

# **Newer emerging SARS-COV2 variant: Omicron EG.5**

Shailendra Yadav, PhD<sup>a</sup>, Kamran Zaman, MD<sup>b</sup>, Prashant Bashyal, MBBS<sup>e</sup>, Rashmi Bhatta, MD<sup>f</sup>, Shailaj Bhandari, MBBS<sup>h</sup>, Aroop Mohanty, MD<sup>c</sup>, Ranjit Sah, MD<sup>d,g,\*</sup>

In December 2019, Wuhan City in China announced the first case of COVID-19 infection. Till date, a total of 690 170 546 cases of COVID-19 infections and 6 902 992 deaths have been recorded. The WHO report indicates that from 12 June to 9 July 2023, there were ~794 000 new COVID-19 infections reported worldwide, along with 4800 fatalities<sup>[1]</sup>. By accumulating mutations, SARS-COV2 is evolving. Hence, it's conceivable that additional variants may appear<sup>[2]</sup>. The COVID-19 virus variants were categorized by the WHO into three groups: variants of concern (VOCs), variants under monitoring (VUMs), and variants of interest (VOIs). There have been three distinct COVID-19 waves documented till now. The L, S, G, GR, and GH clades of SARS-CoV2 dominated the first wave of COVID-19, which started in March 2020. Beginning in March 2021, the second wave was primarily caused by the Delta variant (Alpha-B.1.617). During the second wave of the COVID-19 pandemic, several additional variants with pathogenicity greater than alpha variants (B.1.618 triple mutant), B.1.351 (Beta), and P.1 (Gamma) were also prevalent<sup>[3]</sup>. The third wave of the COVID-19 pandemic has predominantly been the Omicron variant. The first case of Omicron (B.1.1.529) infection was reported from Botswana, South Africa in November 2021. Due to its higher transmissibility and virulence, WHO declared Omicron a VOCs on 26 November 2021. Omicron is the most divergent variants with 26-32 mutations in spike proteins, N terminal domain and, receptor binding sites. These mutations are responsible for higher virulence and transmissibility<sup>[4]</sup>. The genomic surveillance by whole-genomic sequencing during the third wave confirmed the role of Omicron variants (B1.1.529; 98%) in the increase in

Sponsorships or competing interests that may be relevant to content are disclosed at the end of this article.

\*Corresponding author. Address: Tribhuvan University Teaching Hospital, Kathmandu, Nepal. Tel.: +977 982 770 1465. E-mail: ranjitsah@iom.edu.np (R. Sah).

Copyright © 2023 The Author(s). Published by Wolters Kluwer Health, Inc. This is an open access article distributed under the terms of the Creative Commons

Attribution-Non Commercial-No Derivatives License 4.0 (CCBY-NC-ND), where it is permissible to download and share the work provided it is properly cited. The work cannot be changed in any way or used commercially without permission from the journal.

Annals of Medicine & Surgery (2023) 85:5845-5846

Received 11 August 2023; Accepted 28 September 2023

Published online 4 October 2023

http://dx.doi.org/10.1097/MS9.000000000001386

COVID-19 infections. Omicron variants predominated between January 2022 and May 2023, states the Centers for Disease Control and Prevention (CDC). Initially, BA 1.1 dominance occurred in January 2022, followed by BA.2 prevalence in March 2022 and BA.5 prevalence in July 2022. Later, Omicron sub lineages BA.2, BA.4, and BA.5 predominated. WHO has recognized five (BA.1, BA.2, BA.3, BA.4, and BA.5) subvariants of omicron as VOCs<sup>[5]</sup>.

Although the proportion of COVID-19 infections and associated mortality and morbidity notably decreased in 2023, the circulating variants included XBB1.5, XBB1.9.1, and XBB1.16 with the K478R mutation and a longer doubling time. However, the ongoing development of omicron lineages underscores the usefulness of genomic surveillance for keeping track of emerging variants that will aid in the creation of innovative medications and vaccines<sup>[1,6,7]</sup>. Furthermore, decreased testing and reporting could have been a contributing factor in the decline in cases of COVID and deaths. Additionally, barely a small number of nations regularly update their hospitalization and fatality records. Several nations fail to report ICU admissions due to COVID-19 infections. Malta as a whole has seen an increase in hospitalization (20%) during the last 28 days. Pacific nations like Australia reported a 20% increase in COVID-19 cases in  $1 \text{ month}^{[1]}$ .

