World Health Organization

Executive Summary

JN.1 is the most prevalent SARS-CoV-2 variant globally. Considering the available evidence, the additional public health risk posed by JN.1 is still evaluated as low at the global level. Current population immunity globally as well as immunity generated by the XBB.1.5 booster vaccination is expected to remain cross-reactive to this variant, against symptomatic and severe disease. Therefore, the continued spread of this variant alone will unlikely increase the burden on national public health systems compared to other Omicron sub-lineages.

Updated Risk Evaluation of JN.1, 09 January 2023

JN.1 is a descendent lineage of BA.2.86, with the earliest sample collected on 25 August 2023 (1).

As of 5 February 2024, there were 79107 JN.1 sequences submitted to GISAID (1) from 94 countries, representing 89.0% of the globally available sequences in epidemiological week 4, (22 to 28 January 2024). This is a significant rise in prevalence from 64.5% four weeks prior in epidemiological week 52 (25 to 31 December 2023), Table 1. The JN.1 variant is also the most prevalent SARS-CoV-2 variant in all the four WHO regions with consistent sharing of SARS-CoV-2 sequences at epidemiological week 4, i.e. 83.3% for the South East Asian region (SEAR), 71.1% for the Western Pacific region (WPR), 91.7% for the European region (EUR), and 86.0% for the region of the Americas (AMR). There was only a single sequence from the East Mediterranean Region (EMR) and none from the African Region (AFR) in epidemiological week 4.

Table 1: Global proportions of SARS-CoV-2 Variants, week 52 of 2023 to week 4 of 2024

Lineage	Countries§	Sequences§	2023-W52	2024-01	2024-02	2024-03	2024-04
VOIs							
XBB.1.5	138	372049	3.7	3.1	2.1	1.6	1.4
XBB.1.16	128	122335	1.8	1.4	0.8	0.6	0.1
EG.5	107	198985	19.7	14.7	11.8	8.4	4.5
BA.2.86	74	16013	6.4	5.7	5.5	4.5	3.6
JN.1	92	65907	64.5	72.1	77.8	83.0	89.0
VUMs							
XBB	145	115262	0.8	0.9	0.7	0.5	0.1
XBB.1.9.1	126	97131	1.3	0.9	0.7	0.4	0.4
XBB.2.3	119	49917	1.0	0.9	0.5	0.3	0.4
Unassigned	72	29467	0.3	0.1	0.1	0.1	-

Figures by WHO, data from GISAID.org, extracted on 05 February 2024.
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 SARS-CoV-2 Evolution (TAG-VE) continue to recommend that Member States prioritize specific actions to better address uncertainties relating to antibody escape and severity of BA.2.86 and JN.1. The suggested timelines are estimates and will vary from one country to another based on national capacities:

- Conduct neutralization assays using human sera, representative of the affected community(ies), and sera from naive animal models infected with JN.1 live virus isolates (two to four weeks).
- Perform a comparative evaluation to detect changes in rolling or ad hoc indicators of severity (four to 12 weeks).

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 (2).

The risk evaluation below follows the WHO framework (3) and is based on currently available evidence. It will be revised regularly as more evidence and data from additional countries become available.

Overall risk evaluation: **Low**	Based on its genetic features, JN.1 possesses some antigenic advantage evading previous immunity. The available evidence on JN.1 does not suggest additional public health risks relative to the other currently circulating Omicron descendent lineages. While there is a rapid increase in JN.1 infections, and likely increase in cases, available limited evidence does not suggest that the associated disease severity is higher as compared to other circulating variants.		
Indicator	Evidence	Level of risk	Level of confidence
Growth advantage	There are currently 79107 JN.1 sequences available from 94 countries, representing 89.0% of the globally available sequences in epidemiological week 4, (22 to 28 January 2024). This is a significant rise in prevalence from 64.5% four weeks prior in epidemiological week 52 (25 to 31 December 2023). JN.1 variant is also the most prevalent SARS-CoV-2 variant in all the four WHO regions with consistent sharing of SARS-CoV-2 sequences at epidemiological week 4, i.e. 83.3% for the South East Asian region (SEAR), 71.1% for the Western Pacific region (WPR), 91.7% for the European region (EUR), and 86.0% for the region of the Americas (AMR). The driving factors to the high transmissibility of JN.1 remain to be determined. * see footnote for more explanations	High	High
Immune escape	A study from Germany using sera taken in September 2023 from vaccinated and exposed healthy persons found clear neutralization escape against recently circulating variants, but no specific pronounced escape for BA.2.86 or JN.1 (4). A Study from the US on vaccine effectiveness of the monovalent XBB.1.5 COVID-19 vaccine against symptomatic SARS-CoV-2 infection reported a 54% increased protection against symptomatic SARS-CoV-2 infection compared with no receipt of updated vaccine (5).	Moderate	Moderate

