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SHORT COMMUNICATION

Omicron wave in the COVID-19 pandemic

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ABSTRACT

Introduction:

The Omicron variant of the COVID-19 surfaced in November 2021 as the last thanksgiving and spread globally like wildfire. Spike protein mutations have been seen in this variant. The receptor binding domain (RBD) mutation of the Omicron variant raises significant concern in global vaccination programs. S gene dropout is used as a marker for Omicron detection.

Conclusion:

Thorough screening, continuous genomic surveillance, and careful adherence to prevention strategies may be helpful to curb the spread of the virus.

Keywords

Coronavirus, COVID-19, infection, mutation, variants of concern

Introduction

The Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) caused 570,005,017 confirmed cases of COVID-19 infection globally, with a death toll of 6,384,128. [1] The progression of this disease had brought about the evolution of the virus, which led to the emergence of multiple variants with different forms of mutations, changing the development of the coronavirus disease 2019 compared to when it first appeared. Some of the variants of concern (VOC) as classified by the World Health Organization (WHO) are Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1), Delta (B.1.617.2), and the most recent is Omicron (B.1.1.529) which is attributed to be the cause of the new wave in the global pandemic. [2] On November 26, 2021, the WHO declared the newly identified COVID-19 variant, B.1.1.529, as a VOC and renamed it Omicron which was first detected by scientists in South Africa. [1] Subsequently, Omicron spread all over the world [Figure -1]. [3]

The Omicron variation is characterized by 26 and 32 spike protein mutations, many of which are found within the receptor binding domain (RBD). Although three deletions and one insertion in the spike protein are prominent in the Omicron, mutations in other parts are also prominent. [4] S gene as a key target failed to detect during the routine polymerase chain reaction tests for SARS-CoV-2, and a heavily mutated genome is found [5] Some of the mutations are responsible for neutralization antibody escape, and research on previous VOC has shown that these variations might be antigenically significantly different. [4] The RBD of the SARS-CoV-2 Omicron variant, which interacts with human angiotensin-converting enzyme 2 (ACE2), has ten mutations. In contrast, the Delta variant has only two mutations. [6] RBD mutation of SARS-CoV-2 Omicron variant raises significant concern in global vaccination programs. Computer modelling suggests that omicron had the potential to dodge T cell-mediated immunity. [7]

In the PCR test of COVID-19 diagnosis, one of the three target genes is undetected (known as S gene dropout or S gene target failure); used as a marker for Omicron detection without the need of performing a complete genetic analysis. [8]

Studies showed the vaccine efficacy against symptomatic patients infected by the omicron variant is significantly lower comparing the delta variant. According to a study, after two doses, vaccine effectiveness decreased, with minimal vaccine effects seen from 20 weeks after the second dose of any vaccine. Booster doses enhanced the protection against mild infection; however, there are reports of declining protection in the patients after booster doses. [9]

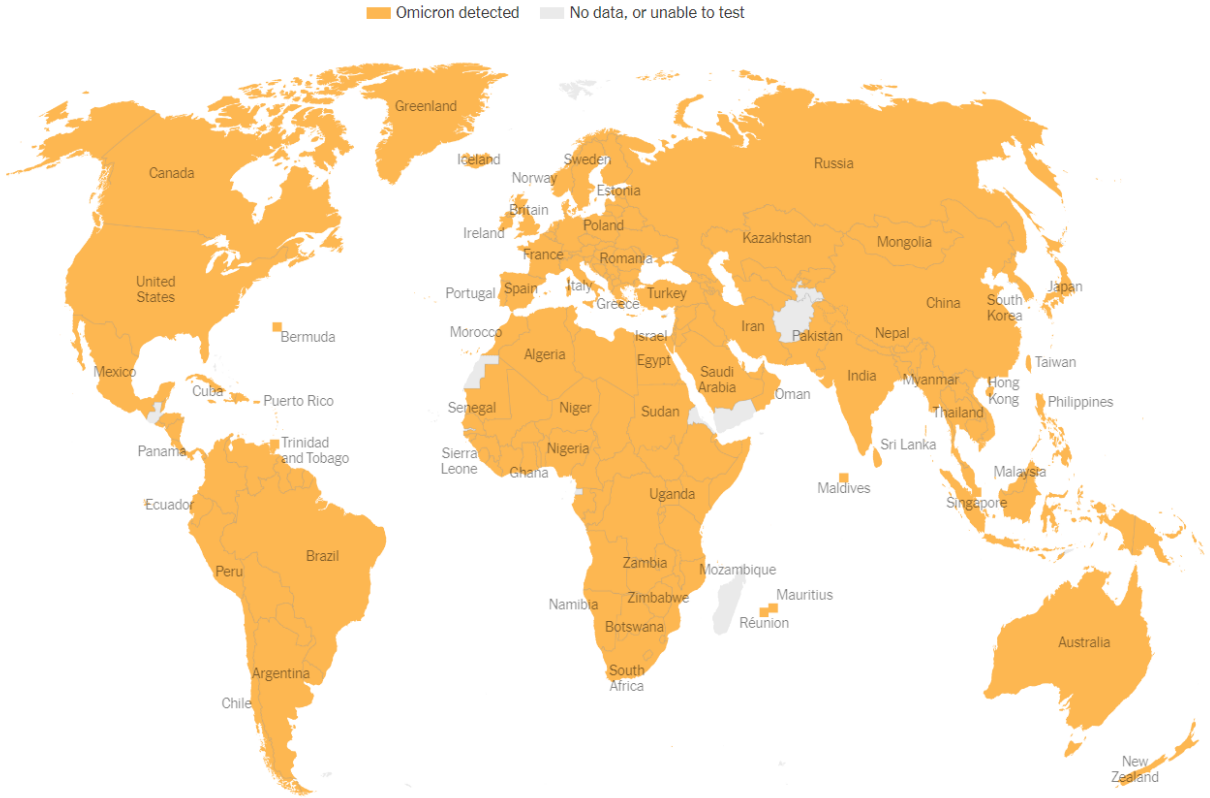

Figure 1: Global spread of Omicron

Conclusion

Governments must take stringent measures to prevent the transmission of the Omicron variation of SARS-CoV-2 by implementing tactics such as thorough screening of international travellers, continuous genomic surveillance, and strain identification by sequencing. As the vaccine's efficacy remains in a dilemma, careful adherence to prevention strategies will be the best way to diminish potential future threats.

Abbreviations

Angiotensin-converting enzyme 2 (ACE2), Coronavirus disease (COVID-19), receptor binding domain (RBD), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), variants of concern (VOC), World Health Organization (WHO)

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Authors' contribution

a. Study planning: JNY, NS

b. Manuscript writing: JM, CJP, JNY, NS

c. Manuscript revision: JM, CJP, JNY, NS

d. Final approval: JM, CJP, JNY, NS

e. Agreement to be accountable for all aspects of the work: JM, CJP, JNY, NS

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Competing interests

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