Electronic Survey about Current Update of CORONAVirus Variants

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ABSTRACT

WHO, in association with partners, expert networks, national authorities, institutions and researchers have been monitoring and assessing the evolution of SARS-CoV-2 since in the month of January 2020.At the current time, this expert group summoned by WHO has indorsed using letters of the Greek Alphabet like Alpha, Beta, Gamma, Delta which will be easier and more applied to be conferred by non-scientific spectators.The efficiency of the current COVID vaccines is fairly high. In fact, it is much advanced than some other vaccines we generally receive. As an aide-memoire, the annual flu vaccine has an efficacy around 40-60 percent from year to year. Numerous theories are on the surface to explain how the Omicron has congregated such a high number of mutations within less time. Few of them are advanced mutation rates within a subgroup of population and then its introduction to a larger population, long term perseverance and evolution of the virus in immune-compromised patients, and epizootic infection in animals from humans, where under dissimilar immune pressures the virus metamorphosed and then got reintroduced to humans.Transmission of SARS-CoV-2 is thought to occur primarily through revelation to respiratory droplets. Breathe out droplets or particles can also deposit the virus onto exposed mucous membranes. Though a numerous number of variants will cause the COVID infection still proper precautionary measures can prevent the transmission of this infection.

Keywords: SARS-CoV-2,OMICRON,Pfizer-BioNTech vaccine, Acquired immunity,Genetic marker, Transmissibility.

INTRODUCTION

All viruses, together with SARS-CoV-2, the virus that reasons COVID-19, change over time. Most variations have little to no impact on the virus' chattels. Though, some changes may disturb the virus's possessions, such as how easily its blowouts, the associated disease harshness, or the recital of vaccines, therapeutic medicines, diagnostic tools, or other public health and social measures. **The first variant** to emerge was the B.1.1.7 variant, which was initially detected in the UK in December 2020. This variant has a higher transmissibility rate than the original SARS-CoV-2 virus and has rapidly spread to other countries worldwide. The B.1.1.7 variant is believed to be around 50% more transmissible than the original virus and has been associated with increased hospitalizations and deaths. **The second variant** to emerge was the B.1.351 variant, first identified in South Africa in October 2020. This variant also has a higher transmissibility rate and is associated with increased hospitalizations and deaths. The B.1.351 variant has been shown to have some resistance to antibodies produced by previous infections or vaccinations, raising concerns about the efficacy of current vaccines against this variant.**The third variant** is the P.1 variant, first identified in Brazil in January 2021.

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This variant is also more transmissible and has been associated with a higher risk of reinfection, meaning that individuals who have previously been infected with the original virus may still be susceptible to this variant. Like the B.1.351 variant, the P.1 variant has also been associated with reduced vaccine efficacy.**The most recent variant** to emerge is the B.1.617 variant, first identified in India in October 2020. This variant has two sub-lineages, B.1.617.1 and B.1.617.2, which have been associated with increased transmissibility and hospitalizations. The B.1.617.2 variant has also been identified in the UK, where it has quickly become the dominant variant, leading to increased concern about its potential spread globally.At the current time, this expert group summoned by WHO has indorsed using letters of the Greek Alphabet like Alpha, Beta, Gamma, Delta which will be easier and more applied to be conferred by non-scientific spectators. When using this naming scheme and referring to the genomic order of SARS-CoV-2 recognized from the first cases (Found in December 2019), the term index viruses should be used.[1]

WHO and its international networks of professionals are monitoring changes to the virus so that if noteworthy amino acid substitutions are recognized, we can inform countries and the public about any variations that may be required to respond to the variant, and prevent its spread. Globally, systems have been reputable and are being wired to detect "signals" of potential VOIs or VOCs and assess these based on the risk posed to global public health. National authorities may choose to electother variants of local interest/concern. At present scenario COVID contagion creates a pandemic and cruel lethal situation globally. Firstcase of Corona virus infection testified in **Wuhan City of China in December 2019**.Beginging from normal fever& common cold it becomes spartan with the symptoms of struggled breathe, tenacious fever, loss of taste &smell etc. It spreads through air from human to human as a form of droplet infection.[2]

METHODOLOGY

We accomplished a Cochrane,PubMed, Google Scholarpursuit in the month of February2023 by using the phrases Corona virus current variants, variants of Corona virus, detonation of corona virus etc.Our research was both time and money-efficient. The search bornea number of scientific papers, including review articles, case reports, case series, and small clinical studies.Along with some regional non-English languagereports we hadcomprehendedthe essence of the articles notwithstanding of publication dates.

