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COVID 19 Omicron: The Origin, Presentation, Diagnosis, Prevention and Control

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Authors' contributions

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

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Review Article

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ABSTRACT

Coronaviruses have become a global health threat over the past two decades as their geographical spread has accelerated. Coronavirus disease 2019, also known as COVID-19, is the severe acute respiratory syndrome coronavirus 2 The epidemic caused by (SARS-CoV-2). The first known case was confirmed in Wuhan, China in December 2019, where he has caused two pandemics in the past. Severe acute respiratory syndrome and Middle East respiratory syndrome are followed by the current COVID-19 outbreak in China. The virus originates from a zoonotic source and is spread by direct and contact transmission. Symptoms range from fever to cough, muscle aches to severe respiratory failure. Diagnosis is confirmed by reverse transcriptase-PCR. Treatment of COVID-19 consists primarily of supportive care and mechanical ventilation in critical cases. Prevention strategies, along with successful disease isolation and community containment, play an important role in reducing the spread of the virus

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among the public. A vaccine has been developed to clear the virus from its host, but it is not yet known whether the vaccine works against the virus's newest subspecies, the Omicron subspecies. This review summarizes the most recent research advances in structure, epidemiology, and etiology. We also focused on mutational patterns, an important feature of viral virology, and examined existing variants, especially its omicron variant. The clinical features of COVID-19, current treatments, and scientific advances to combat the epidemic novel coronavirus were discussed.

Keywords: Novel coronavirus; severe acute respiratory syndrome; diagnosis; omicron.

1. INTRODUCTION

Coronavirus disease 2019 (COVID-19) is a respiratory disease caused by a new coronavirus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; previously called 2019-nCoV). It was first identified in a case of respiratory illness in Wuhan City, Hubei Province, China. First reported to WHO on 31 December 2019. On January 30, 2020, WHO declared his COVID-19 outbreak a global public health emergency. On March 11, 2020, the WHO declared his COVID-19 a global pandemic for the first time since her H1N1 flu in 2009 was declared a pandemic. The disease caused by SARS-CoV-2 was named COVID-19 by the WHO, an acronym derived from "Coronavirus Disease 2019". The name was chosen to avoid stigmatizing the origin of the virus with respect to population, geography, or animal associations. Coronaviruses consist of a large family of viruses, seven of which are known to cause disease in humans. Some coronaviruses that normally infect animals have evolved to infect humans [1-3]. SARS-CoV-2 is likely one such virus and is believed to have originated in large animal and seafood markets. Severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) are also caused by coronaviruses that evolved from animal-to-human transmission. More than 8,000 people were infected with SARS, of which about 800 died from the disease before it came under control in 2003 (mortality rate of about 10%). MERS continues to occur sporadically. Since 2012, a total of 2,465 laboratory-confirmed MERS cases have been reported, with 850 deaths (mortality rate 34.5%).

Humans become infected with SARS-CoV-2 through exposure to respiratory droplets (always within 6 feet) that carry the infectious virus [4,5]. Other transmission methods include contact transmission such as: For example, handshakes and airborne transmission through droplets that remain airborne over long distances (usually 6 feet or more). Viruses released in respiratory secretions such as coughs, sneezes, and speech can infect others through contact with mucous membranes. On 9 July 2020, WHO released an update noting that airborne transmission could play a role in the spread of her COVID-19, especially during "super-spreader" indoor events such as bars. Their relaxed demeanor emphasized the importance of social distancing and masks in prevention. Viruses can also persist on surfaces for varying durations and infectivity, but this is not considered the primary route of transmission. Studies have shown that SARS-CoV-2 was detectable on some surfaces for up to 72 hours, but its infectivity declined over time. Specifically, this study reported that no viable SARS-CoV-2 was measured after 4 hours on copper and 24 hours on cardboard. (Sennimo, Coronavirus disease 2019 (COVID-19), 2021).

