

Review Article

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Omicron Variant: An Acute Public Health Problem

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Abstract

The coronavirus disease 2019 (COVID-19) has persisted as a pandemic for just over two years; vaccines have been developed to prevent the clinical disease and treatment regimens improved upon, but severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) appears to be up to the task, coming up with mutations resulting in multiple variants, alpha, beta, delta, Omicron and so much more. The most important and recent one, the omicron variant, with an amazing 50 genetic mutations, 37 of which are on the spike protein, has emerged as a massive public health problem, rapidly replacing the delta-variant and the predominant variant in many countries, and foretelling a new and likely more devastating wave of the pandemic. To deliver a comprehensive overview to global health authorities and prospective readers worldwide, we detailed in this review, the properties of the Omicron Variant, its infectiousness, and the perils it poses to the general public; we also discuss the situation in Nigerian and the rest of the world alike.

Keywords: Omicron, Variant, Sars-Cov-2, Public health, Mutation, Pandemics

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Introduction

The severe acute respiratory syndrome (SARS), is a respiratory infection with pandemic potentials, the first epidemic of which occurred in 2002. It is not unrelated to the Middle East respiratory syndrome (MERS), the cause of an outbreak of the respiratory disease in 2012 in the Middle Eastern countries causing severe respiratory diseases, and persisting with over 61 new cases recorded in 2020 and 14 hitherto in 2021.^{1,2} The causative agents of these diseases are coronaviruses, named after their crown-shaped structure visible in an electron micrograph.

Of interest, today is the coronavirus disease 2019 (COVID-19) caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus beta-coronavirus of the family Coronaviridae. The cause of the COVID-19 pandemic originated in Wuhan city, China in December 2019. "On 30 January 2020, Dr Tedros Adhanom Ghebreyesus, the Director-General of the World Health Organization (WHO) declared the novel coronavirus outbreak a public health emergency of international concern (PHEIC), WHO's highest level of alarm".³ "At that time, there were 98 cases and no deaths in 18 countries outside China."³ As of the time of writing this manuscript, there have been 275297725 cases worldwide and 5 373 527 deaths.⁴ This depicts the level of public health importance this pandemic has assumed over the past two years.

The SARS-CoV-2 virus such as other highly variable viruses is prone to mutations resulting in multiple variants some with various lineages. The variants are classified by the WHO into variants being monitored (VBM) - Alpha (B.1.1.7 and Q lineages), Beta (B.1.351 and descendent lineages), Gamma (P.1 and descendent lineages), Epsilon (B.1.427 and B.1.429), Eta (B.1.525), Iota (B.1.526), Kappa (B.1.617.1), 1.617.3, Mu (B.1.621, B.1.621.1), and Zeta (P.2), variants of interest (VOIs), variants of concern (VOCs) - Delta (B.1.617.2 and AY lineages), and Omicron (B.1.1.529 and BA lineages), and variants of high consequence (VOHCs). As of today, there are no VOHC.⁵ The mutations that determine the infectivity and antibody resistance of SARS-COV-2 determine the placement of each variant into the above classification, and these mutations occur at the Spike (S) protein receptor-binding domain (RBD).6

Omicron: origin and characteristics

A new variant of the SARS-CoV-2 virus has recently been identified on 23 November in South Africa by researchers utilizing genome sequencing to investigate an alarming rise in the number of cases there. Daily cases went from 274 on 11 November to 1000 a fortnight later and currently number more than 8500.⁷ On the 26th of November, the WHO identified this new variant as Omicron (B.1.1.529) (Figure 1), and as a VOC,⁶ due to the high number of mutations on its S protein leading

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Figure 1. A computer-generated image of the B.1.1.529 (Omicron) variant of Covid-19 (WHO, 2021).

to changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity.⁶

The Omicron (B.1.1.529) differs from other variants in having about 37 mutations on its S protein compared to the Wuhan-Hu-1 spike protein, 13 of these changes are unique while other changes are known from variants of interest and/ or concern⁸ Specifically, 11 mutations, including 6 deletions and 1 insertion, are located in the N-terminal domain (NTD), and mutations N211 Δ and insertions 214EPE are special. Some of the deletions are found in other VOC and most likely contribute to a reduction of antibody binding or an increased expression of the spike protein.9-14 Another 15 mutations are found in the RBD, of which, S371L, G339D, S375F, and S373P are special, and several were previously shown to modulate angiotensin-converting enzyme 2 (ACE2) binding and/or antibody evasion.9-11,13,14 Furthermore, five mutations reside between the RBD and S1/S2site, including the unique mutation T547K and mutation P681H that may modulate cleavage at the S1/S2 site by the host protease furin.^{15,16} Finally, five mutations are present in the S2 subunit, all of them special.8,17