HOW CORONA VIRUS VARIANTS ARE DIFFERENTIATED

The U.S. Department of Health and Human Services established a SARS-CoV-2 Interagency Group to augment coordination among CDC, NIH,FDA, BARDA and DoD. This interagency group is engrossed on the quick characterization of incipient variants and actively monitors their probable impact on critical SARS-CoV-2 countermeasures, including vaccines, therapeutics, and diagnostics.

The SIG meets frequently to evaluate the risk posed by SARS-CoV-2 variants mingling in the United States and to make endorsements about the classification of variants. This evaluation is undertaken by a group of subject matter specialists who assess available data, including variant proportions at the national and regional levels and the potential or known impact of the assemblage of alterations on the efficiency of medical countermeasures, brutality of disease, and ability to spread from person to person.

- VBM– View current VBM in the United States that endure to be scrutinized and characterized by federal agencies
- VOI– Currently, no SARS-CoV-2 variants are elected as VOI
- VOC– View current VOC in the United States that are being meticulouslyobserved and characterized by federal agencies

- VOHC– Presently, no SARS-CoV-2 variants are nominated as VOHC

*Each variant of CORONA virus includes the possible traits of lower classes; variant status might intensify or diminish based on incipient scientific evidence. This page will be updated as needed to show the alternates that belong to each class. The WHO also classifies variant viruses as variants of alarm and variants of interest; U.S. classifications may fluctuate from those of WHO because the impact of variants may differ by location. To assist with public deliberations of variants, WHO proposed using labels entailing of the Greek alphabet (for instance, alpha, beta, gamma) as anapplied way to discuss variants for non-scientific spectators.

VARIANTS

1. VBM

CDC screens all variants circulating in the United States. Variants elected as VBM include those where data directs there is a latent or clear impact on agreed or authorized medical counter measures or that have been allied with more severe disease or amplified transmission but are no longer sensed, or are circulating at very low levels, in the United States. These variants continue to be faithfully scrutinized to identify changes in their scopes and new data are recurrently being analysed.

2. VOI

A variant with exact genetic markers that have been accompanying with changes to

WHO Label	Pango Lineage	Date of Designation		
Alpha	B.1.1.7 and Q lineages	**VOC**: December 29, 2020		**VBM**: September 21, 2021
Beta	B.1.351 and descendent lineages	**VOC**: December 29, 2020		**VBM**: September 21, 2021
Gamma	P.1and descendent lineages	**VOC**: December 29, 2020		**VBM**: September 21, 2021
Delta	B.1.617.2 and AY lineages	**VOC:** June 15, 2021		**VBM:** April 14, 2022
Epsilon	B.1.427 B.1.429	**VOC**: March 19, 2021	**VOI**: February 26, 2021 **VOI**: June 29, 2021	**VBM**: September 21, 2021
Eta	B.1.525		**VOI**: February 26, 2021	**VBM**: September 21, 2021
Iota	B.1.526		**VOI**: February 26, 2021	**VBM**: September 21, 2021
Kappa	B.1.617.1		**VOI**: May 7, 2021	**VBM**: September 21, 2021
N/A	B.1.617.3		**VOI**: May 7, 2021	**VBM**: September 21, 2021
Zeta	P.2		**VOI**: February 26, 2021	**VBM**: September 21, 2021
Mu	B.1.621, B.1.621.1			**VBM**: September 21, 2021

receptor binding, abridged counteraction by antibodies caused against earlier contagion or vaccination, abridged efficacy of treatments, probable diagnostic impact, or foretold increase in transmissibility or disease sternness.Possible traits of a Variant of Interest:

- Explicit genetic markers that are prophesied to affect transmission, diagnostics, therapeutics, or immune outflow.
- Evidence that it is the reason of an increased part of cases or exceptional outbreak clusters.
- Limited pervasiveness or expansion in the US or in other countries.

