



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.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

OPINION

Is Omicron the last SARS-CoV-2 Variant of Concern?

Farid Rahimi,^a and Amin Talebi Bezmin Abadi^b

^aResearch School of Biology, The Australian National University, Ngunnawal and Ngambri Country, Canberra, ACT, Australia

^bDepartment of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran

Received for publication December 10, 2021; accepted January 12, 2022 (ARCMED-D-21-01569).

Millions have died due to the COVID-19 pandemic. The irrepressible propensity of the pandemic, which was highlighted by the outbreak of the Delta variant, should not be underestimated. The Omicron SARS-CoV-2 variant is thought to have originated from Africa. Sequences of the omicron variant show that it carries the highest number of point mutations detected in a betacoronavirus. High hospitalization numbers due to the Omicron variant has retriggered precautionary restrictions and border closures even in countries which have attained herd immunity by mass vaccinations. Surveillance systems for accurate screening of the Omicron variant are needed to guide implementation of hygiene principles and restrictions. Development of vaccines against the variants is important as the pandemic evolves. Whether Omicron is the last variant depends on the success of the local and global public-health strategies against SARS-CoV-2. © 2022 Instituto Mexicano del Seguro Social (IMSS). Published by Elsevier Inc. All rights reserved.

Key Words: Delta variant, Omicron variant, Mutations, Vaccine, SARS-CoV-2, South Africa, Variant of concern.

When the pneumonia of unknown etiology was reported in Wuhan, China, a pandemic of this scale was inconceivable. The virus was called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) as the cause of the coronavirus disease 2019 (COVID-19). This highly transmissible virus infected more than 262 million cases and caused more than 5.2 million fatalities as of 30 November 2021 (<https://www.worldometers.info/coronavirus/>). SARS-CoV-2 is a single-stranded-RNA virus with a genome that is prone to mutations in relatively short periods of time (1). Millions of sequences have shown that only few mutations effectively cause a more severe disease with high transmissibility and infectivity. The viral genetic variations have affected the pandemic course in 2021. The new variants have caused new peaks of infections globally (2–4). Following mass vaccinations in five continents, many countries have eased or lifted the pandemic-related restrictions; however, experts

expected new waves of the positive cases (5–7). Availability of mass-sequencing facilities enabled many countries to actively track emergence of the new SARS-CoV-2 variants (8), leading to discoveries of many variants, including variants of interest (VOIs) or variants of concerns (VOCs) (9).

In late November 2021, news of emergence of a new variant, called B.1.1.529 or Omicron, triggered an urgent WHO meeting on 26 November 2021 to critically assess the various aspects of the variant reported by South Africa (10). The initial patient clusters infected were, however, identified by sequencing in Botswana, confirming that the dominating variant was not Delta. According to the latest news, at least 50 countries have confirmed Omicron cases; however, this number is growing (According to the <https://www.gisaid.org/hcov19-variants/>: December 2021).

The rapid spread of Omicron in South Africa is concerning because of its many mutations. The Omicron genome carries at least 50 new mutations with 30 located in the sequence of the viral Spike protein, which has been the target of developed vaccines (11). Two years into the pandemic, new viral variants have emerged with point mutations mainly in the Spike protein. According to updated GISAID sequence analyses (<https://www.gisaid.org>).

Address reprint requests to: Amin Talebi Bezmin Abadi, PhD, Associate Professor, Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Room 8, First floor, P.O. Box 14115-111, Tehran, Iran; Phone: (+98) 82884883; Lab: (+98) 82884830; E-mail: amin.talebi@modares.ac.ir

20I (Alpha, V1) (B.1.1.7)	20H (Beta, V2) (B.1.351)	20J (Gamma, V3) (P.1)	21A (Delta) (B.1.617.2)	21B (Kappa) (B.1.617.1)	21K (Omicron) (BA.1)	21L (BA.2)	21D (Eta) (B.1.525)	21F (Iota) (B.1.526)	21G (Lambda) (C.37)	21H (Mu) (B.1.621)
Shared mutations										
Sort by: Commonness <input type="radio"/> Position <input checked="" type="radio"/>										
	S: L 18 F	S: L 18 F								
			S: T 19 R			S: T 19 I				
		S: P 26 S				S: P 26 -				
					S: A 67 V		S: A 67 V			
S: H 69 -					S: H 69 -		S: H 69 -			
S: V 70 -					S: V 70 -		S: V 70 -			
					S: T 95 I			S: T 95 I		S: T 95 I
					S: G 142 -	S: G 142 -				
					S: V 143 -	S: V 143 -				
S: Y 144 -					S: Y 144 -	S: Y 144 -	S: Y 144 -			S: Y 144 S
					S: Y 145 D	S: Y 145 D				S: Y 145 N
							S: D 253 G		S: D 253 N	
					S: G 339 D	S: G 339 D				
					S: S 371 L	S: S 371 F				
					S: S 373 P	S: S 373 P				
					S: S 375 F	S: S 375 F				
	S: K 417 N	S: K 417 T			S: K 417 N	S: K 417 N				
					S: N 440 K	S: N 440 K				
			S: L 452 R	S: L 452 R					S: L 452 Q	
					S: S 477 N	S: S 477 N				
			S: T 478 K		S: T 478 K	S: T 478 K				
	S: E 484 K	S: E 484 K		S: E 484 Q	S: E 484 A	S: E 484 A	S: E 484 K	S: E 484 K		S: E 484 K
					S: Q 493 R	S: Q 493 R				
					S: Q 498 R	S: Q 498 R				
S: N 501 Y	S: N 501 Y	S: N 501 Y			S: N 501 Y	S: N 501 Y				S: N 501 Y
					S: Y 505 H	S: Y 505 H				
S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G	S: D 614 G
		S: H 655 Y			S: H 655 Y	S: H 655 Y				
					S: N 679 K	S: N 679 K				
S: P 681 H			S: P 681 R	S: P 681 R	S: P 681 H	S: P 681 H				S: P 681 H
	S: A 701 V							S: A 701 V		
					S: N 764 K	S: N 764 K				
					S: D 796 Y	S: D 796 Y				
			S: D 950 N							S: D 950 N
					S: Q 954 H	S: Q 954 H				
					S: N 969 K	S: N 969 K				