Omicron variants were categorized as Omicron VOCs in an earlier taxonomy. It made it difficult to compare novel variants with parent lineage (BA.1, BA.2, BA.4/BA.5) because they had altered phenotypes<sup>[8,9]</sup>. On 15 March 2023, WHO suggested that Omicron variants be tracked separately as VOIs, VOCs, and VUMs. A novel Omicron variant EG.5, from lineage XBB.1.9.2, has been discovered. It possesses extra mutation in the spike protein. Globally, it is becoming more prevalent. Because the number of infections caused by other variants has greatly decreased, the WHO added this variant as a VUM for COVID-19 tracking on 21 July 2023. There are now seven different VUMs (Table 1). Two variants remain of importance, XBB.1.5, which is progressively falling, and XBB.1.16, which is stable at 20.7% of sequences<sup>[1,10]</sup>.

In the USA, the prevalence of omicron EG.5 was 13%, according to the CDC (until July 8, 2023). Regarding the involvement of EG.5 in escalating COVID-19 infections and fatalities, there is no concrete proof at this time. Its capacity for transmission and virulence (morbidity/mortality) has not yet been established<sup>[11–13]</sup>. Omicron EG.5 infections are yet to be reported in South Asian nations like Bangladesh, India, or Nepal. On 27 July 2023, India reported eight deaths and 1542 cases of COVID-19 infections. About 5 28 913 people have died as a result of COVID-19 infections overall, and around 26 449 active COVID-19 cases at this time<sup>[14–16]</sup>.

<sup>&</sup>lt;sup>a</sup>Malaria Division, ICMR-Regional Medical Research Centre Dibrugarh (ICMR-RMRC Dibrugarh), Dibrugarh, Assam, <sup>b</sup>Department of Microbiology and Molecular Biology, Indian Council of Medical Research—National Institute of Traditional Medicine Belagavi (ICMR-NITM Belagavi), Karnataka, <sup>c</sup>Department of Microbiology, All India Institute of Medical Sciences, Gorakhpur, <sup>d</sup>Dr. D.Y Patil Medical College, Hospital and Research Centre, Dr. D.Y. Patil Vidyapeeth, Pune, Maharashtra, India, <sup>e</sup>Lumbini Medical College, Lumbini, <sup>f</sup>Nepal Medical College, <sup>g</sup>Tribhuvan University Teaching Hospital, Kathmandu, Nepal and <sup>h</sup>Parkside Hospital, Hospital, Wimbledon, London

#### Table 1

Current list of variants under monitoring (VUMs) as per WHO (adopted from Weekly epidemiological update on COVID-19-13 July 2023)<sup>[1,10]</sup>

Variant name	Lineage	Countries detected (21–25-week 2023)	Sequences (21–25-week 2023)	Evidence on transmissibility
BA.2.75 <sup>a</sup>	Omicron	124	121701	Not available
CH.1.1 <sup>a</sup>	Omicron	95	42426	Not available
XBB <sup>a</sup>	Omicron	130	64219	Not available
XBB.1.9.1 <sup>a</sup>	Omicron	98	45603	Not available
XBB.1.9.2 <sup>a</sup>	Omicron	83	24091	Not available
XBB.2.3 <sup>a</sup>	Omicron	64	7020	Not available
EG.5 <sup>a</sup>	Omicron	In the USA	NA	Not available
Other	NA	209	6753503	Not available

<sup>a</sup>Includes descendant lineages, except those individually specified elsewhere in the table. For example, XBB does not include XBB.1.5, XBB.1.9.1, XBB.1.9.2, XBB.1.16, and XBB.2.3.

WHO also recommended that the guidelines for COVID-19 remain unaltered and requested all member countries to continue genomic surveillance via sequencing as the COVID-19 virus will continue to gain mutations and evolve. Based on the recently available evidence, the public health risk by EG.5 is as low as other VOIs. New variants will keep on evolving but there should be no cause for concern till the trajectory follows the path of the pandemic as had happened. Also, understanding the lineage of circulating variants necessitates whole genome sequencing of fresh samples. Additionally, WHO urged member nations to adopt the COVID protocol in public places, create their health-care infrastructures, and continue to operate their current facilities.

#### **Ethics approval**

Ethics approval was not required for this editorial article.