A Variant of Interest might necessitate one or more suitable public health actions, including heightened sequence scrutiny, greater laboratory characterization, or epidemiological soundings to evaluate how easily the virus feasts to others, the cruelty of disease, the worth of therapeutics and whether currently permitted or authorized vaccines offer protection.

3. VOC

A variant for which there is indication of an upsurge in transmissibility, more severe disease, significant lessening in offsetting by antibodies generated during preceding infection or vaccination, reduced efficiency of treatments or vaccines, or diagnostic recognition failures.In addition to the possible traits of a variant of interest, Indicationsandeffect on diagnostics, treatments, or vaccines, widespread meddling with diagnostic test targets, evidence of considerablydiminishedvulnerability to one or more class of therapies, evidence of significantly diminished neutralization by antibodies generated during preceding infection or vaccination.

Evidence of abridged vaccine-induced protection from severe disease

- Indications of increased transmissibility
- Indications of increased disease severity

Variants of concern might require one or more suitable public health actions, such as reported to WHO under the International Health Regulations, broadcasting to CDC, local or provincial efforts to control spread, augmented testing, or research to regulate the effectiveness of vaccines and treatments against the variant. Based on the features of the variant, further considerations may embrace the development of new diagnostics or the amendment of vaccines or treatments.

4. VOHC

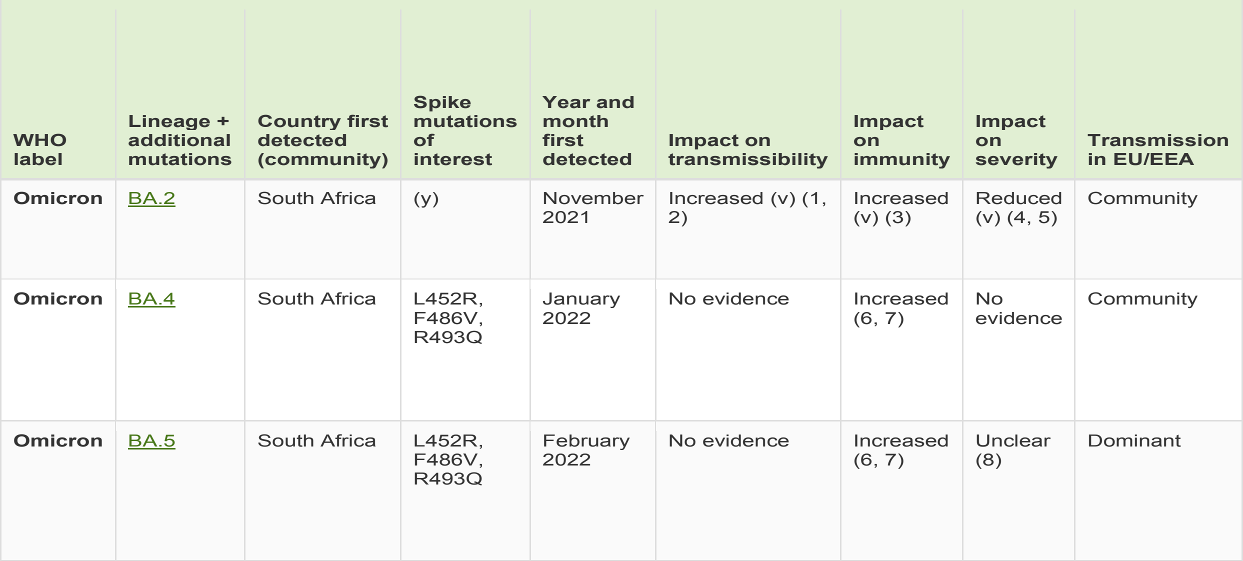
A VOHC has clear proof that deterrence MCMshave pointedly reduced effectiveness relative to formerly circulating variants. Possible features of a variant of high consequence.

