

WHO TAG-VE Risk Evaluation for SARS-CoV-2 Variant Under Monitoring: LP.8.1

Executive Summary

LP.8.1 is currently one of two SARS-CoV-2 variants under monitoring (VUM) with increasing prevalence globally, the other being XEC. Considering the available evidence, the additional public health risk posed by LP.8.1 is evaluated as low at the global level. The recommended COVID-19 vaccines are expected to remain cross-reactive to this variant against symptomatic and severe disease, as LP.8.1 immune escape is comparable to XEC that has been shown to have limited immune escape from JN.1 or KP.2 mRNA booster vaccines. Therefore, the continued spread of this variant alone is unlikely to increase the burden on national public health systems compared to other Omicron sub-lineages.

Initial Risk Evaluation of LP.8.1, 3 February 2025

LP.8.1 is a SARS-CoV-2 variant derived from the JN.1 descendent lineage KP.1.1.3, with the earliest sample collected on 1 July 2024. LP.8.1 is one of seven VUMs tracked by the WHO and was designated as a VUM on 24 January 2025 [1,2]. In comparison to the most recent and currently dominant SARS-CoV-2 variants, KP.3.1.1 and XEC, respectively, LP.8.1 has the following additional Spike mutations: S31- (distinct from XEC only), F186L, R190S, R346T, V445R, and K1086R. The V445R mutation has been shown to enhance binding affinity to hACE2, potentially increasing the variant's transmissibility [3]. Additionally, using pseudoviruses, LP.8.1 was shown to exhibit strong humoral immune evasion comparable to XEC, effectively escaping neutralization by a broad range of antibodies, including some Class 3 monoclonal antibodies [3]. As XEC has been shown to have limited immune escape from JN.1 or KP.2 mRNA booster vaccines [4–6], it is expected that LP.8.1 will mount a similar level of immune response to these vaccines.

As of 2 February 2025, there were 997 LP.8.1 sequences submitted to GISAID [7] from 23 countries, representing 7.0% of the globally available sequences in epidemiological week 2 of 2025 (6 to 12 January 2025). While still low numbers, this is a significant rise in prevalence from 1.9% four weeks prior in epidemiological week 51 of 2024 (16 to 22 December 2024), Table 1. In addition to XEC, LP.8.1 is the only VUM with increasing prevalence in all the three WHO regions that are consistently sharing of SARS-CoV-2 sequences between epidemiological week 51 of 2024 and week 2 of 2025, i.e. an increase from 0.8% to 7.5% for the Western Pacific region (WPR), from 2.2% to 7.9% for the region of the Americas (AMR), and from 1.6% to 2.5% for the European region (EUR). There is only 1 LP.8.1 sequence from the African Region (AFR), and none from the East Mediterranean Region (EMR) and the South East Asia region.

Table 1: Global proportions of SARS-CoV-2 Variants, epidemiological week 51 of 2024 to 2 of 2025

Lineage*	Countries§	Sequences§	2024-51	2024-52	2025-01	2025-02
VOIs						
JN.1	148	310035	16.6	16.6	13.9	13.1
VUMs						
KP.2	92	35598	1.3	1.4	0.9	0.7
KP.3	80	60903	6.2	5.9	6.0	4.5
KP.3.1.1	73	82173	29.4	27.9	27.6	26.9
JN.1.18	104	8592	1.6	1.0	0.2	0.1
LB.1	83	15962	0.4	0.2	0.2	0.1
XEC	60	30858	41.0	42.5	45.7	46.8
LP.8.1	23	997	1.9	3.4	4.3	7.0
Recombinant	148	496867	1.5	0.9	1.0	0.8
Unassigned	69	4289	0.0	0.1	0.1	0.1
Others	120	37556	0.2	0.1	0.1	0.1

Figures by WHO, data from GISAID, extracted on 2 February 2025.

§Number of countries and sequences are since the emergence of the variants.

*The variants listed include descendant lineages, except those individually specified elsewhere in the table.

The VOI and the VUMs that have shown increasing trends are highlighted in orange, those that have remained stable are highlighted in blue, while those with decreasing trends are highlighted in green.