2. COVID 19 AND ITS ORIGIN

“Coronavirus disease 2019, also known as COVID-19, is an epidemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). SARS-CoV-2 is a beta-coronavirus, an enveloped, non-segmented, positive-sense RNA virus (subgenus Sarbecovirus, subfamily Orthocoronavirus). They are enveloped viruses with single-stranded positive-sense RNA genomes and nucleocapsids with helical symmetry. With a genome size of approximately 26-32 kilobases, coronaviruses are among the largest RNA viruses. They have characteristic club-shaped spines protruding from their surface, producing images reminiscent of the solar corona in electron micrographs. This is where the name comes from” [6].

“Coronaviruses (CoV) are divided into four genera: α-/β-/γ-/δ-CoV. α- and β-CoV infect mammals and γ- and δ-CoV infect birds. Recently, six CoVs that also infect humans were discovered: α-CoVs HCoV-229E and HCoV-NL63, β-CoVs HCoV-HKU1 and HCoV-OC43. All of these are of low pathogenicity and cause mild respiratory symptoms similar to the common cold cause illness. The genome sequence of SARS-CoV-2 was found to be 96.2% identical to his CoV RaTG13 in bats, but 79.5% identical to

SARS-CoV. Based on the results of viral genome sequencing and evolutionary analysis, bats have been suggested as the natural host of viral origin, and SARS-CoV-2 may be transmitted from bats to humans via an unknown intermediate host there is. SARS-CoV-2 can use the same receptor, angiotensin-converting enzyme 2 (ACE2), as SARS-CoV to infect humans" [7].

2.1 Epidemiology of Covid 19

"Wuhan, China, experienced the first unknown outbreak of acute respiratory infection since December 12, 2019, possibly linked to a fish market. Several studies have suggested that bats may be potential hosts for SARS-CoV-2. However, so far there is no evidence that SARS-CoV-2 originated in fish markets [8-11]. Conversely, bats are natural hosts for various CoVs, including SARS-CoV-like and MERS-CoV-like viruses. Viral genome sequencing analyzed his COVID-19 whole genome of bat CoV RaTG13 and showed an overall genome sequence identity of 96.2%. It is sold at this fish market. Alignment and phylogenetic analysis of protein sequences also showed that similar receptor residues were observed in many species, likely alternative intermediate hosts such as turtles, pangolins and snacks" [12]. Person-to-person transmission of SARS-CoV-2 often occurs among family members, including relatives and friends who are in close contact with patients and incubators. It was reported that 31.3% of the patients had recently traveled to Wuhan, and that 72.3% of the patients had contact with people in Wuhan among non-resident patients of Wuhan. Transmission among medical personnel occurred in his 3.8% of her COVID-19 patients announced by China's National Health Commission on February 14, 2020. In contrast, SARS-CoV and MERS-CoV infections are said to be primarily due to nosocomial infections end. Health care worker infections were the most common route of transmission of MERS-CoV cases, with 33–42% of SARS cases and patient-to-patient transmission (62–79%). Direct contact with intermediate host animals or consumption of wildlife is also suspected as the main transmission route of SARS-CoV-2. Yet the SARS-CoV-2 source and transmission routine remain elusive.

