



**Biotica
Research
Today**

Vol 3:9 ⁸⁰⁰
2021 ⁸⁰²

C.1.2 Variant: A New Coronavirus Strain Detected across Some Countries

**Jyoti Prakash Sahoo^{1*}, Kailash Chandra
Samal¹, Pranaya Pradhan² and Ankit
Moharana³**

¹Dept. of Agricultural Biotechnology, ²Dept. of Nematology,
³Dept. of Seed Science and Technology, Odisha University of
Agriculture and Technology, Bhubaneswar, Odisha
(751 003), India

 **Open Access**

Corresponding Author

Jyoti Prakash Sahoo
e-mail: jyotiprakashsahoo2010@gmail.com

Keywords

C.1.2, COVID-19, Strain, Variant

Article History

Received in 20th September 2021

Received in revised form 22nd September 2021

Accepted in final form 23rd September 2021

E-mail: bioticapublications@gmail.com

How to cite this article?

Sahoo *et al.*, 2021. C.1.2 Variant: A New Coronavirus Strain Detected across Some Countries. *Biotica Research Today* 3(9): 800-802.

Abstract

Even as the world is facing the repercussions of the deadly Delta variant of COVID-19, the main cause behind the second wave outbreak in India, two other strains of the virus has become a cause of concern globally. C.1.2 COVID-19 variant, first detected in South Africa in May, and Mu also known by its scientific name as B.1.621, first identified in Colombia in January, have been said to be a major cause of concern for the scientists. The World Health Organisation said that it is closely monitoring the new 'variant of interest' Mu or B.1.621 warning that it could be more vaccine-resistant. Mu has been behind the outbreaks in South America and Europe. The new variant exhibits similar spike proteins associated with higher rates of transmissibility, much like the delta variant of the coronavirus, and could potentially have characteristics that would allow C.1.2 to evade vaccine-induced immune responses, but researchers note further observation is needed.

Introduction

The C.1.2 Covid-19 variation was initially found in May in South Africa, although the national institute for communicable diseases in the country published a notice on the "C.1.2 lineage". At MedRxiv, a medical website, a study that is still under review pointed out that the "majority" of provinces in South Africa and "seven other nations spread throughout Africa, Europe, Asia and Oceania" were identified as C.1.2 Covid-19. However, health authorities have not yet established the full extent of the variation dissemination. Although there is a rise in communication, more severe disease, in 'variants of concern' such as the Delta variant,' the 'variants of interest' are often present in community transmission throughout a varied group but are not necessarily more virulent or transmissible. However, it must be noted here that the World Health Organization still needs to designate the reported variety C.1.2 as either a "variant of interest" or a "concern variation" (Sahoo *et al.*, 2021). In addition to several websites in the national and international journals, several popular databases, such as Google, Google Scholar, PubMed, Embassy, ScienceDirect and other academic databases were used to collect the latest data on the infections, mortality and transmissibility of the aggressive and C.1.2 COVID variant.

According to the above mentioned study, the C.1.2 lineage is mutated at a rate of around 41.8 mutations each year, nearly twice as quickly as the present global mutation rate of the other variations. Upasana Ray, a virologist at the CSIR-Indian Institute of Chemical Biology in Kolkata, added: 'There may be more transmissible, and there may be a speedy expansion.' WHO has a classification system of coronavirus variations based on social metrics on their transmissibility, virulence or effectiveness (Figure 1). As there are so many transmutations

in the spike protein, it may lead to an immune escape and, if allowed to proliferate, a global problem for vaccine driving. So far, researchers have shown that C.1.2 sequences have also discovered mutations N440K and Y449H, connected with specific immune escape. It seems like the earlier versions like Beta and Delta, based on these results. Therefore, the serum might not be neutralized as it would with an ancestral strain, although many of these projections are still theoretical. More expertise is needed to correctly assess the effectiveness of existing COVID-19 vaccines against the new strain (Business Standard, 2021).

