70 percent of Omicron epitopes would not be pre-tentious by T-cell acknowledgment, implying that cellular-mediated protection against severe disease will be preserved (Riou, 2022).

Two studies by Liu, J., et al. and Naranbhai, V. et al., looked at T-cell reaction in inoculated people and found that although offsetting responses against Omicron are significantly condensed, cellular immunity is unaffected, with long-lasting CD8+ and CD4+ T cell answers that displayed widespread annoyed-responsiveness for both the Delta and Omicron variants (Liu et al., 2022; Naranbhai et al., 2022). In convalescent non-vaccinated persons, two non-peer-reviewed studies found a drop in attaching antibody stages in opposition to the Omicron recombinant receptor-binding area (WHO Enhancing Readiness for Omicron, 2022) and the N Protein N-terminal domain (NTD) in contrast to other VOCs and the ancestral virus. Binding, on the other hand, was generally retained in vaccinated people (Netzl et al., 2021b).

Nine investigations were performed to measure the effectiveness of the vaccination; however, data-limited four nations (Denmark, South Africa, Canada, and United Kingdom) and four vaccines (AstraZeneca-Vaxzervria, mRNA vaccines, and Ad26.COV2.S). Early evidence reveals that the vaccinations tested do not protect against Omicron infection, illness, or hospitalization as effectively as Delta infection. There is evidence that the primary series' vaccination effectiveness decreases over time, but homologous and heterologous booster doses increase vaccine efficacy (WHO Enhancing response to Omicron SARS-CoV-2 variant, 2022a).

In Scotland, a test-negative strategy by Sheikh, A., et al. (non-peer-reviewed) compared to 25 weeks after the second dose. The third/supporter vaccination dosage was connected to a 57 percent (95 percent CI 55, 60) decrease in the probability of S gene negative (probably Omicron) symptomatic infection, comparable to a VE of 88 percent (95 percent CI 86,89) among S gene-positive circumstances (seemingly Delta) (Sheikh et al., 2021).

One more study by Andrews, N., et al., conducted in Imperial College London, Created on PCR-established characteristic infec-

tions in the United Kingdom, eliminating global passengers and matching by sex, day, and age, researchers examined the comparative danger of indicative infection with Omicron versus Delta for divergent vaccine timetables (two dosages of AstraZeneca-Vaxzervria or Pfizer BioNTech, with or without an mRNA vaccine booster). Preliminary results reveal that Omicron has a more substantial likelihood of infection than Delta after two and three vaccination doses (Andrews et al., 2021).

The United Kingdom health agency calculated vaccine performance estimates predicated on 204,036 symptomatic Omicron instances and 169 888 Delta instances in England. Vaccine efficacy for the Omicron variant was 63 percent (95 percent CI: 59–67 percent) two to four weeks next to dose #2, dipping to 10% (95 percent CI: 6 to 13 percent) later 25 weeks in those who took two dosages of Pfizer BioNTech-Comirnaty, compared to 64 percent (95 percent CI: 63 to 65 percent) for the Delta variant in the similar period (Update, 2021).

A non-peer-reviewed nationwide cohort study from Denmark projected a VE of 55 percent (95%CI 24–74%) and 37 percent (95%CI –70–76%) against Omicron SARS-CoV-2 infection for Pfizer BioNTech-Comirnaty and Moderna- mRNA 1273, correspondingly, with a sign of fading VE over a period in contradiction of Delta infections was significantly advanced (Hansen et al., 2021).

Discovery Health, a South African insurance firm, recently published preliminary findings on vaccine effectiveness in preventing hospitalization. A study limited to patients with COVID-19-like symptoms found that the Pfizer BioNTech-Comirnaty vaccination was 50% effective (95 percent CI: 35–62 percent) in preventing hospitalization (Collie et al., 2021). Various vaccines efficacy against delta and omicron variants has been included in the following (Andrews et al., 2022) (Table 5).