2.2 Genome Structure of Covid 19

The total genome of Wuhan Hu-1 coronavirus (WHCV), a strain of SARS-CoV-2 isolated from a COVID-19 pneumonia patient who is an employee of the Wuhan Seafood Market, is 29.9 kb. SARS-CoV and MERS-CoV, on the other hand, have positive-sense RNA genomes of 27.9 kb and 30.1 kb, respectively. CoV genomes have been shown to contain varying numbers (6–11) of open reading frames (ORFs). Two-thirds of the viral RNA, located primarily in the first ORF (ORF1a/b), translates two polyproteins, pp1a and pp1ab, and encodes 16 nonstructural proteins (NSPs), while the remaining ORFs are Encodes accessory and structural proteins [13,14]. The remainder of the viral genome consists of four essential structural proteins, including the spike (S) glycoprotein, small envelope (E) protein, matrix (M) protein, and nucleocapsid (N) protein, which interfere with the host's innate immune response. It encodes other accessory proteins. Deep metatranscriptome sequencing recently performed at WHCV containing 16 predicted NSPs. WHCV shares several genomic and phylogenetic similarities with SARS-CoV, particularly in the S glycoprotein gene and receptor binding domain (RBD), indicating the ability to directly infect humans. Compared to the known SARS-CoV and MERS-CoV genomes, SARS-CoV-2 is closer to the SARS-like bat CoV in terms of overall genome sequence. Most of the proteins encoded in the genome of SARS-CoV-2 are similar to those of SARS-CoV, but there are some differences. At the protein level, no amino acid substitutions occurred in NSP7, NSP13, envelope, matrix, or accessory proteins p6 and 8b, except for NSP2, NSP3, spike protein, underlying subdomains. H. RBD. Another recent study suggested that mutations in NSP2 and NSP3 are involved in SARS-CoV-2 infectivity and differentiation mechanisms. This will encourage people to study the differences in host tropism and transmission between SARS-CoV-2 and SARS-CoV, as well as to conduct further research on potential therapeutic targets [15].

"Analysis of COVID-19 genotypes in different patients from multiple provinces found that SARS-CoV-2 is mutated in different patients in China. Although the degree of diversification of SARS-CoV-2 is lower than that of the H7N9 avian influenza mutation. Tang et al. A population genetic analysis of 103 SARS-CoV-2 genomes was performed to classify his two main evolutionary forms of SARS-CoV-2, L-type (~70%) and S-type (~30%). L strains derived from S strains are evolutionarily more aggressive and contagious. Therefore, virologists and epidemiologists should closely monitor novel coronaviruses to study their pathogenicity and epidemics" [16].

2.3 Covid 19 Replication and Pathogenesis

ACE2, found in the human lower respiratory tract, is known to be the cellular receptor for SARS-CoV, regulating both interspecies mating and human-to-human transmission. It was isolated from bronchoalveolar lavage fluid (BALF) of COVID-19 patients. SARS-CoV-2 has been confirmed to use the same cell entry receptor ACE2 as SARS-CoV. The virion S glycoprotein on the surface of coronaviruses can bind to ACE2 receptors on the surface of human cells. The S glycoprotein is composed of her two subunits, S1 and S2. S1 uses a key functional domain, the RBD, to determine viral and host range and cellular tropism. S2, on the other hand, mediates fusion of the virus with the plasma membrane through two tandem domains, heptad repeat 1 (HR1) and HR2. After membrane fusion, the viral genomic RNA is released into the cytoplasm, and the uncoated RNA translates two polyproteins, pp1a and pp1ab, which encode nonstructural proteins, and form replication-transcription complexes (RTC). The RTC continuously replicates and synthesizes an interleaved set of subgenomic RNAs encoding accessory and structural proteins. Viral bud assembly is mediated by the endoplasmic reticulum (ER) and Golgi apparatus, newly formed genomic RNA, nucleocapsid proteins, and envelope glycoproteins. Finally, the virion-laden vesicle fuses with the plasma membrane to release the virus [17]. Since binding of the “SARS-CoV-2 spike (S) glycoprotein to the ACE2 receptor is a critical step in viral entry, viral receptor binding affinities are probed with different approaches. Systematic detection of β-CoV receptors revealed human cells expressing ACE2 but not human dipeptidyl peptidase-4 (DPP4) or APN (aminopeptidase N) as a result of increased entry of SARS-CoV-2 was shown to emerge” [18].

Another study by Song and Gui showed that the binding efficiency of S protein and ACE2 was 10- to 20-fold higher than that of SARS-CoV [19].

