
Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

International Journal of Surgery 104 (2022) 106754

Contents lists available at ScienceDirect

International Journal of Surgery

journal homepage: www.elsevier.com/locate/ijsu

Correspondence

# Clinical features of SARS-CoV-2 Omicron BA.2; Lessons from previous observations – Correspondence

*Dear Editor,*

The SARS-CoV-2 Omicron variant (B.1.1.529) was first identified on November 19, 2021 in Gauteng, South Africa. The Omicron variant has spread rapidly from Africa to Europe, Asia, Australia and America (more than 171 countries) in a short time. Thus, the World Health Organization (WHO) announced Omicron as a Variant of Concern (VOC) on November 26, 2021 [1]. The Omicron variant outbreak is replaced with the Delta variant due to its more contagious, higher secondary attacks, and higher vaccine breakthrough rate [2,3]. Omicron variant has several sub-lineages including BA.1, BA.2, BA.3, BA.4, BA.5, and BA.2.12.1.

According to the literature, BA.2 has been detected as a dominant sub-lineage in countries, e.g., Denmark, the United Kingdom, India, the Philippines, and America [4]. BA.2 is about 1.5-fold more contagious than BA.1 and 4.2-fold more contagious than Delta [5]. BA.2 is more of a pathogen than BA.1 that causes more severe inflammation in the lungs [6]. In Denmark, BA.2 increases from 0.1% to 89.2% during ten weeks [7]. Clinical manifestations of BA.1 and BA.2 are most likely similar; nevertheless, there is potential for BA.2 immune evasions [8]. The SARS-Cov2 virus mutation rate is about two mutations per month. These mutations often occur on a spike and ORF1ab genes, affecting the virus's transmissibility, immune evasion, and reinfection with BA.2 after BA.1 infection [3,4]. Global health authorities have reported increasing BA.2 cases; however, our knowledge about BA.2 is limited. Determining the clinical characteristics of individuals infected with BA.2 could provide a new avenue for better management and a productive control program.

According to a comprehensive literature review in major electronic databases such as ISI Web of Science, PubMed, Scopus, and Google scholar, there are four observational studies regarding clinical features of patients infected with Omicron BA.2 sub-lineage data of 18,083 Omicron infected cases [2,3,9,10]. The mean age of BA.2 infected cases was 36.5 ± 2 years. 53.1% of these patients were females. Our estimates showed that there were 58.1% (95%CI: 37.0–76.6) asymptomatic, 32.9% (95%CI: 16.8–54.2) mild, 4.2% (95%CI: 1.2–14.0) moderate as well as 4.2% (95%CI: 2.4–7.3) experienced severe clinical manifestation. For all included cases, the fully vaccinated rate was 56.7% (95%CI: 40.7–71.4). Furthermore, the overall rate of need to ventilation, ICU admission, death, reinfection was 0.8% (95%CI: 0.3–2.2), 0.6% (95%CI: 0.4–1.0), 0.8% (95%CI: 0.4–1.8), 1.4% (95%CI: 0.1–17.2), respectively. Also the average hospitalization length stay was 12.0 ± 3 days. According to our analysis, there are no significant abnormalities in laboratory findings of BA.2 infected patients. Regarding laboratory findings, WBC: 5.29 ± 0.07 (5.15–5.42) X $10^9$ L, Neutrophil: 2.95 ± 0.01 (2.69–3.22) X $10^9$ L, Lymphocyte: 1.38 ± 0.03 (1.00–1.75) X 109 L, Platelet: 220.0 ± 0.16 (212.16–227.84) X $10^9$ L, CRP: 3.15 ± 0.01 (2.94–3.36) mg/L, D-dimer: 0.49 ± 0.05 (0.03–0.95) mg/L, ALT: 16.45 ± 0.2 (15.38–17.52) U/L, as well as, AST: 21.23 ± 0.1 (17.76–24.69) U/L that all being in normal references range. As a result, BA.2 infection does not appear to be severe, which is confirmed in our statistical estimates of clinical features or laboratory findings. Next, we compared the clinical aspects of BA.2 and BA.1. Our findings show that there is no significant difference in gender distribution. (OR: 1.03; 95%CI: 094–1.14; *p*-value: 0.4 for females as well as OR: 0.96 (95%CI: 0.87–1.05; *p*-value: 0.5 in males), ICU admission (OR: 1.63; 95%CI: 0.20–13.8; *p*-value: 0.5), need to ventilation (OR: 1.5; 95%CI: 0.22–8.81; *p*-value: 0.6), reinfections (OR: 0.87; 95%CI: 0.41–1.84; *p*-value: 0.7) between B.2 and BA.1. However, mortality rate was significantly decreased in BA.2 than BA.1 (OR: 0.19; 95%CI: 0.08–0.44; *p*-value: 0.05); also, hospital admission rate was significantly higher in BA.2 compared than BA.1 (OR 1.38; 95%CI: 0.92–2.07; *p*-value: 0.05). Therefore, BA.2 is less severe than previous VOCs, especially the Delta variant; Nevertheless, BA.2 is more contagious than BA.1 but has no meaningful difference in disease severity outcomes. We also showed that BA.2 infected cases who received fully vaccinated tended to be asymptomatic (OR: 2.14; 95%CI: 1.29–3.55; *p*-value: 0.03).