### 11.3. The SARS-CoV-2 Omicron strain demonstrates solid immune escape and viral entry capability

**“We need a concerted research effort, rather than leaping to conclusions based on individual studies. We’ll see new facts and studies every day for several weeks. One research will not suffice to establish anything”** – Soumya Swaminathan, Chief Scientist, World Health Organization, WHO (8 December 2021).

Gu, H., et al. first established that the freshly developed SARS-CoV-2 Omicron variant was particularly opposed to offsetting by recovering sera since initial strain- or Delta-infested people, showing that these people were even susceptible to the recently emerged alternate strain. Several of the first documented Omicron instances were previously fully inoculated or diseased, indicating the existence of advanced re-infection and Omicron variant immune evasion (Gu et al., 2021).

The role of neutralizing antibodies in anti-SARS-CoV-2 resistance is well understood. The RBD region of S protein is one of the main targets of deactivating antibodies as opposed to SARS-CoV-2. The significant level of immune evasion seen in Omicron is most likely due to the high level of mutant S protein and RBD region. Because ACE2 is even needed for infection, RBD-focus on

**Table 5**  
Vaccines efficacy against delta and omicron variants.

Name of the Vaccine	Number of Doses	Percentage of maximum efficacy against delta variant in a particular week	Percentage of maximum efficacy against Omicron variant in a particular week
ChAdOx1nCoV-19(Covishield)	1	42.9(≥4week)	17.7(≥4week)
ChAdOx1nCoV-19(Covishield)	2	82.8((2–4 week)	48.9(2–4 week)
BNT162b2(Pfizer BioNTech)	1	72.3(≥4week)	42.8(0–3 week)
BNT162b2(Pfizer BioNTech)	2	90.9(2–4 week)	65.5(2–4 week)
mRNA-1273(Moderna)	1	60.1(0–3 week)	47.9(0–3 week)
mRNA-1273(Moderna)	2	94.5(2–4 week)	75.1(2–4 week)

vaccines or treatments is successful, though some tweaking is required (Zhang et al., 2021b).

Zhang, X., et al. show that the Omicron variant poses a significant danger to the current preventive and medication strategies. Because the Omicron variant may have previously been distributed for 1 or 2 months, the entire planet ought to go on to observe the virus closely and carefully, particularly in terms of virus mutation progression and accurate transmissibility level. Crucially, Omicron-targeted vaccines and drugs are desperately required to combat this newly developed SARS-CoV-2 VOC (Zhang et al., 2021b).

## 12. Treatments and therapies for omicron variant and their impact

WHO is still working with investigators to figure out how effective treatments are against the Omicron variant. Because they reduce the host's inflammatory response to the virus, corticosteroids and interleukin-6 receptor blockers are predicted to persist in treating individuals with critical and crucial diseases. Some of the monoclonal antibodies created in opposition to SARS-CoV-2 might have lower counteraction in opposition to Omicron, according to preliminary in vitro findings reported in preprints. On 16 December 2021, Roche released a declaration about imdevimab and casirivimab's decreased effectiveness compared to Omicron in vitro experiments (Ronapreve, 2022). Sotrovimab holds action in opposition to Omicron; nevertheless, in 3-fold less effective in counterbalance as evaluated by EC50 (Cameroni et al., 2021).

### 12.1. Recent updates of some major vaccine makers

**Pfizer** is working on an Omicron vaccination that could be available as early as March 2022 (Walsh, 2022).

**Moderna** is working on an Omicron-specific vaccine prepared in March 2022 and a multi-valent vaccination that will protect against up to four different coronavirus types, including Omicron (Reuters Moderna starts trial for Omicron-specific booster shot, 2022).

**J and J (Johnson & Johnson)** evaluated blood line serum from contestants in finished and continuing booster experiments for offsetting action in opposition to the Omicron to assess the vaccine's effectiveness across variations, including Omicron. It's also working on an Omicron-specific variant vaccination, which will advance as needed (Johnson, 2022).

**Sinovac**, if needed, has said that it is capable of quickly mass developing a version as opposed to the Omicron model (Post., 2022).