Impact on MCMs

- Demonstrated failure of diagnostic test boards
- Evidence to suggest a momentous reduction in vaccine effectiveness, a excessively high number of contagions in vaccinated persons, or very low vaccine-induced defence against severe disease
- Suggestively reduced susceptibility to multiple EUA or permitted therapeutics
- More severe clinical disease and enlarged hospitalizations

THE MOST RECENT VARIANT-OMICRON

The Omicron variant (B.1.1.529) was first spotted in specimens collected on the month Nov. 11 in 2021, in Botswana. Experts in South Africa first stated the Omicron variant to the WHO on November 24 in the year 2021. They exposed the variant after COVID-19 infections abruptly began to go up.The WHO grouped Omicron as a VOC. Specialists are keeping a close eye on how the variant spreads or progresses. Experts found that one specific PCR test doesn't recognize one of the three target genes in people infested with Omicron. Because of this, these tests can unambiguously mark positive Omicron cases and, because of



WHO label	Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Impact on transmissibility	Impact on immunity	Impact on severity	Transmission in EU/EEA
Omicron	BA.2	South Africa	(y)	November 2021	Increased (v) (1, 2)	Increased (v) (3)	Reduced (v) (4, 5)	Community
Omicron	BA.4	South Africa	L452R, F486V, R493Q	January 2022	No evidence	Increased (6, 7)	No evidence	Community
Omicron	BA.5	South Africa	L452R, F486V, R493Q	February 2022	No evidence	Increased (6, 7)	Unclear (8)	Dominant

that, can spot this variant faster than with preceding surges.

In the interim, specialists recommend protecting ourselves by getting the vaccine or a booster if we are eligible for it. People should wear mask and continue with social distancing if the COVID-19 community level infection rates are high. Call doctor notices symptoms of Omicron “stealth” variant (BA.2): Scientists call it Omicron BA.2 as contrasting to the original Omicron variant, BA.1. At first, scientists supposed BA.2 wasn’t as contagious as BA.1 and would soon fade away. That didn’t occur, and preliminary in January 2022, BA.2 appeared to be at least as easy to transmit as BA.1.As of the end of February 2022, BA.2 showed signs of spreading more easily than other variants, though it didn’t seem to cause more grave symptoms. The WHO has said that BA.2 is a “variant of concern.”The best defence is still the coronavirus vaccine.[3]

