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Short Communication: The COVID-19 JN.1 variant diagnosed in Egypt.

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Abstract:

JN.1 is a descendant lineage of BA.2.86, with the earliest sample collected on 25 August 2023, JN.1 has been reported in many countries in recent weeks, and its prevalence has been rising quickly worldwide, On 28 December 2023, the Egyptian Ministry of Health and Population announced that two patients were diagnosed with COVID-19 JN.1 variant infection, the two cases were mild infections and did not need hospitalization or Intensive Care Unit. BA.2.86.1 (JN.1's parent lineage) replication kinetics on primary nasal epithelial cells (hNEC). WHO reported that the Level of risk is low, as currently there are no reports of elevated disease severity associated with this variant, JN.1 in comparison with parent BA.2.86 lineage carries the additional spike mutation L455S that significantly enhances immune evasion capabilities.

WHO Recommendations for COVID-19 Vaccine Antigen Composition Given the current SARS-CoV-2 evolution and the breadth of immune responses demonstrated by monovalent XBB.1.5 vaccines, there is only limited data on the cross-neutralization of JN.1 so vaccination programs can continue to use any of the WHO emergency-use listed or prequalified COVID-19 vaccines.

Keywords: COVID-19, JN.1, BA.2.86, XBB.1.5, Egypt.

Introduction:

JN.1 was monitored as a member of the parent lineage, BA.2.86, which is categorized as a variant of interest (VOI). Nonetheless, JN.1 has been reported in many countries in recent weeks, and its prevalence has been rising quickly worldwide. As a result, it currently accounts for the great majority of descendent lineages of BA.2.86 reported to GISAID (1). WHO categorizes JN.1 as a distinct variant of interest (VOI) from the parent lineage BA.2.86 because of its quickly spreading nature (1).

JN.1 is a descendant lineage of BA.2.86, with the earliest sample collected on 25 August 2023 (2). In comparison with the parent lineage BA.2.86, JN.1 has the additional L455S mutation in the spike protein. As of 16 December 2023, there were 7344 JN.1 sequences submitted to GISAID from 41 countries, representing 27.1% of the globally available sequences in epidemiological week 48 (27 November to 3 December 2023) (2).

JN.1 highly reported sequences in France, the USA, Singapore, Canada, the United Kingdom, and Sweden (1). On 28 December 2023, the Egyptian Ministry of Health and Population announced that two patients were diagnosed with COVID-19 JN.1 variant infection, the two cases were mild infections

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and did not need hospitalization or Intensive Care Unit (3).

JN.1 Variant growth and binding:

BA.2.86.1 (JN.1's parent lineage) replication kinetics on primary nasal epithelial cells (hNEC) have been observed to not be higher than other XBB-derived variants (4). It is yet unknown, nevertheless, how much of the increased fitness in primary hNECs and other cell types attributed to JN.1's high transmissibility in humans is due to non-spike mutations, The Omicron XBB.1.5 subvariant exhibits significantly stronger binding to the human ACE2 receptor, like that of BA.2.75 (5).

Growth advantage:

According to WHO the Level of risk is 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 (1).

Wastewater data:

Wastewater data from multiple countries approaching the winter season points to a large wave of SARS-CoV-2 infections in the community, however, that has not resulted yet in pressure on healthcare systems despite significant co-circulation of other viral and bacterial infections (6).

Severity and clinical considerations

WHO reported that the Level of risk is low, as currently there are no reports of elevated disease severity associated with this variant (1), a study from Belgium in ≥65-year-old patients has reported no difference in the odds of hospitalization with JN.1 compared to non-BA.2.86 variant (7), preliminary data from Singapore indicated a lower risk of hospitalization and severity in BA.2.86 elderly and younger cases (8). However, data is currently limited.

Laboratory diagnosis:

The current technologies used to detect COVID-19 in clinical laboratories are classified into main three categories, **I - The polymerase chain reaction (PCR) method**, **II - Immunological or serological methods** (Antigen and Detection) **III - Biochemical and hematological methods** which include **1-** Inflammatory biomarkers, 2. multi-organ damage/failure (Cardiac, Hepatic, and Renal) **(9).**

Most laboratory tests used for COVID-19 patients are:

1. Ferritin: is a significant biomarker for diagnosis of mild infection COVID-19 (71.4 %) (10).

2. LDH: Serum Lactate dehydrogenase LDH level is a good biomarker in COVID-19 mild infection (67.7%) (11).

3. CRP: C-reactive protein (CRP) levels could reflect COVID-19 severity and should be used as a key indicator for disease monitoring (12).

4. D-dimer: Many individuals with diabetes and immunosuppressive diseases face a higher probability of serious complications from COVID-19 infection so Anticoagulation therapy is suggested before the elevation of D-dimer level to avoid serious complications, a study in Egypt showed a high level of D-dimer 36.4% in mil infected COVID-19 patients (13).

5. Neutrophils and Lymphocytes count:

Neutrophilia has a sensitivity of 77.8% and lymphopenia has a sensitivity of 73% for diagnosis or prognosis of mild infection of COVID-19 patients (14).

Antibody escape:

JN.1 in comparison with parent BA.2.86 lineage carries the additional spike mutation L455S that significantly enhances immune evasion capabilities (15)

WHO reported that the Level of risk is moderate, as it is estimated that JN.1 has increased immune evasion relative to its parent BA.2.86.1 lineage that had a similar immune evasion as EG.5 the current most prevalent variant globally (1).

Neutralization assay:

A neutralization assay using rodent sera infected with BA.2.86 showed that NT50 against JN.1 was comparable to that against BA.2.86. However, the NT50 of XBB.1.5 and EG.5.1 breakthrough infection sera against JN.1 were significantly lower than that of HK.3 (2.6- to 3.1-fold) and BA.2.86 (3.8-fold) (16).

In another study, whereas XBB.1, EG.5.1, and BA.2.86.1 neutralization were globally similar in individuals who experienced XBB breakthrough infections, JN.1 displayed higher immune evasion properties compared to BA.2.86.1 (4). JN.1 was 2.9-to-4.3-fold resistant to sera from individuals vaccinated with an XBB.1.5 mRNA vaccine booster (17).

Antibody escape and severity of BA.2.86 and JN.1. The suggested timelines are estimates and will vary from one country to another: • Conduct neutralization assays using human sera, representative of the affected community(ies), and 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) (1).

JN.1 vaccine:

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, there are only limited data on cross-neutralization of JN.1. (18).

Recommendations for COVID-19 vaccine antigen composition

Given the current SARS-CoV-2 evolution and the breadth in immune responses demonstrated by monovalent XBB.1.5 vaccines against circulating variants, the TAG-CO-VAC advises retaining the current COVID-19 vaccine antigen composition, i.e. a **monovalent XBB.1.5** (e.g., hCoV-19/USA/RI-CDC-2-6647173/2022, GenBank: OQ054680.1, GISAID: EPI_ISL_16134259 or WHO Biohub: 2023-WHO-LS-01, GenBank: OQ983940, GISAID EPI_ISL_16760602) as the COVID-19 vaccine antigen, vaccination programs can continue to use any of the WHO emergency-use listed or prequalified COVID-19 vaccines (1).

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