# Consent

Informed consent was not required for this editorial article.

#### Source of funding

No funding was received.

# Author contribution

S.Y., K.Z., A.M.: designed the original draft; P.B., R.B., S.B., R.S.: reviewed the literature; S.Y., K.Z., A.M. critically edited the manuscript. All authors read and approved the final manuscript

# **Conflicts of interest disclosure**

The authors declare no conflict of interest, financial or otherwise.

# Research registration unique identifying number (UIN)

Not applicable.

#### Guarantor

Ranjit Sah (Corresponding author) is taking the full responsibility for the work and/or the conduct of the study, had access to the data, and controlled the decision to publish.

# **Data availability statement**

All data used to support the findings of this study are included in the article.

#### Provenance and peer review

Not commissioned, externally peer-reviewed.

# References

- World Health Organization. COVID-19 weekly epidemiological update, edition 134, 16 March 2023. https://www.who.int/publications/m/item/ weekly-epidemiological-update-on-covid-19
- [2] Pather S, Madhi SA, Cowling BJ, et al. SARS-CoV-2 Omicron variants: burden of disease, impact on vaccine effectiveness and need for variantadapted vaccines. Front Immunol 2023;14:1130539.
- [3] Zaman K, Shete AM, Mishra SK, et al. Omicron BA. 2 lineage predominance in severe acute respiratory syndrome coronavirus 2 positive cases during the third wave in North India. Front Med 2022;9:955930.
- [4] Ma KC. Genomic Surveillance for SARS-CoV-2 Variants: Circulation of Omicron Lineages—United States, January 2022–May 2023. MMWR Morbid Mortal Wkly Rep 2023;72:651–6.
- [5] Markov PV, Ghafari M, Beer M, et al. The evolution of SARS-CoV-2. Nat Rev Microbiol 2023;21:361–79.
- [6] Blomquist PB, Bridgen J, Bray N, et al. Enhancing epidemiological surveillance of the emergence of the SARS-CoV-2 Omicron variant using spike gene target failure data, England, 15 November to 31 December 2021. Eurosurveillance 2022;27:2200143.
- [7] Oude Munnink BB, Koopmans M. Tracking SARS-CoV-2 variants and resources. Nat Methods 2023;20:489–90.
- [8] Sah R, Rais MA, Mohanty A, et al. Omicron (B.1.1.529) variant and its subvariants and lineages may lead to another COVID-19 wave in the world? -An overview of current evidence and counteracting strategies. Int J Surg Open 2023;55:100625.
- [9] Sah R, Mohanty A, Rohilla R, et al. BF.7 Omicron subvariant in India and China: a rising concern - correspondence. Int J Surg 2023;109:606–7.
- [10] WHO adds Omicron EG.5 to variant monitoring as global COVID markers decline further. Accessed on 30 July 2023. https://www.cidrap. umn.edu/covid-19/who-adds-omicron-eg5-variant-monitoring-globalcovid-markers-decline-further
- [11] Statement on the update of WHO's working definitions and tracking system for SARS-CoV-2 variants of concern and variants of interest. Accessed on 01 August 2023. https://www.who.int/news/item/16-03-2023-statement-on-the-update-of-who-s-working-definitions-and-track ing-system-for-sars-cov-2-variants-of-concern-and-variants-of-interest#: ~:text=WHO%20has%20updated%20its%20tracking,variants% 20more%20clearly%20when%20required
- [12] Arumugam VA, Thangavelu S, Fathah Z, et al. COVID-19 and the world with co-morbidities of heart disease, hypertension, and diabetes. J Pure Appl Microbiol 2020;14:1623–38.
- [13] Patel SK, Pathak M, Tiwari R, *et al.* A vaccine is not too far for COVID-19. J Infect Dev Ctries 2020;14:450–3.
- [14] COVID-19 Dashboard Accessed on 01 Aug 2023, 08:00 IST (GMT + 5:30). https://www.mygov.in/covid-19/
- [15] Shrestha S, Khatri J, Shakya S, *et al.* Adverse events related to COVID-19 vaccines: the need to strengthen pharmacovigilance monitoring systems. Drugs Ther Perspect 2021;37:376–82.
- [16] Rabaan AA, Al-Ahmed SH, Sah R, *et al.* Recent advances in vaccine and immunotherapy for COVID-19. Hum Vaccin Immunother 2020;16: 3011–22.