**Sputnik V** is working on an Omicron booster (AFP, 2022b).

## 13. Vaccines efficacy against Omicron

### 13.1. SARS-CoV-2 Omicron variant runaway from combating antibodies is reduced by a homologous or heterologous boosting of deactivated vaccine

So far, one of the most intriguing aspects of the Omicron research has been its alleged capacity to evade immune surveillance. As a result, the scientists took steps to quantify and define the amount of this VOC's immune evasion after infection or immunization. To do so, the researchers examined the nullifying action of serum taken from 10 convalescent people affected by SARS-Delta CoV-2's form authors found strong titers counter to WT virus in all ten sera using VSV-based PsVs, with geometric mean deactivating titers (GMTs) of over 1,100. On the other hand, the Omicron variant was remarkably opposed to offsetting by convalescent plasma. Only three out of ten sera had ID50 titers greater than

the lesser threshold of quantification (LOQ) and a substantial decrease (>26-fold) when matched to WT.

The GMT versus WT was 84, with 80 percent of vaccinees demonstrating affirmative reduction, compared to only 10% of vaccinees successfully inhibiting Omicron. After that, Wang X. et al. tested the nullifying activity of sera from people who had received two dosages of incapacitated whole-virion vaccinations (BBIBP-CorV). This is a stunning first picture of Omicron's ability to evade the immune response (Wang et al., 2022).

### 13.2. Covid-19 vaccines' efficacy against Delta or Omicron infection

3,442 Omicron-confident patients, 9,201 Delta-positive incidents, and 471,545 test-negative controls were included by Buchan, S.A. et al., Vaccine efficacy against Delta infection decreased linearly after two doses of COVID-19 vaccination. Still, it bounced to 93 percent (95 percent CI, 92–94 percent) 7 days later, obtaining an mRNA inoculation for the 3rd dosage. Vaccination with 2 dosages of COVID-19, on the other hand, did not protect in opposition to Omicron. Vaccine efficacy in opposition to Omicron was 37percent (95 percent CI, 19-50percent) 7 days later, having the 3rd dosage of the mRNA vaccine. Buchan, S.A. et al. discovered. Two dosages of the COVID-19 vaccine were incapable of protecting as opposed to Omicron disease. A third dose offers additional security in the short term, albeit not nearly as much as against Delta (Buchan et al., 2022).

### 13.3. Following the 3rd dosage of the mRNA vaccine, kidney transplantation receivers'(KTR's) antibody reaction to the SARS-CoV-2 Omicron variant was lowered

Al Jurdi, A. et al. used 51 adult KTRs to conduct multi-focal point cohort analysis who were given three dosages of BNT162b2 or mRNA-1273. Before and four weeks after the 3rd vaccine dosage, urine and blood samples were taken. anti-viral antibody reactions in opposition to wild-type and variations of SARS-CoV-2 were the critical outcome. Secondary goals included non-intrusive checking for elimination utilizing proteinuria, donor-originated cell-free DNA, serum creatinine, and donor-specialized antibodies and the occurrence of breakthrough SARS-CoV-2 infection. For comparison, sera from pre-pandemic healthy controls and KTRs were employed. After the third vaccine dosage, 67 percent of KTRs generated anti-wild-type spike antibodies, which was like the Alpha (51%) and Beta (53%) variations, but greater than the Gamma (39%) and Delta (25%) versions. Before the third vaccine dosage, no KTRs had offsetting reactions to the Omicron version. In similarity to the wild-type (61%) and Delta (59%) variations, fewer KTRs (12%) had offsetting answers to the Omicron variant after the third dosage. At a median of 89 days, three patients (6%) discovered SARS-CoV-2 infection. Allograft damage, de novo donor-specific antibodies, or allograft rejection did not occur in any KTRs. The third dosage of mRNA vaccines boosts antibody answers against SARS-CoV-2 wild-type and variations in KTRs, although offsetting answers to the Omicron variant remain low (Al Jurdi et al., 2022).

