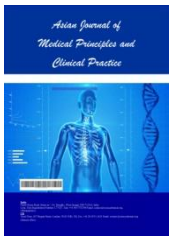

Asian Journal of Medical Principles and Clinical Practice

5(4): 250-259, 2022; Article no.AJMPCP.93240

Current Issue on Omicron COVID-19 Variants

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/93240

Review Article

Received 19 September 2022
Accepted 21 November 2022
Published 24 November 2022

ABSTRACT

Coronavirus Disease 2019 (COVID-19) according to the Nigeria Center for Disease Prevention and Control (NCDC) is a disease contracted from animals (zoonotic disease). Severe acute respiratory syndrome coronavirus (SARS COV-2) is the virus responsible for COVID-19. COVID-19 symptoms may develop within 14 days after infection with the virus and includes fever, headache, cough, difficulties with breathing, loss of smell and taste, and tiredness. In Africa, a new strain of COVID-19 was identified on the 24th of November, 2021 in South Africa and tagged B.1.1.529, it was reported to the World Health Organization (WHO), which later named it Omicron. In December, 2021, the first cases of the Omicron variant were confirmed in Nigeria and has recorded up 45 cases by 20th of the same month. It was reported that this three cases were identified in persons who arrived from South Africa the previous week. The Omicron variant is the dominant, and fast spreading variant of SARS Cov-2 across the world, and seven lineages of the variant has been identified so far since the naming of the strain and they include the Omicron B.1.1.529, BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5 lineages. Laboratory methods for the diagnosis of Omicron sub-variants is the same as those for the general testing of COVID-19 which includes polymerase chain reaction, rapid tests, and additional tests to distinguish between the sub-variants. Patients with the earlier strains of severe COVID-19 are known to respond well to corticosteroids like dexamethasone and IL6 receptor blockers like tocilizumab (Actemra). All preventive measures observed for general SARS-CoV-2 prevention are applicable for Omicron variants prevention and they include vaccination, staying at home, donning a mask in public, avoidance of congested

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places, keeping social distancing, ventilating indoor spaces, controlling potential exposure durations, washing hands frequently and for at least 20 seconds, practicing good hygiene, and avoiding touching the eyes, nose, or mouth with unwashed hands are all preventative measures to lessen the likelihood of Omicron variant infection. All the measures employed in the prevention of COVID-19 outbreak proved to be effective against the Omicron variant also. As efforts continue towards containing the spread and minimizing the emergence of more variants, it becomes necessary to update the public on the current happening regarding the Omicron variant.

Keywords: SARS-CoV-2; omicron; variant; coronavirus; challenges.

1. INTRODUCTION

Coronavirus disease (COVID-19) according to the Nigeria Center for Disease Prevention and Control (NCDC) is a disease contracted from animals (zoonotic disease) [1]. Severe acute respiratory syndrome coronavirus (SARS COV-2) is the virus responsible for COVID-19 [1-2]. According to Dërmaku-Sopjani and Sopjani [3], COVID-19 is at the moment the new public health issue of great concern which is threatening the entire globe [3]. According to reports, the virus was first discovered in bats and then spread to people in China in 2019 by unidentified intermediary species. Although the case fatality rate of COVID-19 is low, report suggested that when compared with its previous ancestors (SARS Cov and Middle east respiratory syndrome), SARS COV-2 spreads faster [3]. SARS-CoV-2 is currently responsible for approximately 1.16 million fatalities and 43.4 million confirmed cases worldwide, posing a major threat to public health on a global scale with still undetermined consequences.

