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Should we be worried about the COVID-19 Delta variant (B.1.617.2)?

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Abstract

Introduction: The World is currently plagued by the COVID-19 pandemic caused by the SAR-CoV-2 virus which started in the last quarter of 2019. The SAR-CoV-2 virus went on to naturally mutate into several variants, each with attributes that made it to spread faster, escaped immune protection, less amenable to vaccine and available therapeutics.

Methods: Standard relevant keywords were used to search online in PubMed and Google Scholar databases and relevant articles pooled for inclusion in the manuscript.

Result: Delta variant emerged as a dominant variant and presently the most predominant variant globally. The Delta variant has been designated as a variant of concern by the World Health Organization (WHO). This manuscript explores the global and local epidemiology of the Delta variant as well as its prevention and control measures.

Conclusion: There is no field of medicine that keeps evolving and changing due to vast knowledge and insight we obtain every day from COVID-19. Much knowledge would be outdated as at the time of going to press.

Keywords: COVID-19, Mutations, New COVID-19 Variants, Delta-variant

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An outbreak of pneumonia was reported in late 2019 from China. The agent responsible was identified as a coronavirus. The virus was first named as severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) virus by the International Committee for Taxonomy of Viruses (1). However, it was not until early March 2021 that the World Health Organization (WHO) declared the disease as a pandemic and also renamed the disease Coronavirus Disease 2019 (2).

Coronavirus Disease 2019 (COVID-19) went on to overwhelm the global community with increasing morbidity and mortality across different regions and countries of the world. As of 20th of February, 2022, there were 418,650,474 confirmed cases of COVID-19, including 5,856,224 deaths as reported by the WHO with a total of 10,279,668,555 vaccine doses administered. Africa has the least cases with 8,264,647 confirmed cases and 246,142 deaths (3).

Mutations of the SARS-COV-2 Virus

One basic property of viruses is that they all naturally mutate over time. This is more relevant now when with SARS-CoV-2, the virus that causes coronavirus disease 2019 (COVID-19). Since the detection of the SARS-CoV-2, thousands of mutations have been identified. These mutations will continue to occur as a form of viral survival in order to allow new strain lineages of the virus to evolve, even though the vast majority of mutations will have little impact (4). However, in some instances the mutations might become of clinical relevance when it fosters survival and replication better than the original strain.

Viruses carrying these mutations can then increase in frequency due to natural selection and when mutant viruses have some advantage, they are named as "variants of interest, a variant of concern, or a variant of high consequences" (5). These mutations can have advantages when looking at SARS-CoV-2 and this is what is being used now to classify these mutated variants into; variants of interest, variant of concern or variant of high consequences. The variants now have faster or more efficient transmission, increase risk of severe disease or death, escape immunity from past infection, escape immunity from vaccination or elude detection of existing tests (4, 5).

The SAR-CoV-2 variants have emerged and would continue to emerge worldwide without

global concerted action. Variant's occurrence due to SAR-CoV-2 mutations are observed through laboratory-based surveillance where pooled samples are sequenced and compared with clinical and epidemiological data. The COVID-19 variants are classified into three classes as follows; a variant of interest, variant of concern and variant of high consequence.

Pango Nomenclature

The Pango nomenclature is used globally to determine the pattern and dissemination of SARS-CoV-2. The website makes available the most up to date Pango lineages and their pattern as well as various software tools which can be used by scientists to conduct analyses on SARS-CoV-2 sequencing data (6).

Variant of interest

This is a variant that has some changes to the receptor-binding domain, reduced effectiveness of prior antibodies from past infection, resistance to available medication, reduce detection capabilities and increased in transmission rate and occurrence of severe or critical diseases (4). The attributes of the variants of interest are the specific genetic markers that are predicted to affect the transmission, diagnostics, therapeutics, or immune escape. Others are the capacity to cause increased incidence of new cases but they have limited prevalence or dissemination to other countries (5).

The selected variants of interest are: WHO Label (None); Pango Lineage: B.1.427 that was first discovered in USA (California), then we have the WHO Label (None); Pango Lineage: B.1.429 also discovered from the USA (California), WHO Label (Eta); Pango Lineage: B.1.525 that was discovered from USA/Nigeria (December 2020) (6). Others are the WHO Label (Iota); Pango Lineage: B.1.526 discovered from the USA/New York (November 2020), the WHO Label (Kappa); Pango Lineage: B.1.617.1 discovered in India (December 2020) and then the WHO Label (None); Pango Lineage: B.1.617.3 discovered in India (October 2020) (6).