	Pre-existing SARS-CoV-2-specific T cells are predicted to cross-recognize BA.2.86, whereby 72% and 89% of CD4 and CD8 SARS-CoV-2 responses are still conserved in BA.2.86 (6). ** see footnote for more explanations		
Severity and clinical/diagnostic considerations	BA.2.86 pseudo-virus has been shown to have high infectivity in CaLu-3 cells, with this phenomenon thought to indicate a change in disease severity (7,8). However, there have been no reports of changes in disease severity in studied patients. A study from Denmark in ≥65-year-old patients has reported no difference in the odds of hospitalization with JN.1 compared to non-BA.2.86 variant (OR: 1.15 [0.74-1.78]) (9). Similar observations were reported by France (10). However, for Singapore, JN.1 elderly and younger cases had a lower risk of hospitalization and severity (11). A recent study assessing the validity of the Panbio™ Rapid Antigen Test for SARS-CoV-2 (Abbott) for its ability to detect JN.1 and other circulating BA.2.86-derived variants from Switzerland reported that the diagnostic test is still useful in detecting infections caused by these variants (12). *** see footnote for more explanations	Low	Low

World Health Organization

Annex:

*** Growth advantage**
Level of risk: High, as the variant is fast growing across all WHO regions with consistent SARS-CoV-2 sequence data sharing and has become the most prevalent variant in some countries.

Confidence: High, as the rapid growth has been reported by several countries in different WHO regions.

**** Antibody escape**
Level of risk: Moderate, as it is estimated that JN.1 has increased immune evasion relative to co-circulating variants.

Confidence: Moderate, as there are increasing data on cross neutralization of JN.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. It is unclear if the severity of this variant is lower as compared to co-circulating variants.

Confidence: Low. Current available data are limited to cell cultures and retrospective observational studies from a few countries. Additional studies would be needed to further assess 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. GISAID. Available from: https://gisaid.org/hcov19-variants/
2. World Health Organization Technical Advisory Group on COVID-19 Vaccine Composition. Available from: https://www.who.int/news/item/13-12-2023-statement-on-the-antigen-composition-of-covid-19-vaccines
3. WHO. SARS-CoV-2 variant risk evaluation, 30 August 2023. Available from: https://apps.who.int/iris/rest/bitstreams/1528680/retrieve
4. Jeworowski LM, Mühlemann B, Walper F, Schmidt ML, Jansen J, et al. Humoral immune escape by current SARS-CoV-2 variants BA.2.86 and JN.1, December 2023. Euro Surveill. 2024 Jan;29(2):2300740. doi: 10.2807/1560-7917.ES.2024.29.2.2300740. PMID: 38214083; PMCID: PMC10785204.
5. Link-Gelles R, Ciesla AA, Mak J, et al. Early Estimates of Updated 2023–2024 (Monovalent XBB.1.5)COVID-19 Vaccine Effectiveness Against Symptomatic SARS-CoV-2 Infection Attributable to Co-Circulating Omicron Variants Among Immunocompetent Adults — Increasing Community Access to Testing Program, United States, September 2023–January 2024. MMWR Morb Mortal Wkly Rep 2024;73:77–83. DOI: http://dx.doi.org/10.15585/mmwr.mm7304a2
6. Alessandro Sette, John Sidney, Alba Grifoni. Pre-existing SARS-2-specific T cells are predicted to cross-recognize BA.2.86. Cell Host & Microbe. Volume 32, Issue 1, 2024. Pages 19-24.e2. ISSN 1931-3128. https://doi.org/10.1016/j.chom.2023.11.010.
7. Qu P, Xu K, Faraone JN, et al. Immune Evasion, Infectivity, and Fusogenicity of SARS-CoV-2 Omicron BA.2.86 and FLip Variants. bioRxiv [Preprint]. 2023 Sep 12:2023.09.11.557206. doi: 10.1101/2023.09.11.557206. Update in: Cell. 2024 Jan 3;: PMID: 37745517; PMCID: PMC10515800.
8. Zhang L, Kempf A, Nehlmeier I, et al. SARS-CoV-2 BA.2.86 enters lung cells and evades neutralizing antibodies with high efficiency. Cell. 2024 Feb 1;187(3):596-608.e17. doi: 10.1016/j.cell.2023.12.025. Epub 2024 Jan 8. PMID: 38194966.
9. Statens Serum Institut, Denmark. Presentation at the WHO Technical Advisory Group (TAG-VE) meeting on 11 December 2023
10. Santé Publique France, France. https://www.santepubliquefrance.fr/maladies-et-traumatismes/maladies-et-infections-respiratoires/grippe/documents/bulletin-national/infections-respiratoires-aigues-grippe-bronchiolite-covid-19-.-bulletin-du-10-janvier-2024
11. Ministry of Health, Singapore. Presentation at the WHO Technical Advisory Group (TAG-VE) meeting on 11 December 2023
12. Geneva Centre for Emerging Viral Diseases, Hôpitaux Universitaires Genève.