## 14. Neutralization

### 14.1. Broad SARS-CoV-2 variants are suppressed by an ultrapotent Receptor-Binding Domain-targeted biparatopic nanobody

A.C. Walls et al. uncovered a panel of SARS-CoV-2 mitigating nanobodies (Nbs). They generated Nb1-Nb2-Fc, a biparatopic thick chain-up antibody that binds the intersecting but distinctive RBD antigenic zones while preserving cross-attraction with all the SARS-CoV-2 receptor-binding domains variants of concern that

were examined. >60 characteristic socializing points altered SARS-CoV-2 pseudo viruses comprising Spikes from the WHO nominated variants Alpha, Beta, Gamma, Delta, Lambda, Kappa, Mu, Omicron, and other pseudo viruses typed virus-comprising Spikes from the WHO defined variants are nullified by Nb1-Nb2-Fc. Neutralization of live SARS-CoV-2 variants was also authenticated, supporting the pseudo-virus concept. Once the virus adapts to human and animal hosts and evolves quickly, antibody attention and a distinctive counteraction method are becoming increasingly important in preventing and treating illness by new variants and reducing virus-related evade. In the long run, these findings suggest that the bi para topic heavy chain antibody is a good candidate for combating the wide range of variations that are currently being studied (Chi et al., 2021).

#### 14.2. Omicron variant treatment with CoronaVac or BNT162b2

HKU344-R346K is an Omicron variant strain with an added R346K mutation, found in 8.5% of GISAID strains. Only 20 parentage and 24 parentages of BNT162b2 beneficiaries, respectively, have noticeable offsetting antibodies to the Omicron variants HKU691 and HKU344-R346K. None of the CoronaVac beneficiaries, on the other hand, did. For BNT162b2 beneficiaries, the geometric mean offsetting antibody titers (GMT) of the Omicron variant isolates (5.43 and 6.42) were 35.7–39.9-fold smaller than the inherited virus (229.4), and both omicron isolates had substantially smaller GMT than the beta and delta variants. There was no noticeable variation in GMT between HKU691 and HKU344-R346K. And Lu L. et al. found that the Omicron version is immune to antibodies induced by BNT162b2 or CoronaVac. The neutralizing susceptibility was unaffected by the different R346K mutations. These findings imply that the Omicron variation is linked to poorer COVID-19 vaccination efficacy (Lu et al., 2021).

Omicron was found to be immune to the BNT162b2 messenger RNA vaccine (Pfizer–BioNTech) in a study of live-virus neutralization testing. As a result, more data on the efficiency of current vaccinations against the omicron form in preventing Covid-19 hospitalization is required. (Collie et al., 2022).

#### 14.3. Plasma neutralizing qualities of the SARS-CoV-2 Omicron variant

Schmidt, F. et al. evaluated nullifying antibody titers in 169 lengthwise gathered plasma models utilizing pseudo types harboring the Wuhan-hu-1 or Omicron variant or a lab setting offsetting-repellent SARS-CoV-2 spike (PMS20). Convalescents who got or won't receive an mRNA vaccination and indigenous people who have accepted 3-dosages of mRNA or 1-dosage Ad26 vaccines had their plasma stored. The samples were obtained one, five, six, and twelve months after the vaccination or illness. Likewise, to PMS20, the Omicron spike protein was more opposed to nullification than Wuhan-hu-1. Convalescing plasma had a 30- to 60-fold decrease in nullifying ability in opposition to PMS20 or Omicron. In plasma from beneficiaries of two mRNA vaccine doses, Wuhan-hu-1 was 30- to 180-fold less efficient in opposition to PMS20 and Omicron. After receiving additional mRNA vaccine doses, those who got contaminated or accepted two mRNA vaccination doses had 38 to 154-fold, and 35 to 214-times rises in neutralizing action in opposition to Omicron and PMS20, correspondingly (Schmidt et al. 2022).