A study carried out by Oran and Topol [4] revealed that COVID-19 symptoms may develop within 14 days after infection with the virus, although one-third of those exposed to the virus are asymptomatic. The WHO report also noted that averagely, symptoms can manifest between 5-6 days after exposure to the virus, although it can take up to 14 days [2]. The symptoms of COVID-19 usually range from fever [5] to headache, cough [6], difficulties with breathing, loss of smell and taste, and tiredness [7-9]. Gandhi et al. [10] reported that COVID-19 symptoms may delay for four to five days before manifesting. While the delay occurs, another research by Byrne et al. noted that the infected person would be able to transmit the virus between day one to four of contracting the disease [11]. For clarity purposes, the WHO categorized COVID-19 symptoms into most common, less common, and serious symptoms [2]. Tiredness, fever, cough and loss or taste and/or smell are classified as the common symptoms, while diarrhea, headache, sore throat, aches and pains, rashes on the skin, or toes or fingers discoloration, and redness, or irritation of the eyes are the less common symptoms, and finally, breath shortness or breathing difficulties, speech or mobility loss, or confusion, and chest pains are regarded as serious symptoms [2]. It is however worthy to note that COVID-19 symptoms vary based on the type of variant contracted by a patient [12].

As the genetic code is altered during genome replication (by genetic mutations or viral recombination), viruses like SARS-CoV-2 continue to evolve. According to the CDC report [13], proper understanding of the terms such as lineage, variant, recombinant, and mutation are necessary to gaining full insight of the subject being discussed. This report described lineage as a collection of genetically distinct viral strains that have a common ancestor, whereas, a variant refers to one or more changes in the DNA of one virus which makes it different from others. The combination of two variants gives rise to a recombinant, while mutation is the changes occurring in the DNA of the virus [13]. According to the WHO [14], each virus undergoes gradual evolution, including COVID-19's causative agent, SARS-CoV-2. The majority of alterations rarely or never affect the virus's characteristics. The virus's characteristics, such as how quickly it spreads, the severity of the accompanying sickness, or the effectiveness of vaccines, therapeutic drugs, diagnostic tools, or other public health and social measures, could be impacted by certain alterations.

With respect to Africa, a new strain of COVID-19 was identified on the 24th of November, 2021 in South Africa and tagged B.1.1.529, which was reported to the World Health Organization (WHO) [13]. According to Musa et al. the variant was later named 'Omicron' by the WHO on November 26th of the same year and categorized as variant of concern (VOC) [15]. A virus is categorized as a VOC if there is evidence of an increase in transmissibility, more severe disease,

a notable reduction in the ability of antibodies produced during prior infections or vaccinations to neutralize the virus, decreased effectiveness of treatments or vaccines, or failures in diagnostic detection [13]. Additionally, the Omicron variant has also been discovered in three more African countries (Botswana in the south, and Ghana and Nigeria in the West) [16]. It was further reported that 19 and 172 Omicron variant instances, have been recorded from Botswana and South Africa respectively, and both countries account for 62% of cases recorded globally [16]. In December, 2021, the first cases of the Omicron variant were confirmed in Nigeria according to Anadulo Agency's report [17]. It was reported that these three cases were identified in persons who arrived from South Africa the previous week. Further report showed that the patients were all asymptomatic, suggesting they could have transmitted the virus to other; prompting contact tracing as at the time of the event [17]. By December 20th, 2021, Nigeria had recorded 45 cases [18]. According to this report, Omicron is currently the dominant variant in Nigeria. This study therefore aims at updating the public on the current developments on Covid-19 Omicron variant with regards to Nigeria.

2. VARIANT NOMENCLATURE

In order to prioritize global research and monitoring, and eventually to guide the ongoing COVID-19 pandemic response, the WHO has been tracking and evaluating the development of SARS-CoV-2 in partnership with partners, specialist networks, national authorities, institutions, and researchers since January 2020 [14]. According to this report, the WHO grouped the emerging strains of SARS Cov-2 into Variants of Concern (VOC) and Variants of Interest (VOI) for the purpose of prioritizing worldwide research and surveillance, and eventually to guide the ongoing COVID-19 pandemic response [14].