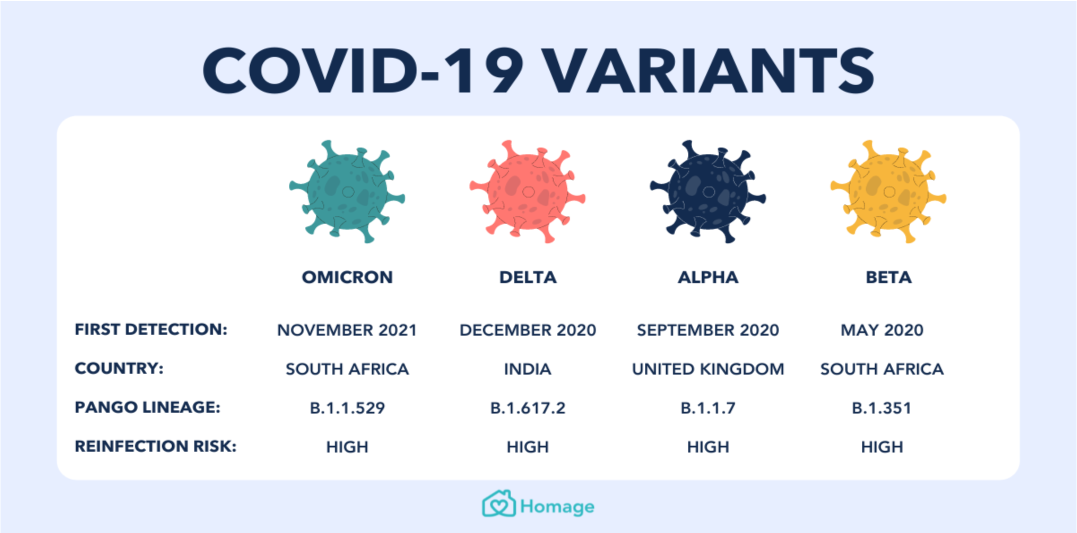
[4]THE FIRST VARIANT

Earlier in the year 2020, when the pandemic was new, we might have heard that there was more than one strain of the novel coronavirus. The theory about dissimilar variants of the new coronavirus came from a study in China. Researchers were studying changes in coronavirus RNA over time to figure out how various coronaviruses are correlated to each other. They observed near about 103 samples of the new coronavirus obtained from people, and they looked at coronaviruses from animals. There were two different types, which the researchers’named “L” and “S.” They’re very analogous, with slight alterations in two places. It looks like the S type originated first. But the researchers say the L type was more common primary in the outbreak.[5]

EARLIER CORONAVIRUS VARIANTS

- **Alpha (B.1.1.7).** In the year late 2020, experts distinguished gene mutations in COVID-19 cases seen in people in southeastern England. This variant has subsequently been stated in other countries, as well as the U.S. Scientists estimate that these mutations could make the virus up to 70% more communicable, meaning it could blowout more effortlessly. Some research has associatedthis variant to a higher risk of death, but the indication isn’t robust.[6]

The mutation on the Alpha variant is on the spike protein, which helps the virus contaminate its host. This is what COVID-19 vaccines aim. These vaccines make antibodies in contradiction of many parts of the spike protein, so it’s unlikely that a single new transformation in the Alpha variant will make the vaccine less operative.[7]



COVID-19 VARIANTS

	OMICRON	DELTA	ALPHA	BETA
FIRST DETECTION:	NOVEMBER 2021	DECEMBER 2020	SEPTEMBER 2020	MAY 2020
COUNTRY:	SOUTH AFRICA	INDIA	UNITED KINGDOM	SOUTH AFRICA
PANGO LINEAGE:	B.1.1.529	B.1.617.2	B.1.1.7	B.1.351
REINFECTION RISK:	HIGH	HIGH	HIGH	HIGH

Homage

- **Beta (B.1.351).** This variant was first found in other countries, together with South Africa and Nigeria. The Beta variant seems to feast more easily than the original virus but doesn't seem to cause inferior illness.
- **Gamma (P.1).** In January 2021, specialistsspeckled this COVID-19 variant in people from Brazil who would travel to Japan. By the end of that month, it was showing up in the U.S.
- **Delta (B.1.617.2).** This variant was marked in India in December 2020. It caused anenormous surge in cases in mid-April 2021, quickly scatteringcrossways the globe.
- **Mu (B.1.621).** Specialists first dotted this COVID-19 variant (pronounced m'yoo) in Colombia in January 2021. Meanwhile then, countries in South America and Europe have informed outbreaks of Mu.[8]
- **R.1.** Scientists first noticed R.1 in numerous countriestogether with Japan. There was aflare-up at a Kentucky nursing home in March 2021, when an unvaccinated health care worker conceded it to about 45 other staff as well as residents.
- **Epsilon**, **Theta**, and **Zeta** were at one point recorded as variants of interest and were demoted by the WHO. They are still being scrutinized.

THE COVID VACCINES ARE HIGHLY ACTIVE

A COVID-19 vaccine is a vaccine envisioned to provide acquired immunity aim to SARS-CoV-2, the virus that causes coronavirus disease the year 2019 (COVID-19). In Phase III trials, several COVID-19 vaccines have confirmed effectiveness as high as 95% in averting symptomatic COVID-19 infections. Nearly twenty vaccines have been accepted by at least one national regulatory authority for public use: nine conformist incapacitated vaccines, two RNA vaccines, one viral vector vaccines, and four protein subunit vaccines.[9]

COVID BOOSTERS UPSURGE IMMUNE RESPONSE

According to CDC data from clinical trials disclosed that a booster shot augmented the body's immune response. With an increased immune response, people should have enhanced protection in contradiction of getting infested with COVID-19, including the Delta variant. Clinical tribunals also exhibited that a booster shot helped avert COVID cases in which symptoms developed.[10]

