Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Omicron B.1.1.529 subvariant: Brief evidence and future prospects

Since the initial report of the coronavirus disease 2019 (COVID-19) in December 2019, subsequent emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants has generated serious concerns [1]. The World Health Organization (WHO) categorized notable SARS-CoV-2 variants into three groups for monitoring purpose, inclusive of 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 (B.1.617.2) were previously identified VOCs until late October 2021 [2].

In November 2021, a substantial surge in COVID-19 cases was detected in South Africa's Gauteng province. This upsurge was accompanied increased S-gene target failure (SGTF) observation during TaqPath-based Reverse-Transcriptase Polymerase Chain Reaction (PCR) testing. Hence, this novel finding suggested a genetically distinct lineage of SARS-CoV-2 has spread in the community. Concurrently, in Gaborone, Botswana, unexpected viral sequences from samples obtained from a group of visitors were observed [3]. On November 24, 2021, these SARS-CoV-2 genomes from South Africa and Botswana were designated as belonging to a new PANGO lineage (B.1.1.529) [4].

On November 26, 2021, WHO announced the newly discovered Omicron variant (B.1.1.529) as a Variant of Concern (VOC), making it the fifth on the list. This novel variant, like other SARS-CoV-2 variants, comprises of several sublineages. Up to August 24, 2022, more than 300 Pango lineages were associated with the Omicron variant. Some prominent subvariants are BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5 [4]. Following South Africa and Botswana, more than 150 countries have reported containing the Omicron variant since January 20, 2022 [5]. Omicron and its subvariants provide additional obstacles in the fight against the COVID-19 pandemic.

1. Genetic structure and mutations

The Omicron variant has fifty shared mutations compared to the standard strain of SARS-CoV-2, including 43 substitutions, six deletions, and one insertion of the nucleotide. At least 27 of these mutations occurred at the S protein, predicted to cause accumulations around the receptor-binding motif [6]. In addition to the 50 shared mutations, ten other locations exhibited high-frequency mutations, including seven non-synonymous and three synonymous nucleotide substitutions [6]. Fig. 1 illustrates the details of spike protein mutations. The other four VOCs showed significantly fewer mutations, with 22, 18, 23, and 29 mutations for Alpha, Beta, Gamma, and Delta, respectively [6].

2. Transmissibility

The SARS-COV-2 Omicron variant caused a quicker spread of COVID-19 than any preceding variants [7]. The Centers for Disease Control and Prevention (CDC) states that anyone infected with Omicron, regardless of vaccination status or the presence of symptoms, poses a greater risk of spreading the virus to others [8]. Spike (S) protein of Omicron variant has receptor binding domain (RBD) mutations that increase its affinity to the human ACE2 receptor, allowing the virus to enter human cells more efficiently. It causes a relatively higher effective reproduction number than the Delta variant, approximately 3.19 times (95% CI 2.82–3.61) [7,9]. Thus, due to the significant expansion of transmissibility and infectivity, Omicron cases have increased rapidly shortly after its introduction. This variant causes several manifestations, which is generally mild and classified as flu-like symptoms. These include fever, sore throat, cough, fatigue, and pains. In addition, symptoms such as muscle or joint pain, loss of taste (anosmia) or smell (ageusia), and runny nose were also typical of earlier variants [10–12]. The Omicron form, on the other hand, has the potential to increase the number of deaths due to its great transmission ability [8].

3. Fear of co-infection and re-infection, and vaccine efficacy against B.1.1.529

Study findings have found the risk of co-infection and reinfection associated with Omicron infestation, even after they have fully recovered from COVID-19 [8]. Omicron emergence (November 1-30, 2021) could increase the reinfection ratio by 1.75 times (95% CI: 1.48 to 2.10) compared with the first wave of COVID-19 spread (June–September 2020) [13]. One study has reported that the SARS-CoV-2 Delta/Omicron co-infections are not uncommon (found in 6 out of 7 samples), especially during high virus co-circulation periods [14]. Co-infections could lead to extended disease duration and severity.

Vaccination is the most recognized public health measure to counteract COVID-19 infection [8]. It is advised for everyone without any absolute contraindications to having their primary round of shots, as well as booster doses. Available vaccines are able to reduce the risk of complications, hospitalizations, and deaths from the Omicron variant [15].

Primary immunization with two doses of ChAdOx1 nCoV-19 (AstraZeneca) or BNT162b2 (Pfizer-BioNTech) vaccine provided only little protection against the Omicron variant's symptomatic disease. After either the ChAdOx1 nCoV-19 or BNT162b2 primary course, a BNT162b2 or mRNA-1273 (Moderna) booster significantly enhanced protection, but that protection faded over time [16].