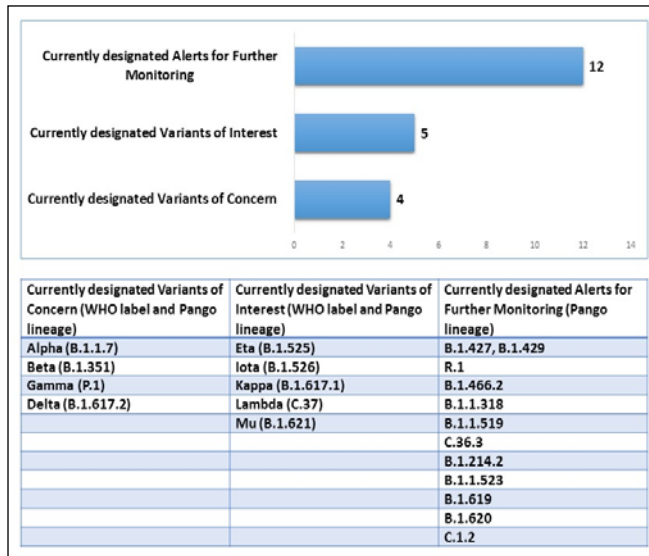


Figure 1: Tracking SARS-CoV-2 variants (Source: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>)

Recent Information and Mutation Rate of C.1.2 Corona Variant

The study reveals a novel version of SARS-CoV-2, which might be more transmissible and prevent protected vaccinations from developing in South Africa and many more other places worldwide. The possible variation of interest, C.1.2, was initially discovered in May this year by scientists from the National Institute for Communicable Diseases in South Africa and the KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP). Since then, C.1.2 has been detected in China, the DRC, Mauritius, the UK, New Zealand, Portugal and Switzerland. According to the study, C.1.2 changed considerably compared with C.1, one of the lines that dominated SARS-CoV-2 infections in the initial wave in South Africa, according to the study now being evaluated by the preprint site MedRxiv (Scheepers *et al.*, 2021). Researchers have claimed that the new version has been discovered and has more mutations than previous concern variants (VOCs) or interest variants (VOI) globally.

They also noted the possible under representation of the prevalence and frequency of variation in and throughout South Africa in the sequences provided in C.1.2. Each month the C.1.2 genome count rose consistently from 0.2% of genome sequenced in May to 1.6% in June and subsequently to 2% in July. The study revealed that the genome in South Africa was up consistent. The analysis shows that the lines of C.1.2 have a mutation rate of around 41.8 per year, which is approx. double that of other variations' present worldwide mutation rate (Sahoo *et al.*, 2021). In the C.1.2 spike area, around 52% of mutations were previously reported in other VOCs and VOIs. SARS-CoV-2 is utilized to infect and inject human cells with the spike protein, and most vaccinations are directed towards that area.

In sequences C.1.2, the mutations N440K and Y449H linked with some antibodies' immunological evasion were also noted. Although these changes are not typical for existing VOC/VOIs, they were related to escape from specific antibodies neutralizing class 3. It was also shown that coupled with alterations in other sections of the virus; these mutations are likely to allow the virus to escape antibodies and prevent immunological response, particularly for individuals with Alpha or Beta versions. A recent study revealed a new strain of coronavirus, which might become a source of concerns like the alpha, beta, and delta versions that have slashed vast waves of new infections and mortality in nations worldwide (Scheepers *et al.*, 2021).

Coronavirus: What is the R Number, and How is It Calculated?

The R number is a means to evaluate the capacity to spread coronavirus or illness. R is the average number of persons who are transmitted to a virus by an infected person. For example, in populations lacking immunity, Measles has an R number of 15. This implies a person is spreading measles to fifteen more on average. In order to determine how readily the virus spreads, the data, such as the number of individuals dying and hospitalized or positive tests for the virus over time, are employed. If the value R is over one, the number of instances increases continuously. However, if the R number is lower, the illness will cease spreading because the epidemic is not infected with enough new individuals. The R number in the United Kingdom now ranges from 0.7 to 0.9; however, regional divisions exist.

For example, the predicted R number in Scotland is somewhat higher than in the previous week, between 0.8 and 1.0. Wales counts 0.6 to 0.9, but it stays 0.75 to 0.95 in Northern Ireland. The figure in England is up slightly from 0.8 to 1.0 (BBC, 2021). Figure 2 shows an updated scenario of Covid in India, including its vaccination status. The nation had predicted its total R-value in India to rise to 1.37 between 9 March and 21 April at the peak of the second wave of the Covid-19 outbreak.

However, according to the study, it fell to 1.18 from 24 April to 1 May, followed by 1.1 from 29 April to 7 May. The R-value was measured at around 0.98 between May 9 and 11. From 14 May to 30 May it fell to 0.82, from 15 May to 26 June it fell to 0.78. However, the R-value increased from 20 June to 7 July to 0.88 and from 3-22 July to 0.95 (BBC, 2021).