According to the U.S CDC report on SARS Cov-2 variant classification, Omicron was designated as a Variant of Concern (VOC) by the SARS-CoV-2 Interagency Group (SIG) of the US government on November 30, 2021 [13]. The factors which formed the basis of this classification are: detection of cases linked to Omicron in numerous nations, including among people with no history of travel, the spike protein's substitutions, both in terms of quantity and position, transmission of the Delta version and its replacement in South Africa, data available for other variants with fewer spike protein mutations that show a decrease in neutralization by sera from vaccinated or recovering people, and details on other variants with fewer spike protein changes that shows a decreased sensitivity to monoclonal antibody therapies [13].

3. CLASSIFICATION

A study conducted by Del Rio et al. [19] described the Omicron variant as the dominant, and fast spreading variant of SARS Cov-2 across the world. The CDC [13] outlined seven lineages of the Omicron variants identified so far since the naming of the strain and they include the Omicron B.1.1.529, BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5 lineages. According to Quarleri et al. [20] and Gowrisankar et al. [21] researches, Omicron B.1.1.529 was the first of Omicron variants to be reported to the WHO by the network for Genomics Surveillance in South Africa on the 24th of November, 2021. Vitiello et al. [22] in their work cited that the first place Omicron was discovered was in Botswana and has emerged to become the most predominant strain in circulation worldwide.

A report by the WHO shows that Omicron is at the moment, the dominant strain of SARS CoV-2 circulating all globally, with over 98% viral sequence shared on Global Initiative on Sharing Avian Influenza (GISAID) after February 2022 [14]. Significant intra-VOC development has resulted from the continued transmission of these VOCs. Additionally, since its classification as a VOC by WHO on 26 November 2021, viruses part of the Omicron complex have continued to undergo changes, resulting to descendent lineages with different genetic constellations of mutations. Each constellation may or may not differ in the public health risk it poses, and each lineage that includes substitutions in important places may require more study to establish if its traits deviate or not from those that define the variety of concern they stem from [14]. Also, WHO has introduced a new group to its variation tracking system, called "Omicron subvariants under monitoring" to communicate to public health agencies internationally, which VOC lineages may require prioritized attention and monitoring. This became necessary following the Omicron VOC's widespread dissemination worldwide and the anticipated rise in viral diversity [14]. The Table below represents WHO new categorization tracking system for the Omicron SARS CoV-2 variant.

Table 1. Omicron sub-variants under tracking by WHO as of September 2022 [14]

Pango lineage[#] (+ mutation)	GISAID clade	Nextstrain clade	Relationship to circulating VOC lineages	Spike genetic features	Earliest documented samples
BA.5.1 (+V445X)	GRA	22B	BA.5 sublineage	BA.5 + S:V445X	07-02-2022
BA.5.2** (+R346X or +K444X)	GRA	22B	BA.5 sublineage	BA.5 + S:R346X or S:K444X	02-05-2022 or 04-04-2022
BA.2.75***	GRA	22D	BA.2 sublineage	BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion BA.2.75.2: BA.2.75 + S:R346T, S:F486S, S:D1199N	31-12-2021
BQ.1****	GRA	22B	BA.5 sublineage (B.1.1.529.5.3.1.1.1.1.1)	BA.5 + S:K444T, S:N460K	04-07-2022
BJ.1*****	GRA	21L	BA.2 sublineage (B.1.1.529.2.10.1.1)	BA.2+S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:V483A, S:F490V, S:G798D, S:S1003I	06-09-2021
BA.4.6	GRA	22A	BA.4 sublineage	BA.4+S:R346T, S:N658S	20-07-2020

Interpretation of Table:

**These sub-variants are tracked under Omicron unless/until adequate evidence emerges that the virus features are substantially different from what is known about the VOC they belong to. If this evidence materializes, WHO will determine whether the classification of the developing variant justifies a separate WHO label after consulting with the TAG-VE (Technical Advisory Group on SARS-CoV-2 Virus Evolution).*