Researchers are keeping an eye on several variants of interest, including Lambda (like the K417N/T). The theory of natural selection can come into play when these mutations become fixed and recurring. The best strategy is to control the pandemic and reduce the transmissibility of viruses within populations otherwise with the preponderance of mutations the probability of natural selection of the best-fit virus variant is imminent (5).

Variants of Concern

This is a variant of SAR-CoV-2 that has the following

attributes; increase transmission rate, a greater proportion of infected persons coming down with severe or critical disease leading to admission or higher mortality and reduction in vaccine effectiveness and or escaped detection by available laboratory methods (7). The variant of concern are as follows; B.1.1.7 (Alpha), B.1.351 (Beta), B.1.617.2 (Delta), P.1 (Gamma) with the WHO Label (Alpha) then the Pango Lineage: B.1.1.7 from the United Kingdom with WHO Label (Beta), there is also the Pango Lineage(s): B.1.351, B.1.351.2 and B.1.351.3 first detected from South Africa with WHO Label (Delta). There is also the Pango Lineage: B.1.617.2, AY.1, AY.2, AY.3 first detected from India with WHO Label (Gamma) and also the Pango Lineage(s): P.1, P.1.1, P.1.2 detected from Japan and Brazil (6, 8, 9). The attributes of variants of concern have some of the attributes of a variant of interest and in addition, also have the following; evidence of impact on diagnostics, treatments, or vaccines, failure or escaped detection by the available laboratory tests, resistance to one or more class of available therapeutic regimens, increase the rate of transmission, greater proportion of occurrence of severe or critical disease and failure of protection from available vaccines (10, 11).

Culpable Mutations of the variant of Concern

The basic mutation occurs in the amino acid of the spike (S) protein in SARS-CoV-2. The spike protein is what vaccinologist used as a target and also it is the same target for the antibody responses during natural SARS-CoV-2 infection, specifically the receptor-binding domain (RBD) of the S protein. Consequently, mutations at the S protein would make early antibodies produced to be ineffective. The Delta variant has several mutations around the S gene, RBD, at the furin cleavage site and in the region of the N-terminal domain known as an 'antigenic supersite' (12).

The Delta or B.1.617.2 variant

The Delta or the B.1.617.2 variant was first detected in India in December, 2020 and within a few months of its detection, this variant has spread to more than 100 countries globally. This is now the dominant variant across the globe including countries with high COVID-19 disease burden like India, the United Kingdom and the United States, amongst others (4).

Delta is presently responsible for greater than 90 % of COVID-19 cases around the world. The Delta variant is about 40-60% more transmissible than the Alpha and almost twice as transmissible as the original Wuhan strain of SARS-CoV-2. Studies have also revealed higher viral particles in the airways of patients infected with the Delta variants (8). Studies have shown that the viral loads in Delta infections are 1,000 times higher than those in infections caused by other

variants. The WHO regards Delta as “the fastest and fittest” variant so far (12). The Delta variant has a greater improve capability of infectiousness and transmissibility as compared to the original SARS-CoV-2-Wuhan virus.

It also has greater capability for severe and critical infection among the unvaccinated with a higher proportion of morbidity and mortality. Even though studies have revealed that fully vaccinated people though susceptible to this infection have milder forms of shorter durations. Getting vaccinated and wearing masks indoors in public spaces helps to reduce the spread of this variant (13).

Variant of high consequences

This variant has significantly decreased effectiveness of preventive and medical countermeasures and compared to other available variants (5). The attributes of variant of high consequences comprise of all those of variants of concern and in addition also the impact on medical countermeasures and demonstrated failure of diagnostics. Other measures are evidence to suggest a significant reduction in vaccine effectiveness, a disproportionately greater percentage of vaccine breakthrough cases, or very low vaccine-induced protection against severe disease (12). They also have significantly reduced susceptibility to multiple emergency use authorization medication or approved therapeutics (undertrials) and they have more severe clinical disease and increased hospitalizations rates. As recommended under the international health regulations (IHR) the occurrence of any variant of high consequences must be notified to the WHO (5). However, at present, this is merely theoretical as there are no SARS-CoV-2 variants that have been designated as a variant of high consequence (8).