#### 14.4. Omicron variant neutralization by vaccine sera and monoclonal antibodies

Wilhelm, A. et al. found that Antibody-facilitated neutralization effectiveness against real SARS-CoV-2Omicron was assessed in vitro and compared to Delta utilizing an isolate taken from a dual

1273-mRNA-immunised journey returned person from Zimbabwe. Neutralization of sera from twice (no booster) or triple BNT162b2-inoculated people (collected 0.5 or 6 months later boosting) indicated reductions of 11.4, 37.0, and 24.5 times, correspondingly. The monoclonal antibodies imdevimab and casirivimab, which are presently in use, effectively prevented Delta infection. However, Omicron was not neutralized, possibly due to amino acid substitutions. In difference to the already spreading Delta form, vaccine-elicited sera had a significantly lower neutralizing efficiency against Omicron, showing T-cell-based protection as an essential obstacle to preventing dangerous COVID-19. SARS-CoV-2 genotyping might be required prior to starting mAb therapy because Omicron was impervious to casirivimab and imdevimab. Variant-focussed vaccines and mAb therapies might be needed of the hour to deal with COVID-19 (Wilhelm et al., 2021).

## 15. Therapeutic options

The neutralization results will be available in the coming days, but real-world data will take longer to arrive. Corticosteroids and IL6 Receptor Blockers, according to the WHO, will continue to be useful in the therapy of individuals with acute COVID-19. Other remedies will be assessed to make sure if they are beneficial in the context of the Omicron variant's alterations to the virus (WHO Update on Omicron, 2022b).

**Paxlovid by Pfizer**, the novel chemical (PF-07321332), is used with ritonavir, a remodeled HIV/AIDS medicine. The protease inhibitor PF-07321332 inhibits the 3CLpro SARS-CoV-2 protease (gene NSP5), limiting the infection's capacity to multiply in host cells. The Omicron variant's NSP5 gene structure is unaltered; therefore, no significant reduction of efficacy should be expected for the Pfizer medication (Balloux, 2022). In vitro research in a recent preprint suggests that the effectiveness of specific main protease (Mpro) inhibitors like PF-07321332 is unaffected in existing COVID-19 versions (Ullrich et al., 2021).

**Molnupiravir lagevrio by Merck** is a nucleoside analog, which implies it imitates several of the structural elements of RNA and causes copying errors during viral RNA replication. Given the enormous modifications in their spike protein, the Omicron variant might be more sensitive to Molnupiravir than prior SARS CoV-2 lineages. As a result, Omicron might be more susceptible to "mutational meltdown." (Balloux, 2022).

**GlaxoSmithKline's Sotrovimab** According to preliminary evidence, it is anticipated to be capable of combating the Omicron variant. A range of variants that contribute to mutations in Omicron had been tested in the lab. In addition, one of the spike's target locations is thought to be unaffected in Omicron (H., K., 2022).

#### 15.1. Regeneron's Ronapreve could be less effective against Omicron to the mutations (H., K., 2022)

**Eli Lilly's antibody treatment** has already been demonstrated ineffective compared to other variants. It recommends opposition to employing one of their antibodies, bamlanivimab, to treat the Delta strain on its own, but claims it can yet be treated with a combination. It anticipates Omicron results in the following weeks (H., K., 2022).

**Gilead's Remdesivir** By targeting the viral RNA polymerase, it directly inhibits SARS-CoV-2 reproduction in interior infected cells. Gilead's research indicates that it will remain to work out in opposition to the latest omicron form (Gilead Gilead Statement on Vekury, 2022).

**Monoclonal Imdevimab and Casirivimab** are ineffective when used against Omicron (a small-scale preliminary study from a German lab) (Ciesek, 2022).

## 16. Favipiravir in covid-19 treatment

The recent review article by Gaonkar, S.L., et al. summarizes the role of favipiravir as an excellent curing option against SARS-CoV-2 disease (Gaonkar and Hakkimane, 2021).

## 17. Some initial out breaks of Omicron

### 17.1. The United States of America

On 26 November 2021, the WHO assigned B.1.1.529 as a variation of concern (WHO Classification of Omicron, 2021), and on 30 November 2021, the US SARS-CoV-2 Interagency Group (SIG) did the same. The initial instance of COVID-19 linked to the Omicron variant was described in the United States of America on 1 December 2021. As of 8 December, at least one Omicron variant case had been detected in 22 states, with several indicating community transmissions. One hospitalization and no deaths were reported among 43 instances with initial follow-up. To restrict the propagation of SARS-CoV-2, comprising variants like Omicron, and to guard counter acute sickness and mortality after COVID-19, contemporary preventative techniques such as inoculation, screening, increased air circulation, examination, isolation, and separation are proposed (CDC Team, 2021).