The mutations by the genomic regions include:

- "Spike protein: A67V, Δ69-70, T95I, G142D, Δ143-145, Δ211, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F (Half (15) of these 30 changes are located in the receptor binding domain-RBD (residues 319–541))
- 2. ORF1ab
- 3. nsp3:K38R, V1069I, Δ1265, L1266I, A1892T
- 4. nsp4:T492I
- 5. nsp5:P132H
- 6. nsp6:Δ105-107, A189V
- 7. nsp12: P323L
- 8. nsp14: I42V
- 9. Envelope protein: T9I

- 10. Membrane protein: D3G, Q19E, A63T
- 11. Nucleocapsid protein: P13L, Δ31-33, R203K, G204R".¹⁸

As observed, most of the mutations are on the S protein and have resulted in vastly increased infectivity, transmission, and severity of the Omicron variant. Compared to the delta variant which has only five mutations in its spike protein, the omicron variant is about 2.8 times as infectious as the delta strain and 13 times as infectious as the alpha variant.⁶

In this present study, we discuss the origin, and characteristics of the Omicron variant, the present public importance in Nigeria, and other countries, and the way forward to overcome the prevalence of the Omicron variant.

Omicron in Nigeria

Nigeria Centre for Disease Control (NCDC) on December 1st confirmed the first three cases of Omicron variant in Nigeria.¹⁹ The Omicron variant is also referred to as B.1.1.529 lineage. It was confirmed in travellers returning from South Africa who arrived in Nigeria. The monotonous travel test is essential for all international travellers and Genomic sequencing at the NCDC through its National Reference Laboratory (NRL), Abuja and network of other testing laboratories confirmed Nigeria's first case of the Omicron variant, also known as the B.1.1.529 lineage. The sample obtained for the stipulated day two test for all travellers to Nigeria was positive for this variant in three persons with a history of travel to South Africa. But of recent, NCDC stated no person has died of B.1.1.529 SARS-CoV-2 lineage in Nigeria as the variant surges across the country.

Omicron in other countries

The SARS-CoV-2 omicron strain, first discovered on November 24 in South Africa, has already been discovered in 57 countries. Early evidence suggests that omicron is more transmissible than earlier strains, especially because it has surpassed delta as the most common variety in South Africa, and there is evidence that it is associated with a higher risk of reinfection.²⁰ The first incidence of B.1.1.529 was reported in the United States on December 1, 2021, in a person returning from a trip to South Africa. On December 2, 2021, a second case was reported in an individual with no prior overseas travel history who similarly attended a convention in the days leading up to symptom start. In addition to Europe, the Omicron variation has been found in travel-related cases in the United Kingdom, Brazil, Canada, Australia, Hong Kong, Israel, Sweden, Japan, and Norway. Individuals without a history of travel to southern Africa have been reported in a few nations, including the United States.

Furthermore, by December 14, Omicron appears to have surpassed all other strains as the most prevalent. Without assuming that behaviour will alter in response to the variation, a million infections each day by December 24 will have doubled in 2.5 days.²¹ With some geographical changes, the growth rate in Denmark has been fairly similar, with a doubling period of about 2–3 days, reaching about 39% of all COVID-19 cases on December 14.²² Switzerland is not far behind, and Germany is not far behind either.²³ On December 17th Omicron appears to have become the most common variation in Scotland.²⁴ On December 13th it became the most common strain in Ontario.²⁵ On December 13, the strain appears to have overtaken the most common strains in the United States, expanding at a rate of 0.42 per day.²⁶ This was one day before the CDC announced that the strain had been discovered under invariant surveillance.²⁷ The strain may become the most prevalent in Belgium around December 25th,²⁸ and the Netherlands appears to be on the same track.²⁵ Other nations may lack timely information since their PCR tests do not employ Thermo Fisher TaqPath Assay or an equivalent to indicate Omicron. To detect Omicron or other developing strains, researchers recommend sampling at least 5% of COVID-19 patient samples.²⁹

Way forward

The exact characteristics of the Omicron version are unknown at this time. Given the spike mutations found in other VOCs, it is especially concerning that Omicron may have evolved with the potential to spread more easily among people and to withstand currently effective antibody treatments. This situation emphasizes the significance of maintaining current public health prevention measures, such as mask use, frequent ventilation, physical distance, and hand washing. These procedures are effective in stopping the spread of other variants, and they should be useful in stopping the spread of the Omicron variant, as well. Early diagnosis and quarantine are also important elements in limiting virus transmission during a pandemic.³⁰

