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Characterization of SARS-CoV-2 Omicron XBB.1.5 sub-lineage: A review

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Abstract

The COVID-19 pandemic is characterized by the highly infectious severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), Omicron variant, which was first reported in Botswana and quickly spread as the dominant variant worldwide during early 2022, the start of 2023 brings a new subvariant of the Omicron variant of SARS-CoV-2, known as XBB.1.5. The Omicron XBB.1.5 subvariant is a sublineage of the XBB variant, a recombinant of two BA.2 sublineages, with an additional spike receptor-binding domain (RBD) change, S486P.

It is demonstrated that XBB.1.5 is just as immunologically evasive as XBB.1, the Omicron subvariant with the largest immune escape to date, using pseudotyped viral neutralization experiments. There is currently no data on real-world vaccine effectiveness against severe disease or death. At this time, there are no indications that XBB.1.5's infection severity differs from that of earlier Omicron sub-lineages that were circulating. The gold standard for COVID-19 diagnosis is reverse transcription-quantitative polymerase chain reaction (RT-qPCR) testing using upper respiratory tract swabs or saliva. there are no vaccine effectiveness (VE) estimates for XBB.1.5 yet, no specific data are currently available on the effectiveness of COVID-19 antiviral therapeutics.

Keywords: COVID-19, SARS-CoV-2, Omicron variant, XBB.1.5,

Introduction:

coronavirus disease 2019 (COVID-19) has been widely spreading in China in December 2019, and even in many other countries [1]. The WHO reported that more than 750 million cases of COVID-19, including approximately 6.83 million deaths, had occurred as of January 30, 2023 (https://covid19.who.int/) [2].

SARS-CoV-2, the virus that causes COVID-19, is constantly changing and accumulating mutations in its genetic code over time. New variants of SARS-CoV-2 are expected to continue to emerge. Some variants will emerge and disappear, while others will emerge and continue to spread and may replace previous variants [3].

The COVID-19 pandemic is characterized by the highly infectious severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron variant, which was first reported in Botswana and quickly spread as the dominant variant worldwide during early 2022 [4]. From August 2022, Omicron became classified into five main lineages, including BA.1, BA.2, BA.3, BA.4,

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BA.5, and several sublineages including, BA.1.1, BA.2.12.1, BA.2.11, BA.2.75, and BA.4.6 [5].

When compared to earlier SARS-CoV-2 variations, the BA.5 subvariant of the Omicron was the main subvariant producing COVID-19 between July and December 2022 in most countries. It also demonstrated a large escape from antibody neutralization [6,7].

The BA.4 sublineage BA.4.6, the BA.2 sublineage BA.2.75.2, the BA.2 lineage recombinant XBB.1, and the BA.5 sublineages BF.7 and BQ.1.1 have all been discovered in individuals with COVID-19 during the year 2022, These variants have the R346T mutation in the spike (S) protein [6,7]. The start of 2023 brings a new subvariant of the Omicron variant of SARS-CoV-2, known as XBB.1.5 [8]. The Omicron XBB.1.5 subvariant is a sublineage of the XBB variant, a recombinant of two BA.2 sublineages, with an additional spike receptor-binding domain (RBD) change, S486P [8,9].

The Omicron variety of SARS-CoV-2, B.1.1.529, currently has over 600 Pango lineages, making it impossible to list them all alphabetically by name [9]. However, it has been referred to as the "Kraken" subvariant in the media as a result of the increase in COVID-19 cases brought on by the XBB.1.5 Omicron infection in the US [10]. The word "Kraken" refers to the name of a legendary northern European giant sea monster, which was the topic of the apocalyptic poem by Lord Alfred Tennyson, published in 1830 [11].

XBB.1.5 Rapid Risk Assessment, 24 February 2023:

XBB.1.5 is a descendent lineage of XBB, which is a recombinant of two BA.2 descendent lineages. From 22 October 2022 to 21 February 2023, 45 193 sequences of the Omicron XBB.1.5 variant have been made available from 74 countries. Most of these sequences are from the United States of America (72.2%). The other countries include the United Kingdom (7.3%), Canada (5.0%), Germany (2.7%), Austria (1.8%), Denmark (1.1%), and France (1.0%) [12,13].

Growth rate:

XBB.1.5 (using the mutational proxy described under the heading The XBB.1.5 variant above) currently exhibits a daily growth advantage of 12% (95%CI 11-13%) in the US compared to other circulating variants, according to estimates provided by covSPECTRUM [14], based on data reported by the US to GISAID EpiCoV [15]. Comparatively, the daily growth advantage for BQ.1.1 is 5.6% (95%CI 5.3-5.7%), for CH.1.1 it is 5.0% (95%CI 4.6- 5.3%), and for XBB (excluding XBB.1.5) it is 4.2% (4.0-4.3%).