*** Additional genetic changes outside of the spike protein: N:G30-, N:S33F, ORF9b:D16G, ORF9b:M26-, ORF9b:A29I, ORF9b:V30L. This clade includes BF.x sublineages such as BF.7.*

**** The following other mutations are found outside the spike protein: ORF1a:S1221L, ORF1a:P1640S, ORF1a:N4060S, ORF1b:G662S, and E:T11A.*
***** Represents a parent lineage of BE.1.1.1., having further mutations outside the spike protein which include N:E136D, ORF1a:Q556K, ORF1a:L3829F, ORF1b:Y264H, ORF1b:M1156I, and ORF9b:P10F.*

****** The following additional mutations are found outside of the spike protein: M:D3Y, N:T282I, ORF1a:K47R, ORF1b:G662S, ORF1b:S959P, and ORF7a:I110T.*

[#] *Incorporates descendant clades.*

4. STRUCTURE AND VIRULENCE OF OMICRON VARIANT

The novel Beta coronavirus SARS-CoV2 is an enclosed, single-stranded RNA virus with a helical symmetry nucleocapsid. The angiotensin-converting enzyme 2 (ACE2) is the host cell receptor for SARS-CoV2 [23-24]. In a study conducted by Mohamadian et al. [25], it was reported that there are three major proteins in SARS-CoV-2. The body's pentameric ion channels are built by a small protein complex called the envelope (E) protein. The main structural protein is the M protein. The spike (S) protein is composed of the head S1 and stem S2 subunits. The S protein facilitates the virus's attachment to ACE2 receptors on the surface of host cells. Trus et al. [26] in their research showed that the N terminus of the S1 heterotrimer often binds to molecules of carbohydrates on the cell surface. However, only angiotensin II and aminopeptidase N are targeted by the C terminal domain. Cevik et al. [27] cited that the respiratory epithelium is SARS-CoV-2's main target tissue. Headache, muscle aches, fever, and respiratory issues are among the non-specific symptoms caused by the virus's replication and discharge from the lungs. Clarifying where infections take place may be made possible by the distribution of ACE2 receptors in diverse organs. For example, ACE2 receptors are produced by the intestinal epithelium and blood vessel endothelial cells, which are indicative of digestive complaints and cardiovascular problems [28].

Weiss et al. [29] suggested to keep in mind that structural proteins, such as those in the spike, envelope, membrane, and nucleocapsid, are crucial for the processes of virulence, pathogenicity, and virion assembly. The host cell protease cleaves the receptor-attached S protein once the S protein binds to cell surface receptors, which causes the membranes of the host cell and the virus to converge. Utilizing host resources, viral RNA induces viral genomes and proteins as well as specialized RNA polymerase. Viral particles are produced, exocytosed, and discharged as new virions as a result of the viral M protein combining with the endoplasmic reticulum [30]. The SARS-CoV-2 spike initiates cell entry through interactions with ACE2 and TMPRSS2 at the cathepsins in endosomes or the plasma membrane and is a key predictor of viral infectivity says Hoffmann et al. [31]. The vast mutation in Omicron variant which is over 50 mutations in the spike protein surface is suggested to be responsible for its dominance, virulence, and spread across the globe [32-33]. Additionally, Omicron has been found to include more than 60 insertions, substitutions, and deletions, making it the SARSCoV-2 variation with the largest mutation area [34]. Prior to this report, WHO cited that it is yet unknown if Omicron infections result in more severe disease than infections with other variations, such as Delta. According to preliminary data, hospitalization rates are rising in South Africa, but this may not be attributable to a specific Omicron infection but rather to an increase in the overall number of infections [35].

5. CLINICAL SIGNS AND SYMPTOMS OF OMICRON INFECTION

Scribner's study revealed that night sweats is a specific symptom of the Omicron variant [36], especially with the BA.5 sub-variant added *Quann* [37]. Additionally, compared to other strains, a loss of taste and smell appears to be unusual [38]. According to a study conducted by the Centers for Disease Control between December 1 and 7, "the most often reported symptoms [were] cough, weariness, and congestion or runny nose," making it challenging to differentiate between a less harmful variety or other virus [39]. The Zoe COVID app users' most common complaints, according to research released in London on December 25, 2021, were "a running nose, headaches, weariness, sneezing, and sore throats" [40].