“In SARS-CoV, trimeric S protein cleavage is triggered by cell surface-associated transmembrane protease serine 2 (TMPRSS2)” [20] and cathepsins, whereas in SARS-CoV the putative molecule is Promoted membrane invagination. 2 Endocytosis is still unknown. To the date of this review, it has been reported that SARS-CoV-2, while readily transmissible, causes less severe human infections than SARS-CoV in humans. Number of infected people based on the latest WHO report (more than 80,000 worldwide as of March 1, 2020 update). A global outbreak may be due to the following factors: First, an unknown pneumonia outbreak occurred during a large population gathering during the Chinese New Year. Second, more consistent molecular mechanisms of viral binding and entry pathways need to be elucidated, which may hinder the development of targeted therapies. Third, the available data suggest that SARS-CoV-2 may be less virulent than SARS-CoV and MERS-CoV, with COVID-19 mortality rates currently analyzed 3.4%, lower than the SARS mortality rate (9 March). .6%). MERS (~35%) [21]. Therefore, the potential mechanisms for transmission between humans and pathogenic mechanisms of the SARS-CoV-2 are under intensive studies.

3. MUTATION PATTERN OF COVID 19

All viruses naturally mutate over time and Sars-CoV-2 is no exception. Since the virus was first identified a year before him, other mutations have emerged, most of which are "passengers" and have little effect. However, viruses occasionally mutate so that they can survive and reproduce. This does not change the behavior of the virus, it just carries the virus with the changing environment. Viruses with these mutations may emerge more frequently due to natural selection under an appropriate epidemiological framework [22]. This seems to be the case for the variant known as 202012/01 that spread to the UK and a similar and different variant recently seen in South Africa (501.V2).

Infections with these strains are more severe due to their increased contagiousness, and the impact of Covid-19 disease on hospitalization and mortality is estimated to be high, especially for the elderly and those with comorbidities [23-25]. The mutants have different origins, but they all share mutations in the gene that encodes the spike protein that the virus uses to attach and enter human cells. That's why it looks like.

3.1 Variants of Covid 19

- Viruses are constantly changing through mutation. When a virus has one or more new mutations, it is called a variant of the original virus.
- When the virus undergoes one or more mutations that alter its behavior in some way, new strains arise, but when the virus undergoes mutation, variants arise