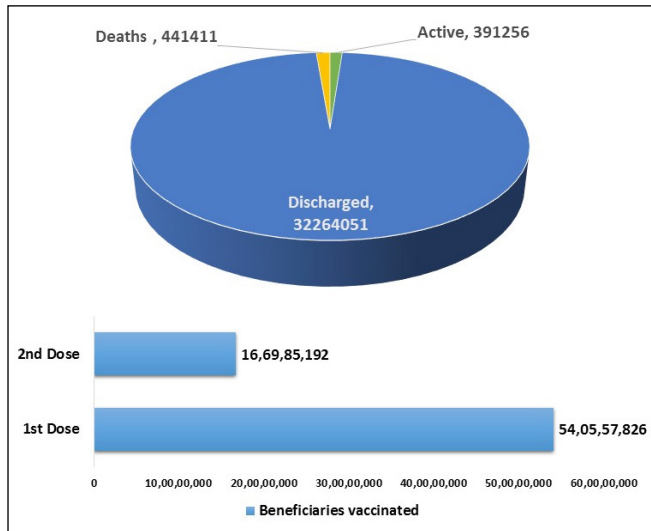


Figure 2: COVID scenario and vaccination status of India on 8th Sept. 2021 (Source: <https://www.mohfw.gov.in/>)

The Effects of Virus Variants on COVID-19 Vaccines

The majority of viral alterations have little or no effect on virus infection and disease capabilities. However, it may influence the features of a virus, such as transmission or severity, depending on where the mutations are situated in the virus' genetic material. At least some protection from new variations of the virus is predicted from the COVID-19 vaccines presently in research or have been authorized since these vaccines evoke a broad immune response, including a spectrum of antibodies and cells. Vaccines should thus not be entirely useless if modification or mutation is reported in the virus. If one of these vaccinations proves less effective against one or more variations, the mix of the vaccines can be changed to protect them. Data on new variations of the COVID-19 virus are still being gathered and analyzed.

Manufacturers and vaccine-related programmes may need to react to developments with the Virus COVID-19: for example, when in development, vaccines may need to include several strains, booster injection, and other vaccine modifications are necessary. Tests must also be devised and maintained to evaluate any change in efficacy and must be ample and varied enough so that the results can be interpreted. In order to understand their impact, studies on the impact of vaccines as deployed are equally necessary. Since the beginning of the

COVID-19, the world health organization has been monitoring the mutations in the coronavirus. It remains essential to stop the spread at the source. Continue working against new variations by lowering the quantity of viral transmission and consequently reducing possibilities for virus mutations to minimize transmission, including frequent hand washing, mask-wearing, physical distance, proper ventilation and avoiding crowded spaces or shutdown. The rapid and broadest feasible increase in vaccine manufacture and deployment will also be critical measures to protect individuals from exposure to the virus and risk of new variations. Vaccination of high-risk people in all areas should be given priority to increase world protection against novel variations and reduce transmission risks (Sahoo *et al.*, 2021).

Conclusion

While it is too early to determine if the C.1.2 variety can be classed as a variant of concern, investigators observed that it had many of the same features as corona viral versions of alpha, beta, and delta. News of a possible Delta variation is unhelpful as COVID-19 continues to be an incredibly high number average in the USA and throughout the globe, despite several authorized coronavirus vaccinations. Hesitancy in the vaccine and delayed approval contribute too many instances of unvaccinated and young people.

References

- BBC, 2021. Coronavirus: What is the R number, and how is it calculated?. Available at: <https://www.bbc.com/news/health-52473523>. Accessed on: 6th September 2021.
- Business Standard, 2021. The new variant, C.1.2, maybe more infectious, evade vaccine protection: Study. Available at: https://www.business-standard.com/article/current-affairs/new-variant-c-1-2-may-be-more-infectious-evade-vaccine-protection-study-121083000572_1.html. Accessed on: 6th September 2021.
- Sahoo, J.P., Mishra, A.P., Pradhan, P., Samal, K.C., 2021. Misfortune Never Comes Alone-The New "Black Fungus" Accompanying COVID-19 Wave. *Biotica Research Today* 3(5), 318-320.
- Sahoo, J.P., Mishra, A.P., Samal, K.C., 2021. Triple Mutant Bengal Strain (B. 1.618) of Coronavirus and the Worst COVID Outbreak in India. *Biotica Research Today* 3(4), 261-265.
- Scheepers C, Everatt J, Amoako DG, *et al.*, 2021. The continuous evolution of SARS-CoV-2 in South Africa: a new lineage with rapid accumulation of mutations of concern and global detection. *medRxiv*. DOI: <https://doi.org/10.1101/2021.08.20.21262342>.