WHO and its Technical Advisory Group on Virus Evolution (TAG-VE) continue to recommend that Member States prioritize specific actions to better address uncertainties relating to antibody escape and severity of LP.8.1:

- Conduct neutralization assays using human sera, representative of the affected community(ies), and sera from naive animal models infected with LP.8.1 live virus isolates.
- Perform a comparative evaluation to detect changes in rolling or ad hoc indicators of severity.

WHO and its Technical Advisory Group on COVID-19 Vaccine Composition (TAG-CO-VAC) continue to regularly assess the impact of variants on the performance of COVID-19 vaccines to inform decisions on updates to vaccine composition [8].

The risk evaluation below follows the published WHO framework for risk evaluation of SARS-CoV-2 variants [9] and is based on currently available evidence. This risk evaluation will be revised regularly as more evidence and data from additional countries become available. With declining prevalence of VOIs, and VUMs increasingly unable to meet the VOI definition, WHO, on 29 November 2024, began conducting risk evaluations for VUM designations in addition to VOI designations.

To support member states in addressing the risk posed by COVID-19 during the transition from the response to a public health emergency of international concern to its management within broader disease prevention and control programmes, the WHO Director General's latest standing recommendations remain in effect from 9 August 2023 until 30 April 2025 [10].

Overall risk evaluation: Low	<p>LP.8.1 is growing rapidly compared to co-circulating variants, but possesses comparable antigenic advantage as XEC in evading previous immunity. There is no significant increase in cases attributable to LP.8.1 infections, and there are no reports to suggest that the associated disease severity is higher as compared to other circulating variants.</p> <p>The available evidence on LP.8.1 does not suggest additional public health risks relative to the other currently circulating Omicron descendent lineages.</p>		
Indicator	Evidence	Level of risk	Level of confidence
Growth advantage	<p>There are currently 997 LP.8.1 sequences available from 23 countries, representing 7.0% of the globally available sequences in epidemiological week 2 of 2025 (6 to 12 January 2025). While still low numbers, this is a significant rise in prevalence from 1.9% four weeks prior in epidemiological week 51 (16 to 22 December 2024).</p> <p>While LP.8.1 is increasing in prevalence, the most prevalent SARS-CoV-2 variant tracked by the WHO, XEC, is also increasing in prevalence and represented 46.8% in epidemiological week 2 of 2025, compared to 41.0% in epidemiological week 51 of 2024.</p> <p>Using a logistic regression model [11], compared to KP.3.1.1, LP.8.1 was estimated to have a higher relative growth advantage than co-circulating variants XEC, LF.7, LF.7.2.1, MC.10.1, NP.1, and LP.8 [3]. The higher growth advantage is thought to arise from enhanced ACE2 engagement efficiency to a level similar to KP.3 [3].</p> <p>* see footnote for more explanations</p>	Moderate	Moderate
Immune escape	<p>Using pseudoviruses, LP.8.1 was shown to exhibit strong humoral immune evasion comparable to XEC, effectively escaping neutralization by a broad range of antibodies, including some Class 3 monoclonal antibodies [3]. However, as XEC has been shown to have limited immune escape from JN.1 or KP.2 mRNA booster vaccines [4–6], it is expected that LP.8.1 will mount a similar level of immune response to these vaccines</p> <p>** see footnote for more explanations</p>	Low	Low

Severity and clinical/diagnostic considerations	<p>There are no reported or published studies on the impact of LP.8.1 on clinical outcomes.</p> <p>*** see footnote for more explanations</p>	Low	Low
---	---	-----	-----

Annex:

*** Growth advantage**

Level of risk: Moderate, as while the variant is growing substantially across all WHO regions with consistent SARS-CoV-2 sequence data sharing, XEC, the most prevalent SARS-CoV-2 variant, is also increasing in prevalence.

Confidence: Moderate, as even though we are seeing growth in three WHO regions, there have been no detections in the remaining regions.

**** Antibody escape**

Level of risk: Low, as it is estimated that LP.8.1 has comparable immune evasion relative to co-circulating variants such as XEC, which has been reported to have limited immune escape from JN.1 or KP.2 mRNA booster vaccines.

Confidence: Low, as there is only a single study using pseudoviruses with data on cross neutralization of LP.8.1. Additional laboratory studies from different regions of the world would be needed to further assess the risk of antibody escape in settings with different population immunity backgrounds.