### 17.2. Norway

On 30 November 2021, a native lab in Oslo alerted the Norwegian Institute of Public Health (NIPH) of a coronavirus disease (COVID-19) incidence with an alleged SARS-CoV-2 Omicron variant of concern (VOC) (Phylogenetic Project of Labeled Worldwide Outburst Lineages (Pangolin) description B.1.1.529 BA.1) infection. The issue was possible because of the Christmas event gathering on 26 November 2021. According to the laboratory, some guests came back from South Africa on 24 November 2021 and attended the laboratory (Brandal et al., 2021).

### 17.3. Spread of omicron variant

In the coming days and weeks, the growth rate (in absolute numbers and relative to Delta) will become apparent, but the variety has the potential to spread quickly. According to preliminary modeling from UK organizations, the central forecast for omicron widening time is 0.1 to 0.4 per day, with a swift multiplying period of 2 to 3 days (UKGOVT SPI-M-O: Consensus Statement on COVID-19, 2021).

The SARS-CoV-2 virus's Omicron variation is much more capable of spreading than that of the basic virus, and it is unclear how easily Omicron transmits relatively to Delta. As claimed by CDC (Centre for Disease Control and Prevention in the United States), everybody with Omicron infection is expected to transfer the disease to every-one else, especially if they have been immunized or have no symptoms (CDC Omicron Variant: What You Need to Know, 2022). Some estimates show that Omicron could transmit 3 to 6 times as many individuals as Delta during that period, based on the emergence of COVID-19 instances and sequence data (Callaway and Ledford, 2021).

Corresponding to a recent analysis conducted by the UK Health Security Agency, the Omicron variation may have a shorter infection period before becoming infectious than the Delta variant (UKGOVT, 2022). Omicron's quick displacement of existing Delta viruses in Gauteng and South Africa is an important data point. However, Omicron was discovered when Delta transmission was low. It had limited competition; it will be critical to track events

on every side of the planet to see if Omicron could outperform Delta (Kupferschmidt, 2022).

Investigations of households and links in the United Kingdom identified that Omicron index incidents had the highest vulnerability of transmitting to contacts than Delta index cases. The most recent findings show a higher risk of residential transfer based on routine testing data. According to regular proximity tracing findings, the family secondary exposure figure for Omicron is 15.8% (95% CI: 14.3% – 17.5%) and 10.3 percent (95%CI: 10.1% – 10.55%) (UKSHA SARS-CoV-2 variants of concern and variants under investigation in England, 2022). In a domestic setting, a study in Denmark indicated that when an index incident was affected with the Omicron variant, secondary attack rates were higher than when an index incident was affected with the Delta variant (31 percent vs 21 percent) (Lyngse et al., 2021). A blend of variables, having immune-bypass and possibly intrinsic higher transmissibility, are likely to be responsible for the observed rapid growth rate. In contrast, there is increasing evidence of natural and vaccine-derived immunity-based immune evasion against transmission (Pearson et al., 2021).

According to a non-peer-reviewed study from South Africa, Omicron is 36.5 percent (95 percent CI 20.9–60.1) higher transmissible than Delta, and Omicron jeopardizes 63.7 percent (95 percent CI 52.9–73.9) of herd immunity built by previous infection and vaccination (Yang, 2021).

Omicron infects human bronchial tissue more quickly and effectively than Delta (Chan et al., 2021). According to a study from Hong Kong University, Omicron outperforms Delta in race tests employing cells resulting from the humanoid nose, but not lung-derived cells, and another analysis from the UK Genotype to Phenotype (G2P) conglomerate identified that Omicron outperforms Delta in race analysis employing cells obtained from the humanoid nose, but not lung-resultant cells (Peacock et al., 2022). It indicates a growing benefit in the higher respiratory region, minimum in part, could provide a transmitting benefit independent of immune evasion. As indicated by preliminary results by the Republic of Korea, where Omicron's in sequence time was 2.22 days, shorter serial intervals may also contribute to a higher growth rate (95 percent CI 1.48–2.97) (Kim et al., 2021), matched to Delta's 3.26 days (95 percent CI 2.92–3.6) (Hwang et al., 2021).

