



What is known about the SARS-CoV-2 Omicron BA.2 Sub-Variant?

Zafran Khan^{1,2,3,*#}; Daniya Ualiyeva^{2,4,5,#}

¹State Key Laboratory of Respiratory Disease, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, China.

²University of Chinese Academy of Sciences, Beijing, China.

³Center for Biotechnology and Microbiology, University of Swat, Pakistan.

⁴Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China.

⁵Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan.

***Corresponding Author(s): Zafran Khan**

State Key Laboratory of Respiratory Disease, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, 510530, China.

Email: zafrankhan807@yahoo.com & zafran@gibh.ac.cn

These authors contributed equally to this work

Received: Jul 03, 2022

Accepted: Jul 19, 2022

Published Online: Jul 21, 2022

Journal: Annals of Epidemiology and Public health

Publisher: MedDocs Publishers LLC

Online edition: <http://meddocsonline.org/>

Copyright: © Khan Z (2022). *This Article is distributed under the terms of Creative Commons*

Attribution 4.0 International License

Introduction

In November 2021, for the first time, a new variant omicron (B.1.1.529) of SARS-CoV-2 was reported to World Health Organization (WHO). It quickly became evident that the four genetically distant variants (BA.1, BA.1.1, BA.2, and BA.3.1) of viral lineages existed. Each of them had a unique set of mutations. In the beginning, the BA.1 was the most circulating variant worldwide. During this winter, the BA.1 was considered responsible for an entirely record-shattering spike in cases [5].

As the omicron surge subsided, at the start of 2022, the new BA.2 variant became predominant with a high transmissibility

rate in some countries, i.e. Denmark, India, England and the Philippines. Scientists suspect that BA.2 rapid spread is due to eight unique mutations on the spike protein genes, which make the BA.2 differs from BA.1 (**Figure 1**). These mutations speed up the transmission of BA.2 rather than being better able to evade immunity. For example, in Denmark, individuals infected with BA.2 were substantially more involved in infecting the nearby individuals or those who shared a common apartment than those with BA.1. Also, the researcher found that in England, the individuals infected with BA.2 took less time on average, thus accelerating the spread across the communities. Another

Cite this article: Khan Z, Ualiyeva D. What is known about the SARS-CoV-2 Omicron BA.2 Sub-Variant?. A Epidemiol Public Health. 2022; 5(2): 1083.



study reported that in Hong Kong, the estimated time of BA.1 in a public housing complex was 1.28 days to replicate. However, Hong Kong was suffered relatively higher from earlier variants are now getting pummeled by BA.2 again [1].

BA.2 rapid transmission is driving increases in the cases. However, it is also hard to disentangle the sub variant's effects from other factors. For example, Europe has just eased the COVID-19 protection measures, enabling any coronavirus variant to spread rapidly. Also, vaccinated individuals may experience waning immunity, especially if they are not boosted. While the countries, i.e. Hong Kong, which kept out the COVID-19 till now, were unable to build the herd immunity by infection in the last waves, with additional non vaccinated older individuals, putting the country at high risk.

On the other hand, in the United States, the COVID-19 cases are dropping dramatically, despite the BA.2 greater fraction of those dwindling cases. On March 12, the Centers for Disease Control and Prevention (CDC) estimated that the BA.2 is accountable for 23% of cases. The United States eased the COVID protection measure, which may lead to the possible risk of BA.2 spread. However, it is still unclear whether it may cause high morbidity and hospitalization [2].

During the early omicron wave, the BA.2 was difficult to track in positive PCR test and was nicknamed "stealth variant". In the beginning, the infection was either caused by the Delta or BA.1/omicron. The three genes were used to detect the coronavirus to detect the positive case. The BA.1 mutation caused it to come up negative for one of those three genes. That offered an easy way to distinguish the variants: Delta would test positive for all three genes, whereas BA.1 would test positive for only two. Nevertheless, BA.2 lacked the mutation that caused BA.1 to come up negative for one gene. That meant that when looking at PCR test results, BA.2 was indistinguishable from Delta - hence the "stealth variant" nickname. However, now that Delta has gone from dominant to rare, it is easy to distinguish the two versions of Omicron on a PCR test. Viruses that test positive for only two genes are BA.1, and those that test positive on all three are BA.2 [2]. The record-high surge of BA.1 was due to its evasion from the immune response activated by early strains. The antibodies produced during the early infections could not bind to the sub-variants. Though, individuals infected by the

BA.1 developed antibodies, which was able to abolish the BA.1 and lasted for several months.

When BA.2 upsurges to prominence, scientists worried that novel mutation in BA.2 will allow them to evade the immune response generated by the BA.1 infection. However, the scenario was fortunately different. The WHO claims that the immune response generated by the BA.1 provide strong protection against the BA.2. It is also speculated that the countries, i.e. United States, that have come through major spikes of BA.1 infection may immune and shield them from the major spike of BA.2 [5].