***** Severity and clinical considerations**

Level of risk: Low, as currently there are no reports of elevated disease severity associated with this variant.

Confidence: Low. Currently there are no studies assessing the impact of this variant on clinical outcomes. Although, there is regular co-ordination and data sharing between all WHO Regional colleagues, countries, and partners, reporting of new hospitalizations and ICU data with the WHO has decreased substantially, therefore caution should be taken when interpreting severe cases due to this decrease in reporting.

References

1. World Health Organization Tracking SARS-CoV-2 Variants Available online: <https://www.who.int/activities/tracking-SARS-CoV-2-variants/> (accessed on 5 December 2024).
2. Coronavirus Disease (COVID-2019) Situation Reports: Coronavirus Disease (COVID-19) Weekly Epidemiological Updates and Monthly Operational Updates Available online: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports>.
3. Liu, J.; Yu, Y.; Yang, S.; Jian, F.; Song, W.; Yu, L.; Shao, F.; Cao, Y. Virological and Antigenic Characteristics of SARS-CoV-2 Variants LF.7.2.1, NP.1, and LP.8.1 2024.
4. Arora, P.; Happle, C.; Kempf, A.; Nehlmeier, I.; Stankov, M. V.; Dopfer-Jablonka, A.; Behrens, G.M.N.; Pöhlmann, S.; Hoffmann, M. Impact of JN.1 Booster Vaccination on Neutralisation of SARS-CoV-2 Variants KP.3.1.1 and XEC. *Lancet Infect Dis* **2024**, *24*, e732–e733, doi:10.1016/S1473-3099(24)00688-1.
5. Wang, Q.; Mellis, I.A.; Wu, M.; Bowen, A.; Gherasim, C.; Valdez, R.; Shah, J.G.; Purpura, L.J.; Yin, M.T.; Gordon, A.; et al. KP.2-Based Monovalent mRNA Vaccines Robustly Boost Antibody Responses to SARS-CoV-2 2024.
6. Chen, W.; Tompkins, K.R.; Windsor, I.W.; Martinez, L.T.; Ramos, M.; Li, W.; Shrivastava, S.; Rajput, S.; Chang, J.S.; Sahasrabudhe, P.; et al. Immunologic and Biophysical Features of the BNT162b2 JN.1- and KP.2-Adapted COVID-19 Vaccines 2024.
7. Khare, S.; Gurry, C.; Freitas, L.; Schultz, M.B.; Bach, G.; Diallo, A.; Akite, N.; Ho, J.; Lee, R.T.C.; Yeo, W.; et al. GISAID's Role in Pandemic Response. *China CDC Wkly* **2021**, *3*, 1049–1051, doi:10.46234/ccdcw2021.255.
8. WHO World Health Organization Technical Advisory Group on COVID-19 Vaccine Composition Available online: <https://www.who.int/news/item/13-12-2023-statement-on-the-antigen-composition-of-covid-19-vaccines>.
9. World Health Organization *SARS-CoV-2 Variant Risk Evaluation*, 30 August 2022; World Health Organization: Geneva, 2023;
10. Standing Recommendations for COVID-19 Issued by the Director-General of the World Health Organization (WHO) in Accordance with the International Health Regulations (2005) (IHR) Available online: [https://www.who.int/publications/m/item/standing-recommendations-for-covid-19-issued-by-the-director-general-of-the-world-health-organization-\(who\)-in-accordance-with-the-international-health-regulations-\(2005\)-\(ihr\)](https://www.who.int/publications/m/item/standing-recommendations-for-covid-19-issued-by-the-director-general-of-the-world-health-organization-(who)-in-accordance-with-the-international-health-regulations-(2005)-(ihr)).
11. Chen, C.; Nadeau, S.A.; Topolsky, I.; Manceau, M.; Huisman, J.S.; Jablonski, K.P.; Fuhrmann, L.; Dreifuss, D.; Jahn, K.; Beckmann, C.; et al. Quantification of the Spread of SARS-CoV-2 Variant B.1.1.7 in Switzerland. *Epidemics* **2021**, *37*, 100480, doi:10.1016/j.epidem.2021.100480.