Binding to the human ACE2:

According to a preliminary study, XBB and XBB.1.5 have very similar antigenic properties, while XBB.1.5 exhibits significantly stronger binding to the human ACE2 receptor, similar to that of BA.2.75 [16]

Immune escape properties:

The most antibody-resistant variations to date, along with BQ.1 * variants, are XBB* variants. [17] It is demonstrated that XBB.1.5 is just as immunologically evasive as XBB.1, the Omicron subvariant with the largest immune escape to date, using pseudotyped viral neutralization experiments. [18] According to these data, sera from people who had breakthrough infections of BA.1, BA.5, or BF.7 and received three doses of the inactivated vaccine (Coronavac) or who had BA.5 infections after receiving three or four doses of the mRNA vaccine (BNT162b2 or mRNA-1273) did not result in high levels of neutralization titers against XBB.1.5. [19] There is currently no data on real-world vaccine effectiveness against severe disease or death.

Severity:

At this time, there are no indications that XBB.1.5's infection severity differs from that of earlier Omicron sub-lineages that were circulating. It is lower than Delta VOC based on body weight, pulmonary function, the efficacy of viral spread in the respiratory tissues, and histopathological assessments reported in a preprint study [20].

Diagnostics:

The gold standard for COVID-19 diagnosis is reverse transcription-quantitative polymerase chain reaction (RT-qPCR) testing using upper respiratory tract swabs or saliva because of this test's high sensitivity and specificity for SARS-CoV-2[21]. According to WHO, the diagnostic accuracy of routinely-used RT-PCR assays does not appear to be impacted by Omicron [22], and FIND, the global alliance for diagnostics, maintains a directory of diagnostic assays functional for different SARS-CoV-2 variants [23].

The US Food and Drug Administration (FDA) reports reduced, but not failed,

performance for the DxTerity SARS-CoV-2 RT PCR CE Test (DxTerity Diagnostics, Inc.) for the Omicron variant and sub-variants as well as reduced performance for the Clip COVID Rapid Antigen Test (Luminostics, Inc.) [24]. However, studies on the performance of diagnostic tests especially for XBB.1.5 are required since some assays may be affected by the mutations that Omicron lineage XBB.1.5 possesses. As a result, laboratories are recommended to validate the effectiveness of their current tests.

Laboratory biomarkers:

For every COVID-19 wave or mutation, five laboratory biomarkers must be investigated to detect the severity of infection and follow-up:

1. Ferritin: By directly suppressing the immune system and promoting inflammation, elevated ferritin levels have the potential to trigger a cytokine storm. According to reports, COVID-19 lethal results are associated with cytokine storm syndrome, Serum ferritin level is a good biomarker of infection in COVID-19 which increased in 71.4 % of moderate infected patients [25].

2. CRP: C-Reactive Protein (*CRP)* levels were positively correlated with mild COVID-19 infection of lung lesions with a sensitivity of 90.2%. CRP levels could reflect disease severity and should be used as a key indicator for disease monitoring [26].

3. D-dimer: a high level of D-dimer 36.4% in out-hospitalized patients with COVID-19, so 36.4% of outpatients and patients under home observation need Anticoagulation therapy to decrease the complications of COVID-19 infection, Since it is well-known that people with diabetes and immunosuppressive illnesses have a higher risk of developing major problems from COVID-19 infection, anticoagulation medication is advised before the elevation of D-dimer levels to prevent serious complications[27].

4. LDH: Serum Lactate dehydrogenase LDH level is a good biomarker of infection in COVID-19 Outpatients and patients under home observation increased by 67.7%, many other studies revealed LDH is a good marker for COVD-19 hospitalized patients and severe infection [28].

5. **peripheral Leukocyte:**

Neutrophils are immune cells that are well known to be present in various lung diseases, including viral respiratory disease [29]. Several cohort studies have reported that lymphopenia can predict prognosis in COVID-19 patients [30]. 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 (Outpatients and patients under home observation) [31].

Vaccination uptake data:

While there are no vaccine effectiveness (VE) estimates for XBB.1.5 yet, the currently available vaccines remain effective against severe disease due to previous and current Omicron variants dominant in the EU, with some evidence of waning over time. [32].

Therapeutics:

No specific data are currently available on the effectiveness of EU-authorised COVID-19 antivirals nirmatrelvir/ritonavir or remdesivir for XBB.1.5.

However, recent data indicate that the susceptibility of XBB to nirmatrelvir, remdesivir, and molnupiravir (authorized in the US) is similar to ancestral strains [33]. The effectiveness of monoclonal antibodies targeting the spike protein is expected to be considerably limited [34].

Conflict of interest:

There are no conflicts of interest.

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