6. DIAGNOSIS

A report by Berger [41] shows that the likelihood of identifying a case is greatly influenced by a nation's sequencing rate. For instance, South Africa sequences more samples than any other country in Africa, but much less frequently than the majority of Western countries. Geddes [42], added that it might take up to two weeks for a viral sequence to return in locations with the necessary technical capacity, thus reliable statistics on verified cases lag the reality of the problem. Before thorough sequencing, Denmark and Norway consider cases discovered by their alternative qPCR test, which is quick and tests several genes, to be adequate for classifying it as an Omicron [43].

Laboratory methods for the diagnosis of Omicron sub-variants is the same as those for the general testing of COVID-19 which includes polymerase chain reaction and rapid tests however,

additional testing is needed to distinguish the sub-variants from one another and from other COVID-19 variations. Important for epidemic control is the use of quick and accurate diagnostic tools to identify the virus and then select appropriate and efficient containment measures and treatments. The best approach for identifying whether a patient has Omicron is still reverse transcriptase-polymerase chain reaction (RT-PCR), the gold-standard test for laboratory diagnosis of SARS-CoV-2. Omicron mutations have primarily affected the S gene. By looking for the S genes that encode the spike glycoprotein, SARSCoV2 can also be found. The main emphasis of the RT-PCR diagnostic kits that have been given approval for use is the E, Rd, Rp, and N genes [44]. It is feasible to determine if the results of an RT-PCR test are positive or negative by using the most widely used RT-PCR kits. Depending on the test, the S gene mutation might or might not produce a positive result. To find the new mutation, patients might be advised to have their DNA sequenced [45].

7. TREATMENT

Patients with the earlier strains of severe COVID-19 are known to respond well to corticosteroids like dexamethasone and IL6 receptor blockers like tocilizumab (Actemra). In 2021, the effect on other treatments' efficacy was being evaluated [35]. Similar testing and research are ongoing in relation to treatments using monoclonal antibodies (mAbs) [46]. Preclinical findings on in vitro pseudotyped viral data show that some mAbs with highly conserved epitope designs nonetheless have neutralizing effectiveness for major Omicron substitution mutations. Related findings are supported by cryo-electron microscopy and X-ray data. McCallum et al. [47] stated that these findings highlight the significance of focusing on conserved epitopes when developing vaccines and treatments, as well as the structural approach and molecular basis for the evasion of humoral immunity displayed by the Omicron antigenic shift. The S309 mAb, the parent mAb of sotrovimab, neutralized Omicron with just 2-3-fold less potency than other clinical mAbs or mAb combinations, which all experienced loss of neutralizing power of 1-2 orders of magnitude or larger in comparison to the prototypic virus [47]. According to new information, Omicron would result in significant humoral immune evasion, whereas neutralizing antibodies that target the conserved portion of the virus continue to be the most effective [48]. *Cameroni and team cited that* just three out of the 29 mAbs studied in a different study had intact potency, indicating that most monoclonal antibodies directed by receptor-binding motifs (RBMs) lost their *in vitro* neutralizing effectiveness against Omicron. Also, several widely neutralizing sarbecovirus mAbs, such as sotrovimab (VIR-7831), S2X259, and S2H97, neutralized Omicron by recognizing antigenic sites beyond the RBM [49]. However, because sotrovimab is only partially effective against the BA.2 Omicron sublineage, the U.S. Assistant Secretary for Preparedness and Response (ASPR) office discontinued supplying the antibody therapy to states where BA.2 was predominate in early 2022 [50].