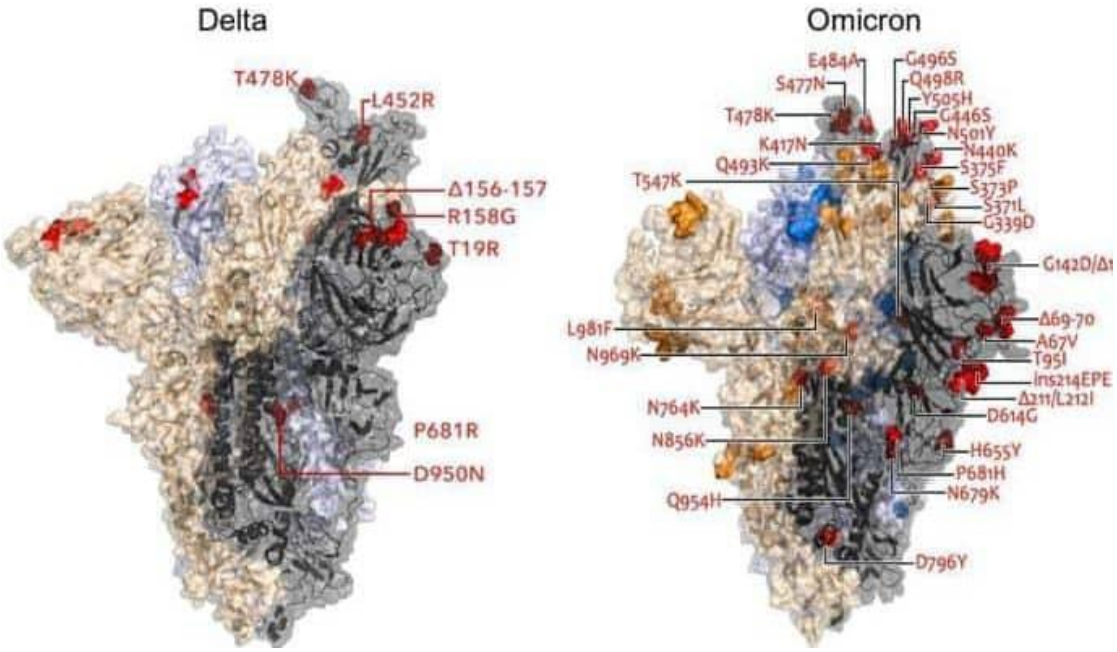

Fig. 1. A comparison of Delta and Omicron variant spike mutation
(Image source: Modified rom covid- 19 Genomics UK consortium)

- The various variants of COVID 19 include
- will be

3.1.1 Delta variant from India

This variant is believed to have first emerged in India in October 2020. It's since spread to the U.S. and currently has more than 6% of sequenced cases in the U.S., Dr. Anthony Fauci said at a recent news briefing. It also has increased transmissibility compared to other variants, according to the World Health Organization.

3.1.2 Alpha variant: UK variant

The U.K. strain, called B.1.1.7, was first reported in the U.S. in late December, and it spreads faster and easily than other variants, according to the CDC. It is now in all 52 states and territories and is the dominant variant in the U.S. The CDC has also said it has "potential increased severity based on hospitalizations and case fatality rates

3.1.3 Beta variant: South African variant

This variant, known as B.1.351 or Beta, emerged independently from the U.K. strain but shares some of its mutations, according to the CDC. Data indicates that it first emerged in South Africa in October 2020 and has since spread to other countries, including the U.S. In late January. This variant could also make re-infection more likely; a vaccine study in South Africa found 2% of people who'd already had a version of the coronavirus had been reinfected with a variant. It also has an estimated 50% increase transmission.

3.1.4 Gamma variant

The Brazilian variant, P.1, was first detected in mid-January 2020 in travelers to Japan from the Amazonas state of Brazil. It appears to contain mutations that raise concerns about its transmissibility and potential for reinfection, according to the CDC. Manaus, the largest city in the Amazon region, saw a surge in cases in December 2020, despite 75% of the population already having been infected by October.

3.1.5 Omicron variant

This variant might spread more easily than other variants, including delta. But it’s not yet clear if omicron causes more severe disease. It’s expected that people who are fully vaccinated likely can get breakthrough infections and spread the virus to others.

A new strain occurs when a virus goes through one or more mutations that change its behavior in some way, but a variant develops when a virus goes through a mutation of any kind.

4. COVID 19 OMICRON

"The new COVID- 19 variant called the Omicron variant also know as B.1.1.529 variant has been named a variant of high importance by WHO based on the evidence that it has several mutations that may have an impact on how it behaves. There is still significant uncertainty regarding Omicron and a lot of research has been going on to evaluate its transmissibility, severity and reinfection risk this is because when a virus is circulating widely and causing numerous infections, the likelihood of the virus mutating increases. The more opportunities a virus has to spread, the more opportunities it has to undergo changes" [26].

Vaccines so has so far been observed to reduce the rate but it has not been recorded to stop the virus but is very important that people get vaccinated when the vaccine is made available to them and continue to follow existing protocols on preventing the spread of the virus, including social distancing, wearing masks, regular handwashing and keeping indoor areas well ventilated [27-31].

The Omicron variant has now been detected in many countries around the world and Nigeria is no exception. The WHO reported that the Omicron Variant might be in some other countries even though it hasn't been discovered yet.