Figure 1. Mutations shared among the variants of interest and concern.

org/hcov19-variants/), of 183 submitted sequences, 124 (67%) were reported in South Africa until 30 November 2021. Comparison of the sequences of all the variants of concern and variants of interest shows that Omicron shares many mutations with four other VOCs, including Alpha, Beta, Gamma, and Delta (Figure 1. <https://covariants.org/shared-mutations>). For example, P681H is shared among Omicron and two VOCs (Alpha and Delta). D614G, the most common mutation, is present also in the

Omicron genome. These Omicron mutations has raised concern among the scientists and decision-makers, calling for adaptation of strategies in the fight against SARS-CoV-2. Initial assessments suggest that the Omicron variant could more avidly bind to the human host cells than the former dominant variants, including Alpha and Delta (12,13). The Omicron mutations have implications for its functional biology, potentially adversely affecting the vaccine effectiveness worldwide. If the effectiveness of

the approved vaccines are affected, the Omicron variant may not be the last VOC we encounter during this pandemic.

Whether hospitalizations due to the Omicron variant will increase globally is unpredictable now. However, considering restoring some public-health countermeasures is prudent to avoid further casualties, even in countries with optimal rates of full vaccination. Detection and spread of the Omicron VOC in many more countries is expected; however, avoiding case surges with Delta and Omicron variants is ideal to assist the healthcare facilities in many countries. Nevertheless, some experts predict that the disease due to the Omicron VOC is less severe than with other variants. Emergence of the Delta variant was not reported opportunely, but Omicron was quickly reported by the relevant authorities. Subsequently, border closures and counter-responses were implemented to curb the spread of the variant (14).

While mass production of the vaccines in 2021 is an important health measure against the pandemic, persistent emergence of the new SARS-CoV-2 variants will likely require additional countermeasures, including longer quarantine periods, physical distancing especially indoors, travel bans, mask wearing, and targeted vaccination campaigns. Reducing the chance of emergence of new viral variants may be difficult; however, preventing uncontrolled spread of the virus may facilitate this ideal aim. Sequencing facilities to accurately screen and track the spread of the variants is necessary for guiding the public-health countermeasures. Developing vaccines with broader efficacies is critical, considering the emergence of the variants such as Omicron.

Conflict of Interest

None.

Funding

None.

Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.arcmed.2022.01.001](https://doi.org/10.1016/j.arcmed.2022.01.001).

References

1. Hu B, Guo H, Zhou P, et al. Characteristics of SARS-CoV-2 and COVID-19. *Nat Rev Microbiol* 2021;19:141–154.
2. Tang JW, Tambyah PA, Hui DS. Emergence of a new SARS-CoV-2 variant in the UK. *J Infect* 2021;82:e27–e28.
3. Zhang W, Davis BD, Chen SS, et al. Emergence of a novel SARS-CoV-2 variant in Southern California. *JAMA* 2021;325:1324–1326.
4. Hodcroft EB, Zuber M, Nadeau S, et al. Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. *Nature* 2021;595:707–712. doi:10.1038/s41586-021-03677-y.
5. Planas D, Veyer D, Baidaliuk A, et al. Reduced sensitivity of SARS-CoV-2 variant Delta to antibody neutralization. *Nature* 2021;596:276–280.
6. McCallum M, Walls AC, Sprouse KR, et al. Molecular basis of immune evasion by the delta and kappa SARS-CoV-2 variants. *Science* 2021:eabl8506 Preprint. doi:10.1101/2021.08.11.455956.
7. dos Santos MC, Júnior ECS, de Almeida J, et al. First reported cases of SARS-CoV-2 sub-lineage B. 1.617.2 in Brazil: an outbreak in a ship and alert for spread. 2021.
8. Tang JLW, Toovey OTR, Harvey KN, et al. Introduction of the South African SARS-CoV-2 variant 501Y.V2 into the UK. *J Infect* 2021;82:E8–E10.
9. Koyama T, Platt D, Parida L. Variant analysis of SARS-CoV-2 genomes. *Bull World Health Organ* 2020;98:495–504.
10. Steinhäuser G. Omicron variant drives rise in Covid-19 hospitalizations in South Africa hot spot: The Wall Street Journal; 2021. Available from: <https://www.wsj.com/articles/omicron-variant-drives-rise-in-covid-19-hospitalizations-in-south-africa-hot-spot-11638185629>. (Access November 29, 2021).
11. Yang J, Wang W, Chen Z, et al. A vaccine targeting the RBD of the S protein of SARS-CoV-2 induces protective immunity. *Nature* 2020;586:572–577.
12. Del Rio C, Malani PN, Omer SB. Confronting the Delta variant of SARS-CoV-2, summer 2021. *JAMA* 2021;326:1001–1002.
13. Grint DJ, Wing K, Houlihan C, et al. Severity of SARS-CoV-2 Alpha variant (B.1.1.7) in England. *Clin Infect Dis* 2021:ciab754. doi:10.1093/cid/ciab754.
14. Güvendik MO, Kavak G. World closing its doors to African countries due to omicron: Anadolu Agency; 2021. Available from: <https://www.aa.com.tr/en/americas/world-closing-its-doors-to-african-countries-due-to-omicron/2434131>. (Access November 30, 2021).