



# Are We Facing a New Outbreak Caused By Sars-Cov2 Omicron Xbb.1.16 (Arcturus) Variant?

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## Abstract

Coronavirus disease 2019 has brought about a great threat to global public health. More than 762 million confirmed cases have been reported according to the statistics of the World Health Organization (WHO), including over 6 million deaths. By the end of February 2023, an XBB sublineage named XBB.1.16 emerged and was detected in various countries especially India, USA and UK. XBB.1.16 had an effective reproduction number (Re) that was 1.27 and 1.17 times higher than XBB.1 and XBB.1.5, respectively. Also, XBB.1.16 is very resistant to a variety of antiSARS-CoV-2 antibodies as well as XBB.1 and XBB.1.5. We conclude that we could face a new pandemic in the coming months. Coronavirus disease 2019 (COVID-19) has brought about a great threat to global.

**Keywords:** Covid-19; Sars-Cov2; Pneumonia; Omicron; Xbb.1.16; Arcturus; Variant

## Introduction

Coronavirus disease 2019 has brought about a great threat to global public health. More than 762 million confirmed cases have been reported according to the statistics of the World Health Organization (WHO), including over 6 million deaths. By the end of February 2023, an XBB sublineage named XBB.1.16 emerged and was detected in various countries especially India, USA and UK. XBB.1.16 had an effective reproduction number (Re) that was 1.27 and 1.17 times higher than XBB.1 and XBB.1.5, respectively. Also, XBB.1.16 is very resistant to a variety of anti-SARS-CoV-2 antibodies as well as XBB.1 and XBB.1.5. We conclude that we could face a new pandemic in the coming months. Coronavirus disease 2019 (COVID-19) has brought about a great threat to global.

Public health that has been surging for almost 4 years. More than 762 million confirmed cases have been reported according to the statistics of the World Health Organization (WHO), including over 6 million deaths [1]. By the end of February 2023, certain sublineages of the SARS-CoV-2 omicron XBB variant harboring the F486P substitution in the spike (S) protein (e.g. XBB.1.5 and XBB.1.9) were predominant worldwide [2]. Therefore, an XBB

sublineage named XBB.1.16 emerged and was detected in various countries especially India, USA and UK [3]. There are 2 substitutions at the S protein in XBB.1.16: E180V in the N-terminal domain, and T478R in the receptor-binding domain Compared to XBB.1.5. Also, XBB.1.16 has two substitutions in the S protein: E180V is in the N-terminal domain, and T478R in the receptor-binding domain Compared to XBB.1.5. XBB.1.16 had an effective reproduction number (Re) that was 1.27 and 1.17 times higher than XBB.1 and XBB.1.5, respectively, suggesting that XBB.1.16 will spread worldwide in a near future [4,5]. Also, the WHO classified XBB.1.16 as a variant under surveillance on March 30, 2023. In addition, a strong resistance of XBB.1.16 to BA.2 breakthrough infection sera and BA.5 was shown by neutralization tests [4-7]. A recent study suggests that XBB.1.16 is very resistant to a variety of anti-SARS-CoV-2 antibodies as well as XBB.1 and XBB.1.5 [4]. The same study suggests that compared to XBB.1 and XBB.1.5, XBB.1.16 has a greater growth advantage in the human population, while XBB.1.16's ability to exhibit deep immune evasion is comparable to XBB.1 and XBB.1.5. The acquired ability of XBB.1.16 may be due to different antigenicity of XBB.1.5; and/or mutations in the non-S viral protein(s) which may contribute to increased viral growth

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efficiency (4.7). This may lead us to conclude that we could face a new pandemic in the coming months. What we need to do is stop the spread of the XBB.1.16 or arcturus variant virus by (1) maintaining prevention measures including wearing masks, frequent ventilation, keeping physical distance, and washing hands; (2) developing variant-specific vaccines or vaccines containing several mutations which may be used to prevent the XBB.1.16 infection and transmission.

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## Conflicts of Interest

The authors declare no conflict of interest.

## Author's Contributions

Literature search, manuscript preparation and editing was done by R.A.A, manuscript review was carried out by A.B. The supervision was done by M.C and the whole manuscript was read and approved by all the author's.

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