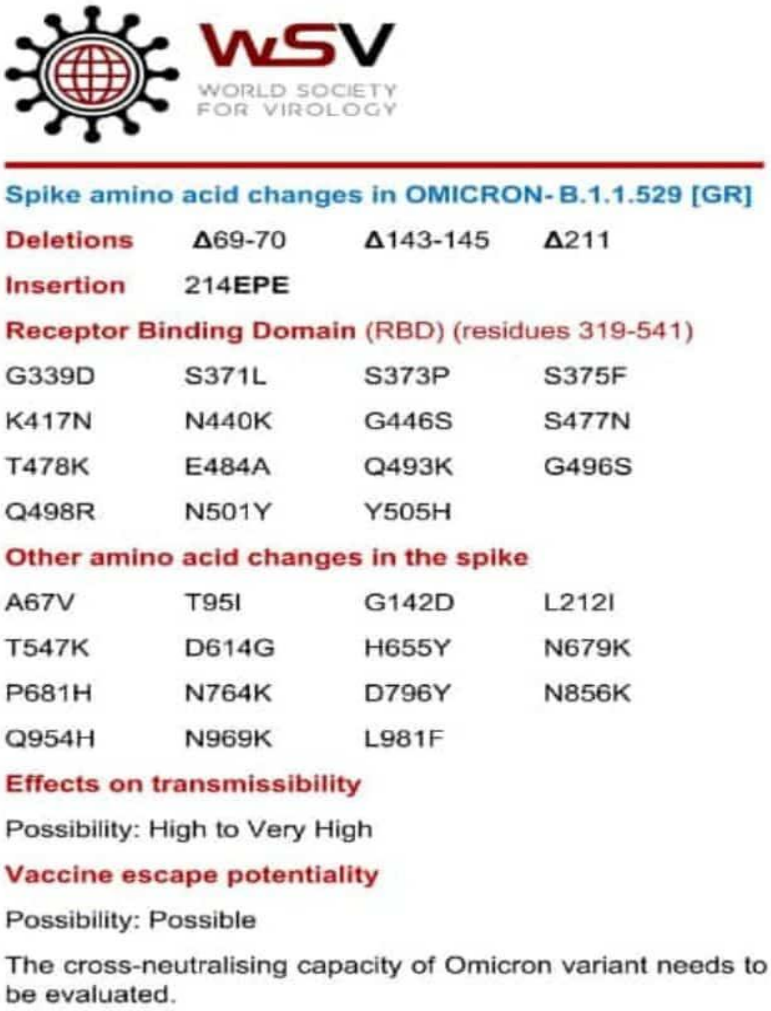

Fig. 2. Spike amino acid changes in Omicron
(Source: World Society for Virology)

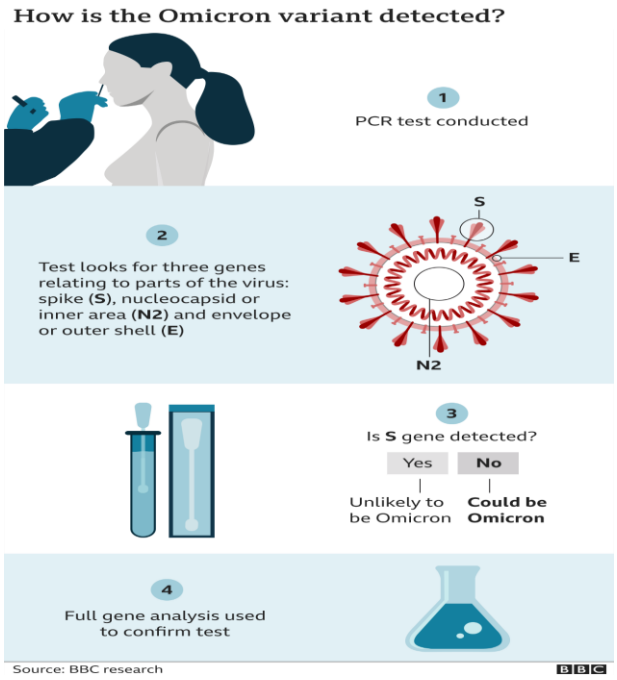

Fig. 3. Detection of omicron variant

The B.1.1.529 variant was first reported to WHO from South Africa on 24 November 2021. The epidemiological situation in South Africa has been distinguished by three well defined peaks in reported cases, the latest of which was primarily the Delta variant which has had an increasingly steep infection rate in recent weeks, corresponding with the detection of B.1.1.529 variant. The first known confirmed B.1.1.529 infection was from a specimen collected on 9 November 2021.