Higher percentages of asymptomatic infection could also contribute to infectious transmission. An experiment had vaccine trial participants from South Africa suggested. Altogether, a more significant portion (16%) of frequently examined asymptomatic persons were discovered to be contacted with the virus in the era of Omicron majority, relative to 2.6 percent in the course of Delta and Beta supremacy (Garret et al., 2021).

## 18. Measures for effective control of Omicron variant

The exact characteristics of the Omicron variant are currently unknown. Given the spike mutations found in other VOCs, it's especially alarming because Omicron may have developed the ability to propagate effortlessly among humans and elude existing effective antibody treatments. Epidemiological research suggests that the breakdown of PCR examinations aiming at the spike gene is growing together with the number of incidents affected with Omicron. To stop the Omicron variant from spreading, it's also vital to improve diagnosis accuracy so that diagnosed cases can be isolated and treated quickly.

### 18.1. Increasing Covid-19 vaccine coverage

Despite the fact that specific estimates indicate that Omicron will spread quickly in South Africa, it could mark the start of a

new pandemic wave worldwide. The impact of this variety and what it signifies for the current epidemic remain unknown. The state of affairs with the Omicron increase in South Africa may be very distinct from that in other nations. In South Africa, for instance, only approximately 24% of the population is adequately inoculated. This figure is significantly lower than the global average immunization rate of 42% (Hanson, 2021). This could hasten the spread of Omicron in South Africa.

### 18.2. Developing variant-specific vaccines

The Omicron variant's arrival in South Africa has been connected to a higher probability of SARS-CoV-2 re-infection. Suggesting that the Omicron variant may be related to a significant power to thwart immunity from earlier infection (Pulliam et al., 2021b). According to these studies, current COVID-19 immunizations might not be as successful in opposition to the omicron type of SARS-CoV-2 as opposed to other SARS-CoV-2 variants. In the time to come, further knowledge concerning the efficacy of existing COVID-19 vaccines will be needed. Although it is unknown if the Omicron spike mutations influence the efficiency of presently available vaccines, immunizations established on wild-type SARS-CoV-2 are less efficient in avoiding modified viruses (Pilišvili et al., 2021).

According to a recent study by He C. et al., the immunization centered on the modified spike had a tremendous amount of offsetting antibodies as opposed to mutant viruses but then a smaller level of offsetting antibodies in opposition to wild-type SARS-CoV-2 (He et al., 2021d). In brief, these findings emphasize the significance of creating variation-particular vaccines centered on the mutant spike, particularly for the omicron variant.

### 18.3. Disruption of SARS-CoV-2 variant multiplication

The exact characteristics of the omicron variant are at present unknown. Given the spike mutations found in other VOCs, it's especially concerning that Omicron may have come with the potential to spread more easily among people and to withstand currently effective antibody therapies. This situation emphasizes maintaining current public health preventive procedures, such as surgical mask use, bodily distance, and hand cleaning. These procedures successfully stop the spread of other variations, and they should also help control the omicron variant (He et al., 2021b).

## 19. Conclusion

In the appearance of omicron advent, we can apply our experience of covid-19 to control the omicron variant. Still, the Variant's spreading capability, origin, and immune-dodging ability remain unknown. It's also unclear whether further variants based on Omicron may emerge in the future. Omicron, however, will undoubtedly not be the last SARS-CoV-2 Variant. The COVID-19 pandemic has become difficult to control owing to the constant advent of new SARS-CoV-2 mutations. Fortunately, we have a wealth of expertise and strategies for dealing with novel coronaviruses, and we know what we need to do to prevent viral variations from spreading.

### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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### Further Reading

- WHO Tracking SARS-CoV-2 variants. <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> (accessed 21 January 2022).