4. Recommendations and implications

To combat the spread of the Omicron variant (and any other possibly emerging variants), sufficient pandemic preparedness, mutation surveillance, and control measures should be used with caution. It is

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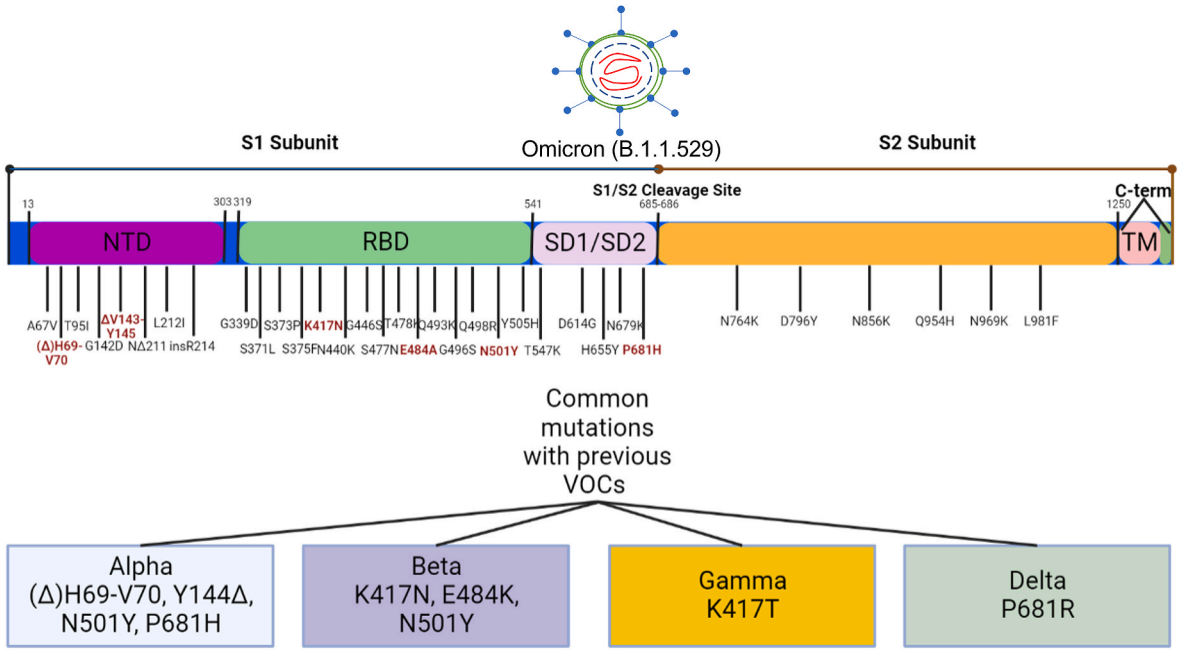

Fig. 1. Details of spike protein mutations in Omicron B.1.1.529.

suggested that governments do the following: notify WHO of any new cases or clusters of cases involving VOC infection as soon as possible, conduct field investigations and laboratory assessments to better understand the potential effects of the VOC on COVID-19 epidemiology, severity, diagnostic methods, immune responses, antibody neutralization, or other relevant characteristics, as well as evaluating the efficacy of public health and social measures, [4]. In addition, more effort should be put into monitoring and sequencing the spread of SARS-CoV-2 mutations. Finally, the results of complete genome sequences and associated metadata can be deposited into a freely accessible resource like Global Initiative on Sharing All Influenza Data (GISAID).

Individuals should be guided to practice public health and social measures that have been shown to reduce the risk of acquiring COVID-19 [4]. These include washing their hands frequently, keeping their distance from others, using adequate ventilation in enclosed spaces, limiting their time spent in crowded areas, using face mask, and getting vaccinated.

In conclusion, humanity may be forced to live with COVID-19; thus, vaccination campaigns must continue, and appropriate routine behavioral changes will become increasingly crucial for adopting safety measures and other necessary disease prevention and control measures as the "new normal" lifestyle of our world.

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Author contribution

RAF: the conception and design of the study. RAF, MB and TPU: made the first draft. RAF: updated the manuscript. RAF and TPU: reviewed the final draft and edited final. All authors have critically reviewed and approved the final draft and are responsible for the content and similarity index of the manuscript.

Consent

N/A.

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Ramadan Abdelmoez Farahat*
Faculty of Medicine, Kafrelsheikh University, Kafrelsheikh, Egypt

Mohamed Baklola
Faculty of Medicine, Mansoura University, Mansoura, Egypt

Tungki Pratama Umar
Faculty of Medicine, Sriwijaya University, Palembang, Indonesia

* Corresponding author. Faculty of Medicine, Kafrelsheikh University, Kafrelsheikh, 33511, Egypt.
E-mail address: ramadan.med_2587@med.kfs.edu.eg (R.A. Farahat).