Although some predictions suggest that the rapid spread of Omicron in South Africa could indicate the onset of a new pandemic wave around the world, the impact of this variety and what it signifies for the current epidemic remain unknown. In reality, the condition of Omicron spread in South Africa may differ significantly from that in other nations. In South Africa, for example, only approximately 24% of the population is properly vaccinated.³¹ This figure is significantly lower than the global average immunization rate of 42%.³¹ This could hasten the spread of Omicron in South Africa, underscoring the country's urgent need for increased vaccine coverage. Although the COVID-19 vaccinations' potency against variant viruses has decreased,³²⁻³⁵ it has been demonstrated that the vaccines are still useful in preventing serious infections, hospitalization, and death.³⁶⁻³⁸ It is also worth noting that low antibody levels in people who have been infected with SARS-CoV-2 or who have been vaccinated against it may encourage the evolution and selection of new variations. Several studies have found that serum neutralizing antibodies drop considerably six months after immunization and that further vaccination with a booster dose can restore and even improve vaccine efficacy.^{39,40} As a result, we feel that including an additional boosting dosage of the COVID-19 vaccine in the vaccination regimen would surely aid in the control of Omicron infection and spread.

The appearance of the Omicron variant in South Africa has been linked to an increased risk of SARS-CoV-2 reinfection, suggesting that the Omicron variant may be relevant to a significant ability to circumvent immunity from past infection.⁴¹ Furthermore, there is a lot of interest in seeing if the current COVID-19 vaccinations can protect against the Omicron version. According to the most recent research, COVID-19 vaccinations provide less immunity to the omicron form than other VOCs.⁴² Meanwhile, compared to the wild-type SARS-CoV-2, vaccinated individuals' sera had a 40% reduced neutralizing power against the Omicron variant.⁴³ These findings suggested that current COVID-19 vaccinations may not be as effective against the Omicron form of SARS-CoV-2 as they are against other SARS-CoV-2 variants. More data about the effectiveness of current COVID-19 vaccines need to be further investigated in the future. In the future, further information about the efficacy of current COVID-19 vaccines will be needed.

Conclusion

The origin, transmission capability, and immune-escape potential of the Omicron variety remain unknown in the aftermath of its appearance. It is also unclear whether further varieties based on Omicron may emerge in the future. However, there is no doubt that the Omicron version of SARS-CoV-2 will not be the last. The COVID-19 pandemic has become more difficult to control due to the constant appearance of new SARS-CoV-2 mutations. Fortunately, we

Review Highlights

What Is Already Known?

SARS is the first epidemic that occurred in 2002. It is related to the MERS that caused an outbreak of the respiratory disease in 2012 in the Middle Eastern countries, persisting with over 61 new cases recorded in 2020 and 14 hitherto in 2021. COVID-19 is caused by the SARS-CoV-2 virus betacoronavirus of the family Coronaviridae. The COVID-19 pandemic originated in Wuhan city, China in December 2019.

What Does This Study Add?

SARS-COV-2 virus similar to other highly variable viruses is prone to mutations resulting in multiple variants some with various lineages. The variants are classified by the WHO into VBM - Alpha (B.1.1.7 and Q lineages), Beta (B.1.351 and descendent lineages), Gamma (P.1 and descendent lineages), Epsilon (B.1.427 and B.1.429), Eta (B.1.525), Iota (B.1.526), Kappa (B.1.617.1), 1.617.3, Mu (B.1.621, B.1.621.1), and Zeta (P.2), VOI, VOC - Delta (B.1.617.2 and AY lineages), and Omicron (B.1.1.529 and BA lineages), and VOHC. The SARS-CoV-2 omicron strain, first discovered on November 24 in South Africa, has already been discovered in 57 countries. The NCDC on December 1st confirmed the first three cases of Omicron variant in Nigeria. It was confirmed in travellers returning from South Africa who arrived in Nigeria. The way forward from this global pandemic is early diagnosis and an efficient quarantine system to limit virus transmission. Also, an additional boosting dosage of the COVID-19 vaccine in the vaccination regimen would surely aid in the control of Omicron infection and spread.

have a wealth of expertise and strategies for dealing with novel coronaviruses, and we know what we need to do to prevent viral variations from spreading. Human society would win the war against COVID-19 with worldwide coordination and speedy data sharing.

Authors' Contributions

All authors contributed equally to researching for and the writing and proofreading of this manuscript, with EAA, contributing to the 'Abstract', 'Introduction', 'Omicron: Origin and Characteristics' and ROA the 'Omicron in Nigeria', 'Omicron in Other Countries, 'Way forward', and 'Conclusion'.

Conflict of Interest Disclosures

The authors declare that they have no conflict of interest.

Ethical Approval

Not applicable.

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