Our recent statistical investigation of retrospective observational studies suggested that BA.2 is clinically less severe than previous waives. There are no significant differences between BA.2 and BA.1 concerning age, sex, SARS-CoV-2 reinfection, or hospitalization with severe clinical characteristics; however, the hospital admission rate was higher in BA.2 while the mortality rate was less than BA.1, which represents BA.2 more contagious but not severe than BA.1. Our findings are consistent with previous documents. We have shown that BA.2 cases that have previously received full vaccination often tend to present the BA.2 infection in asymptomatic form. Therefore, mass vaccination could be a helpful strategy in stimulating a robust immune response against Omicron BA.2.

## Provenance and peer review

Not commissioned, internally peer-reviewed.

## Data statement

Not applicable for this study.

## Ethical Approval

Not applicable for this study.

## Sources of funding for your research

Not applicable for this study.

https://doi.org/10.1016/j.ijsu.2022.106754
Received 20 June 2022; Accepted 1 July 2022
Available online 5 July 2022

## Research Registration Unique Identifying Number (UIN)

1. Name of the registry: Not applicable
2. Unique Identifying number or registration ID: Not applicable
3. Hyperlink to your specific registration (must be publicly accessible and will be checked): Not applicable

## Author contribution

Saeed Sahebi contribue in review and editing. Masoud Keikha contribue in conceptioal, study design, review of the literatures, writing the draft and revision.

## Guarantor

Not applicable for this study.

## Declaration of competing interest

There is no conflict of interest.

## References

[1] S. Arora, V. Grover, P. Saluja, Y.A. Algarni, S.A. Saquib, S.M. Asif, K. Batra, M. Y. Alshahrani, G. Das, R. Jain, A. Ohri, et al., Literature review of omicron: a grim reality amidst COVID-19, Microorganisms 10 (2) (2022) 451.

[2] H. Zhang, Z. Weng, Y. Zheng, M. Zheng, W. Chen, H. He, X. Ye, Y. Zheng, J. Xie, K. Zheng, J. Zhang, et al., Epidemiological and Clinical Features of SARS-CoV-2 Omicron Variant Infection in China: A Retrospective Study. https://doi.org/10.2139/ssrn.4128857, 2020.

[3] D. Loconsole, F. Centrone, A. Sallustio, M. Accogli, D. Casulli, D. Sacco, R. Zagaria, C. Morcavallo, M. Chironna, et al., Characteristics of the first 284 patients infected with the SARS-CoV-2 omicron BA. 2 subvariant at a single center in the apulia region of Italy, january–march 2022, Vaccines 10 (5) (2022) 674.

[4] Y. Hirotsu, M. Maejima, M. Shibusawa, Y. Natori, Y. Nagakubo, K. Hosaka, H. Sueki, H. Mochizuki, T. Tsutsui, Y. Kakizaki, Y. Miyashita, et al., Classification of Omicron BA. 1, BA. 1.1 and BA. 2 sublineages by TaqMan assay consistent with whole genome analysis data, medRxiv (2022), https://doi.org/10.1101/2022.04.03.22273268.

[5] F.P. Lyngse, C.T. Kirkeby, M. Denwood, L.E. Christiansen, K. Mølbak, C.H. Møller, R.L. Skov, T.G. Krause, M. Rasmussen, R.N. Sieber, T.B. Johannesen, et al., Transmission of SARS-CoV-2 omicron VOC subvariants BA. 1 and BA. 2: evidence from Danish households, medRxiv (2022), https://doi.org/10.1101/2022.01.28.22270044.

[6] D. Yamasoba, I. Kimura, H. Nasser, Y. Morioka, N. Nao, J. Ito, K. Uriu, M. Tsuda, J. Zahradnik, K. Shirakawa, R. Suzuki, et al., Virological characteristics of SARS-CoV-2 BA. 2 variant, bioRxiv (2022), https://doi.org/10.1101/2022.02.14.480335.

[7] J. Fonager, M. Bennedbæk, P. Bager, J. Wohlfahrt, K.M. Ellegaard, A.C. Ingham, S. M. Edslev, M. Stegger, R.N. Sieber, R. Lassauniere, A. Fomsgaard, et al., Molecular epidemiology of the SARS-CoV-2 variant omicron BA. 2 sub-lineage in Denmark, 29 november 2021 to 2 january 2022, Euro Surveill. 27 (10) (2022), 2200181.

[8] J. Huang, G. Zeng, Epidemiology of the SARS-CoV-2 variant Omicron BA. 2–vigilance needed, Euro Surveill. 27 (13) (2022) 22, 00254.

[9] H. Xu, X. Huang, H. Xu, M. Sun, X. Liu, M. Zhang, X. Zhang, C. Niu, H. Tian, J. Li, H. Hu, et al., Clinical characteristics of hospitalized patients in Binzhou, China during periods of the SARS-CoV-2 Omicron variant BA. 2 predominance: a single-centered, retrospective, observational study, bioRxiv (2022), https://doi.org/10.21203/rs.3.rs-1648125/v1.

[10] J.A. Lewnard, V.X. Hong, M.M. Patel, R. Kahn, M. Lipsitch, S.Y. Tartof, et al., Clinical outcomes associated with SARS-CoV-2 Omicron (B. 1.1. 529) variant and BA. 1/BA. 1.1 or BA. 2 subvariant infection in southern California, Nat. Med. (2022), https://doi.org/10.1038/s41591-022-01887-z.

Saeed Sahebi
*Student Research Committee, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran*

Masoud Keikha*
*Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran*

* Corresponding author.
*E-mail address:* keikham971@mums.ac.ir (M. Keikha).