

Clinical characteristics and novel mutations of omicron subvariant XBB in Tamil Nadu, India – a cohort study



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Summary

Background Despite the continued vaccination efforts, there had been a surge in breakthrough infections, and the emergence of the B.1.1.529 omicron variant of SARS-CoV-2 in India. There is a paucity of information globally on the role of newer XBB variants in community transmission. Here, we investigated the mutational patterns among hospitalised patients infected with the XBB omicron sub-variant, and checked if there was any association between the rise in the number of COVID-19 cases and the observed novel mutations in Tamil Nadu, India.

Methods Nasopharyngeal and oropharyngeal swabs, collected from symptomatic and asymptomatic COVID-19 patients were subjected to real-time PCR followed by Next Generation Sequencing (NGS) to rule out the ambiguity of mutations in viruses isolated from the patients ($n = 98$). Using the phylogenetic association, the mutational patterns were used to corroborate clinico-demographic characteristics and disease severity among the patients.

Findings Overall, we identified 43 mutations in the S gene across 98 sequences, of which two were novel mutations (A27S and T747I) that have not been reported previously with XBB sub-variants in the available literature. Additionally, the XBB sequences from our cohort had more mutations than omicron B.1.1.529. The phylogenetic analysis comprising six major branches clearly showed convergent evolution of XBB. Our data suggests that age, and underlying conditions (e.g., diabetes, hypertension, and cardiovascular disease) or secondary complications confers increased susceptibility to infection rather than vaccination status or prior exposure. Many vaccinated individuals showed evidence of a breakthrough infection, with XBB.3 being the predominant variant identified in the study population.

Interpretation Our study indicates that the XBB variant is highly evasive from available vaccines and may be more transmissible, and potentially could emerge as the 'next' predominant variant, which likely could overwhelm the existing variants of SARS-CoV-2 omicron variants.

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