

# STUDY SHOWS COVID-19 VARIANT XBB IS HIGHLY INFECTIOUS, FAVOURS BOOSTER DOSE TO PROTECT PEOPLE

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

To enjoy additional benefits

CONNECT WITH US

September 15, 2023 12:23 am | Updated 12:40 am IST - CHENNAI

COMMENTS

SHARE

READ LATER

Image used for representative purpose only. File | Photo Credit: SHIV KUMAR PUSHPAKAR

A cohort study, which has indicated that one of Omicron's subvariant, XBB, is highly evasive from available vaccines as 81.1% of the studied infected persons were vaccinated, has highlighted the urgent need for polyvalent vaccines. It also underscores the need for continuous genomic surveillance of SARS-COV-2 to keep a close watch on the emergence of new variants in the community.

Tamil Nadu's State Public Health Laboratory (SPHL), where a whole genome sequencing (WGS) laboratory is functioning, decided to take a closer look at samples that tested positive for XBB variants of Omicron reported from September 2022 to January 2023.

This was following a surge in COVID-19 cases during September 2022 with reports of several breakthrough infections and re-infections in the community.

The findings and recommendations of the study — clinical characteristics and novel mutations of Omicron subvariant XBB in Tamil Nadu, India — a cohort study - was recently published in The Lancet Regional Health-South East Asia.

T.S. Selvavinayagam, Director of Public Health and Preventive Medicine, was the study's lead author.

Of the 2,085 COVID-19 samples sequenced during that period, 420 were reported as XBB (20.14%) variants in the State.

Of this, 244 were selected based on collective information to study the clinico-demography of the cohort and 98 were selected for sequence studies. XBB.3 was the predominant sub-lineage of XBB identified in the study population, infecting 139 individuals; 57% of the total cases in the cohort. Next was XBB.1 that was seen in 56 individuals.

The researchers found that for 200 of the 244, this was their first exposure while for 44 others, it was their second COVID-19 encounter among which 25 were infected with XBB.3 variant.

Based on the data, XBB.3 appeared to be more virulent and prevalent within the study cohort, it said.

One of the key findings was that XBB sub-variants were evasive against available vaccines and may be more transmissible, one of the authors, S. Raju, who is the deputy director of SPHL said.

About 81% of the infected persons were vaccinated of which 78.2% were vaccinated with two or more doses and 2.9% were partially vaccinated with a single dose.

Analysis found that age and underlying conditions such as diabetes, hypertension and cardiovascular disease or secondary complications increased susceptibility to infection rather than vaccination status or prior exposure — 52 individuals reported a single underlying condition and 24 had two or more underlying conditions.

The findings advocated the need to develop bivalent/multivalent booster vaccine for the entire population to protect them from emerging variants of concerns.

The study identified 43 mutations in the S gene across 98 sequences. Of these, two were novel mutations (A27S and T7471) that were not reported previously with XBB sub-variants in the available literature.

Continuous surveillance of viral mutations is critical to identifying emergence of new variants and for developing an effective vaccine.

“The WGS lab will continue to monitor the genomic surveillance of SARS-CoV-2 virus circulating in the community and intends to forecast early warning signals of impending threat due to the emergence of new variants of coronavirus in the community, thereby help reduce the disease burden in the State,” he said.

COMMENTS

SHARE

[Chennai](#) / [Coronavirus](#)

BACK TO TOP

Comments have to be in English, and in full sentences. They cannot be abusive or personal. Please abide by our [community guidelines](#) for posting your comments.

We have migrated to a new commenting platform. If you are already a registered user of The Hindu and logged in, you may continue to engage with our articles. If you do not have an account please register and login to post comments. Users can access their older comments by logging into their accounts on Vuukle.

**END**

Downloaded from [crackIAS.com](#)

© **Zuccess App** by crackIAS.com