COVID-19 variants: Global and local epidemiology

Viruses constantly change through mutation. As expected, multiple variants of SARS-CoV-2 have been documented globally In the United States of America; 99% of COVID-19 cases are caused by the Delta variant as at the time of drafting this manuscript. Also, as at mid-February 2021, there were about 55 different lineages of SARS-CoV-2 known to be circulating in Nigeria and they are changing rapidly. The heterogeneity of SARS-CoV-2 shows an importation of COVID-19 virus into Nigeria from different regions of the world and this leads credence to the statewide community transmission of SARS-CoV-2 in Nigeria (13). A total of 29 cases with the B.1.1.7 variant of concern strain that was initially detected in the United Kingdom and shown to be linked to increase in transmissibility, have so far been detected in Nigeria. These strains were detected from patients from five states of southwestern Nigeria.

The specimen noted with B.1.1.7 variant were collected from cases in early 2021. In the early February of 2021, some recent SARS-CoV-2 genomes were seen to have new mutations and they were defined as a new variant B.1.525. As of mid-February 2021, they have been reported from the United Kingdom, Denmark, United States of America, Canada, France, Australia, Jordan, Singapore, Finland, Belgium, Spain, Ghana and Nigeria. The COVID-19 variant of B.1.525 was first detected in late November of 2021 from a case admitted in Lagos State, Nigeria. (5, 8, 11, 13). This has also been detected among cases in five states in Nigeria. The B.1.525 cases have similarly been detected in some Nigerians visiting countries abroad. However, the B.1.525 a novel strain that has not yet been classified as a variant of concern but further molecular studies are still being pursued (13).

Transmissibility of the Delta variant

Delta is 40-60% more transmissible than Alpha. Delta is twice as transmissible as the original Wuhan strain of SARS-CoV-2. A greater load of viral particles has been recovered from the nasopharynx of patients infected with the Delta variant. There is a thousand-fold increase in viral loads from individuals infected with Delta as compared to the other variants. The WHO regards Delta as “the fastest and fittest” variant at the time of drafting this manuscript (5, 12).

How deadly is the Delta variant compared to the other variants of concern?

Surveys in the United Kingdom reveal that the Delta variants account for more than 90% of current COVID-19 cases. The clinical manifestations of the Delta variant show the diversity of manifestation from the other strains of COVID-19 variants even though this does not infer a severity of the clinical presentation. The flu-like symptoms of fever, malaise, sore throats, headache predominates while anosmia and cough are lesser in occurrence (12). Hearing impairment, coagulation disorders, gastrointestinal disturbances have also been reported in severe cases.

However, current research has not shown a positive association between increased hospitalization and death versus the occurrence of Delta variant (12). A study from Scotland shows that there is a 100% increase in hospitalization in the unvaccinated population infected with Delta as compared to Alpha. Two doses of vaccines are effective at preventing hospitalization and death. Protective antibodies of vaccinated are lower against the Delta variant as compared to the original Wuhan virus (12). Delta variant was 2.9 times less susceptible to protective antibodies following vaccination than the original strain. Most convalescent serum samples and all vaccination serum samples showed detectable



neutralization activity mRNA vaccines more effective on variants (12).

Treatments Strategies for the Delta variant

As at the time of drafting this manuscript there was no approved treatment for COVID-19 and its variants, however, various different therapeutics are at various phases of clinical trials. The anti-SARS-CoV-2 monoclonal antibody treatments for COVID-19 variants are as follows; bamlanivimab plus etesevimab, casirivimab plus imdevimab and sotrovimab (13).

How can we control the Delta Variant?

The Delta variant has emerged and is likely going to replace the other variant of concern. It is therefore important to control it by enforcing non-pharmacologic preventions like use of face masks, hand washing, reduction mass gathering, surveillance at point of entries and massive vaccination (12). Africa presently has registered a 12-fold increase in vaccine deliveries in the last two weeks of July, 2021. Africa should manufacture its own vaccines and also improve on its genomic surveillance and sequencing and improved therapeutics (12, 13).

Should we be worried about the Delta variants?

Globally the emergence of variants of concern should be a source of concern anywhere, more so in resources poor settings where there is suboptimal diagnostics, lack of routine sequencing of pooled samples, low level of operational researches. Globally the behavior of COVID-19 and its variants are still evolving and being studied. An effective treatment has not been finally approved and target for vaccination has not been achieved. This scenario may create a recipe for disaster if not handled well (12).

Conclusion

COVID-19 has emerged as a pandemic and it is still constituting mortalities and morbidities globally as of now. Variants of COVID-19 would continue to emerge and evolve and how we control them is the function that depends largely on the non-pharmacological methods we adopted, our ability for massive equitable vaccination distribution and to a lesser extent the pharmacological methods we adopt globally. This is a clarion call for healthcare providers and policymaker that an infection anywhere is an infection everywhere.

Conflict of interest

None declared

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