CONCLUSION

In conclusion, the emergence of coronavirus variants has highlighted the continued threat posed by the virus to global public health. These variants are more transmissible, associated with increased hospitalization and death rates, and have reduced vaccine efficacy. It is essential that public health measures are continued and scaled up to mitigate the spread of the virus and its variants, and that global efforts are made to increase vaccine access and distribution to reduce the spread of the virus worldwide.[11]

LIST OF ABBREVIATIONS

- EUA-Emergency Use Authorization
- SARS-CoV-2 -Severe Acute Respiratory Syndrome Coronavirus 2
- VBM-Variants Being Monitored
- VOI-Variant of Interest
- VOC-Variant of Concern
- VOHC-Variant of High Consequence
- GISAID-Global Initiative on Sharing All Influenza Data
- NIH -National Institutes of Health
- FDA -Food and Drug Administration
- BARDA -Biomedical Advanced Research and Development Authority

CONFLICT OF INTEREST-Have no conflict of interest relevant to this article

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ETHICAL CLEARANCE – Not required

REFERENCES

1. Tracking SARS-CoV-2 variants [Internet]. [cited 2023 Feb 6]. Available from: https://www.who.int/activities/tracking-SARS-CoV-2-variants
2. Dipankar Maiti, & Balaji M S. (2022). Statement of the Problem: A Study to Evaluate the Effectiveness of Video Assisted Teaching (VAT) on Knowledge Regarding Prevention of Corona Virus Among Staff Nurses Working in AH & RC, B G Nagara, Karnataka. *International Journal of Nursing Education*, *14*(3), 56–62. https://doi.org/10.37506/ijone.v14i3.18351
3. Variants of Coronavirus [Internet]. [cited 2023 Feb 6]. Available from: https://www.webmd.com/covid/coronavirus-strains
4. SARS-CoV-2 variants of concern as of 26 January 2023 [Internet]. [cited 2023 Feb 6]. Available from: https://www.ecdc.europa.eu/en/covid-19/variants-concern
5. COVID Variants: What You Should Know | Johns Hopkins Medicine [Internet]. [cited 2023 Feb 6]. Available from: https://www.hopkinsmedicine.org/health/conditions-and-diseases/coronavirus/a-new-strain-of-coronavirus-what-you-should-know
6. Prompetchara E, Ketloy C, Tharakhet K, Kaewpang P, Buranapraditkun S, Techawiwattanaboon T, et al. DNA vaccine candidate encoding SARS-CoV-2 spike proteins elicited potent humoral and Th1 cell-mediated immune responses in mice. PLoS One. 2021 Mar 1;16(3 March).
7. Akkız H. The Biological Functions and Clinical Significance of SARS-CoV-2 Variants of Corcern. Front Med (Lausanne) [Internet]. 2022 May 20 [cited 2023 Feb 6];9:849217. Available from: http://www.ncbi.nlm.nih.gov/pubmed/35669924
8. Colson P, Delerce J, Beye M, Levasseur A, Boschi C, Houhamdi L, et al. First cases of infection with the 21L/BA.2 Omicron variant in Marseille, France. J Med Virol. 2022 Jul 1;94(7):3421–30.
9. Coronavirus disease (COVID-19): Vaccines [Internet]. [cited 2023 Mar 22]. Available from: https://www.who.int/news-room/questions-and-answers/item/coronavirus-disease-(covid-19)-vaccines
10. Chu L, Vrbicky K, Montefiori D, Huang W, Nestorova B, Chang Y, et al. Immune response to SARS-CoV-2 after a booster of mRNA-1273: an open-label phase 2 trial. Nat Med [Internet]. 2022 May 1 [cited 2023 Mar 22];28(5):1042–9. Available from: https://pubmed.ncbi.nlm.nih.gov/35241844/
11. Colson P, Delerce J, Beye M, Levasseur A, Boschi C, Houhamdi L, et al. First cases of infection with the 21L/BA.2 Omicron variant in Marseille, France. J Med Virol. 2022 Jul 1;94(7):3421–30.