One of the striking features of omicron variants is that they can evade the vaccine generated immune response and surge the cases to the peak. However, the vaccine still protects the folk against the severity of disease, especially individuals who received the booster dose. However, the vaccine remained highly effective against the hospitalizations throughout the surge of the omicron variant. Also, it is found that the BA.2 is susceptible to some of the monoclonal antibodies, such as Evusheld used by AstraZeneca to treat COVID-19. Though the combination therapy of etesevimab and bamlanivmab as a single dose were unable to neutralize the BA.2 in lab experiments [3].

Currently, a new interesting study by Kawaoka and his collaborators at UW-Madison and the National Institute of Infectious Diseases, Tokyo, used the most clinically approved antibodies treatments in combination against the BA.2 in non-human primate cells. They tested the seven monoclonal antibodies, three combinations of antibodies, and three antiviral treatments against the BA.2 variant. They found that the antibodies therapy against the BA.2 was more effective than BA.1 or BA.1.1. However, the results they obtained could be translated into clinical settings is still a question mark (?). Also, they tested the clinically available antiviral compounds. They found that the BA.2 are susceptible to intravenous drug remdesivir and the active ingredients in two anti-COVID-19 pills, Paxlovid and Merck's molnupiravir, and were nearly as effective against BA.1 as they are against the original strain of SARS-CoV-2 [4].

Existing anti-COVID treatments are typically un-efficacious against new variants compared to early strains. This warrants a new and effective treatment that could potentially manage the ongoing unprecedented upsurge of the new BA.2 variant.

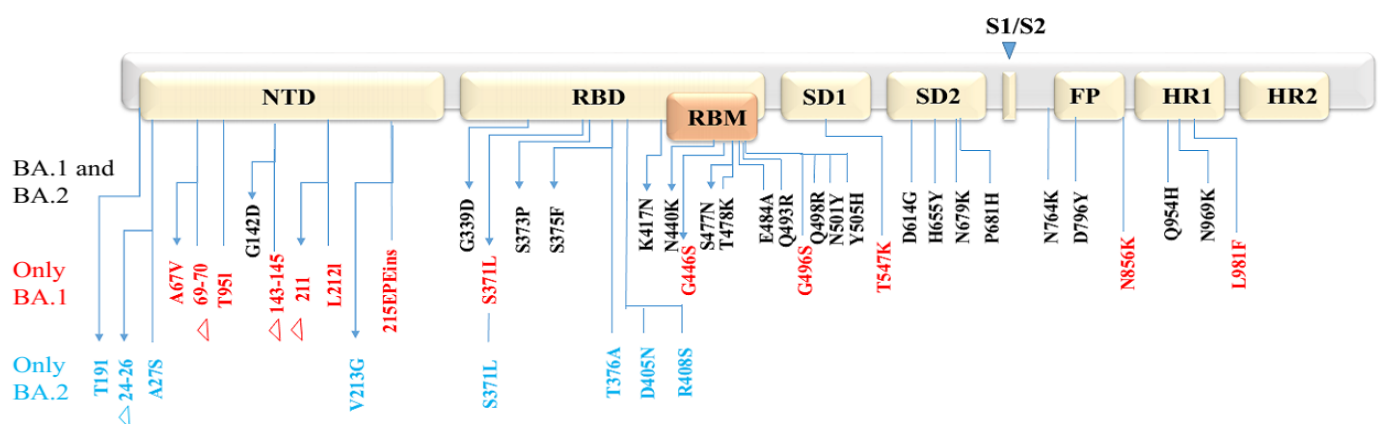


Figure 1: The mutations of spike protein in the omicron sub-lineages BA.1 and BA.2 in the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). NTD denotes (N-Terminal Domain), RBD (Receptor-Binding Domain), RBM (Receptor-Binding Motif), SD1 (Sub-domain 1), SD2 (Sub-Domain 2), FP (Fusion Peptide), HR1 (Heptad Repeat 1), and HR2 (Heptad Repeat 2).

Conflict of interest: The authors declare no conflict of interest.

References

1. CoVariants. Overview of variants/mutations. 2022.
2. Liu L, Iketani S, Guo Y, Chan JFW, Wang M, et al. Striking antibody evasion manifested by the Omicron variant of SARS-CoV-2. *Nature*. 2022; 602: 676-681.
3. World Health Organization. Weekly epidemiological update on COVID-19. 2022.
4. Yu J, Collier AY, Rowe M, Mardas F, Ventura JD, et al. Neutralization of the SARS-CoV-2 Omicron BA.1 and BA.2 Variants. *N Engl J Med*. 2022; 16: 1579-1580.