8. PREVENTION

8.1 Interruption of Variant Transmission

All measures observed for general SARS-CoV-2 prevention are applicable for Omicron variants prevention and they include vaccination, staying at home, donning a mask in public, avoidance of congested places, keeping social distancing, ventilating indoor spaces, controlling potential exposure durations, washing hands frequently and for at least 20 seconds, practicing good hygiene, and avoiding touching the eyes, nose, or mouth with unwashed hands are all measures to lessen the likelihood of infection [51]. He et al. [52] reported that these steps have been shown to be successful in stopping the spread of other variants, and they should be successful in stopping the Omicron variant as well. Additionally, prompt quarantine and early diagnosis are important elements that help reduce virus transmission during a pandemic. Epidemiological data indicate a correlation between the rise in Omicron infection cases and the failure of PCR tests that target the spike gene. To stop the spread of the Omicron variety, it is crucial to increase diagnostic accuracy so that detected cases may be quickly isolated and treated.

8.2 Specific-variant Vaccine Development

It was reported by Pulliam et al. [53] that the appearance of the Omicron variation in South Africa has been linked to a higher risk of SARS-CoV-2 reinfection, suggesting that the Omicron variant may have a significant potential to circumvent protection from past infection. Additionally, there is a lot of interest in how well the COVID-19 vaccinations of today can guard against the Omicron version. Recent research

revealed that the COVID-19 vaccinations offered lower protection against the Omicron form than other VOCs. Similarly, compared to the wild-type SARS-CoV-2, the sera from vaccine recipients demonstrated a 40 percent reduced neutralizing power against the Omicron variant [54]. According to these findings, the current COVID-19 vaccines may not be as effective against the Omicron variation of SARS-CoV-2 as they are against other SARS-CoV-2 variants. The efficiency of the present COVID-19 vaccinations needs to be further studied in the future, according to further evidence. These findings emphasize how critical it is to create variant-specific vaccinations based on the altered spike, particularly for the Omicron variant [52]. As a result, using the altered spike of the Omicron variant as a basis, we are creating the particular vaccinations against the SARS-CoV-2 Omicron variant. To prevent Omicron infection and transmission, vaccine candidates that were designed based on the other variants but had one or more Omicron mutations may also be employed. For instance, some unofficial information suggests that Moderna has created two candidates for a multivalent vaccine: candidate mRNA1273.211 is thought to contain a number of mutations seen in both the Omicron and Beta variants, and mRNA1273.213 is thought to have included a specific number of mutations seen in the Omicron, Beta, and Delta variants [55]. Further research is required to see how well these potential vaccinations protect against the Omicron form. Measures were taken to proffer protective means to those at greater risk, as well as to make available rapid diagnostic kits in schools, work places, and government offices.

8.3 How Nigeria is Monitoring the Omicron Variant

According to the report of the WHO [56], Nigeria moved swiftly by compulsorily isolating travelers from COVID-19 endemic regions as well as regions where the new variants have been reported. Furthermore, in order to promptly detect variations, genome monitoring technique was modified to sequence samples from travelers who tested positive upon arrival in Nigeria [56]. The use of all available mass media for speedy awareness creation, and increasing the ability to spot cases even faster to break the cycle of transmission were other steps taken by the NCDC. WHO [56] also reported that Nigeria is enhancing its genomic monitoring capabilities to promptly detect and characterize novel variations. The information from this also informs our regulations, like the requirement for international travelers to submit to testing.

All of these steps and other measures which include ongoing investigation into the potency of vaccines and stepping up measures in preparation of future outbreaks, proved to be effective against COVID-19 earlier variants as well as the Omicron variants. They have also been applied towards the Omicron variant monitoring and control by the NCDC [56]. Nigeria is strongly in engagement with African nations as well as those from other areas to improve her outbreak readiness.

9. CONCLUSION

It is noteworthy in the time we are, to update the public on the current stance of the Omicron variant of COVID-19, and to encourage each one to step up proper measures not only for the prevention of more variant emergence, but also to work with all concerned institutions towards further reduction of its spread.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/93240