This variant has numerous mutations, some of which are worrisome. Preliminary evidence suggests an increased risk of reinfection with this variant compared with other variants of concern. I'm here. The number of cases of this variant appears to be increasing in almost all provinces of South Africa. Current SARS-CoV-2 PCR diagnostics continue to detect this variant. Several laboratories have shown that the widely used PCR test fails to detect one of the three target genes (referred to as S-gene dropout or S-gene target failure), this check is used to detect 1's until the sequence is confirmed as a marker this variant. Available. Using this approach, this variant was detected earlier than previous recurrences, suggesting that this variant may have a growth advantage [26]. People who have recovered from COVID-19 may develop natural immunity to the virus, but previous infections may not provide protection against Omicron compared to other variants of concern such as Delta. There is., but it is not yet known how long it will last or to what extent the person will be protected [32]. Nigeria has registered a total of 45 Omicron cases as of 20 December 2021 said Ruka Rawal of the Nigeria Center for Disease Control (NCDC) at a virtual media briefing on Friday.

Nigeria now ranks third in the list of African countries, behind South Africa and Botswana (1,296 and 291 cases respectively). On 1 December 2021, Nigeria joined the growing number of African countries that have registered cases of the Omicron subspecies, also known as the B.1.1.529 strain.

Iluyemi 2021 noted that the first case of the Omicron variant was detected in a South African traveler to Nigeria, and the NCDC noted that subsequent cases detected were not from travelers but from within Nigeria [33]. Variant Delta remains the most prevalent since the outbreak of COVID-19, with 2,237 cases of him detected in Nigeria as of 20 December 2021.

5. DIAGNOSIS OF COVID 19 OMICRON VARIANT

A polymerase chain reaction (PCR) test swab that is sent to the lab for analysis is used to detect the infection-causing variant (Omicron, Delta, or other variant).

The UK is using a technique called genome sequencing to detect Omicron variants. Another way to detect the Omicron variant is the Rapid Flow Test or Lateral Flow Test (LFT), which can also be used at home. PCR is then performed to detect mutants. During testing, scientists will have to determine whether the virus is related to the virus as her three genes. The spine (S), the nucleocapsid or inner region (N2), and the shell or outer shell (E). If the S gene is not detected, meaning the variant is likely an Omicron, full genetic analysis is used to confirm the test [34-36].

6. PREVENTION AND CONTROL OF COVID 19

The most important thing you can do is reduce your risk of exposure to the virus. To protect yourself and your loved ones, make sure to:

1. Wear a mask that covers your nose and mouth. Make sure that your hands are clean when you put on and remove your mask.
2. Keep a physical distance of at least 1 metre from others.
3. Avoid poorly ventilated or crowded spaces.
4. Open windows to improve ventilation indoors.
5. Wash your hands regularly.
6. When it's your turn, get vaccinated. WHO-approved COVID-19 vaccines are safe and effective.

7. CONCLUSION

The coronavirus is thought to have existed in animals prior to the first and most recent human infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), with cases increasing daily to this day. It is not yet fully known whether vaccination completely reduces the risk of infection, as cases of reinfection after vaccination have also occurred. The literature reviewed for this purpose shows that vaccination remains an effective means of containing the spread of infection, but adherence to preventive measures is also effective in containing the spread of viral surges.

CONSENT AND ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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