# Characteristics of SARS-CoV-2 Omicron BA.5 variants in Shanghai after ending the zero-COVID policy in December 2022: a clinical and genomic analysis

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**Abstract**

An unprecedented surge of Omicron infections appeared nationwide in China in December 2022 after the adjustment of COVID-19 response policy. In this study, we report the clinical and virological characteristics of SARS-CoV-2 Omicron BA.5 infections among children in Shanghai during the outbreak in late December 2022. We sequenced the 64 SARS-CoV-2 positive samples obtained from hospitalized children. The genomic monitoring revealed that the current outbreak was driven by the BA.5.2.48 and BF.7.14 subvariants. Additionally, children with BA.5.2.48 infection were more frequently observed to experience vomiting/diarrhea compared to those with BF.7.14 infection. The high-frequency unique non-synonymous mutations were present in BA.5.2.48 (N: Q241K) and BF.7.14 (nsp2: V94I, nsp12: L247F, S: C1243F, ORF7a: H47Y) with respect to their parental lineages. Of these mutations, C1243F mutation in S protein, L247F mutation in nsp12, and H47Y mutation in ORF7a protein were predicted to have a deleterious effect on the protein function. Besides, H47Y mutation was also found to increase the stability of ORF7a protein. Therefore, attention should be paid to these specific mutations, especially for H47Y mutation, which could serve as a viral immune escape strategy due to the potential immunomodulatory ability of the ORF7a protein. Continuous genomic monitoring and clinical manifestation assessments of the emerging variants will be crucial for effective responses to the ongoing COVID-19 pandemic.

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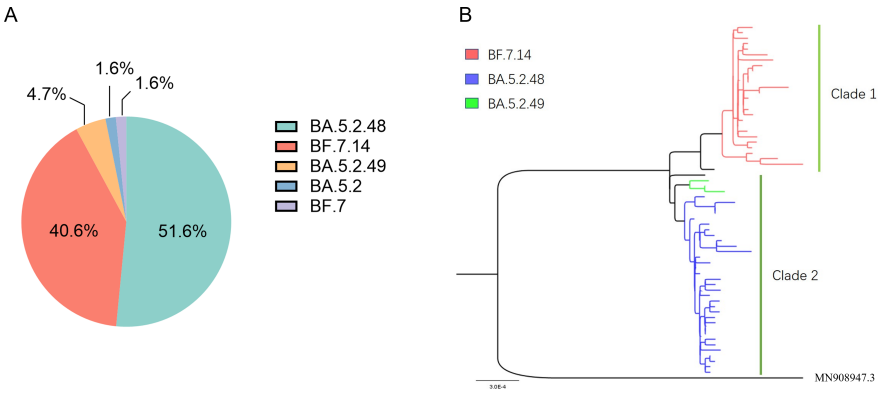


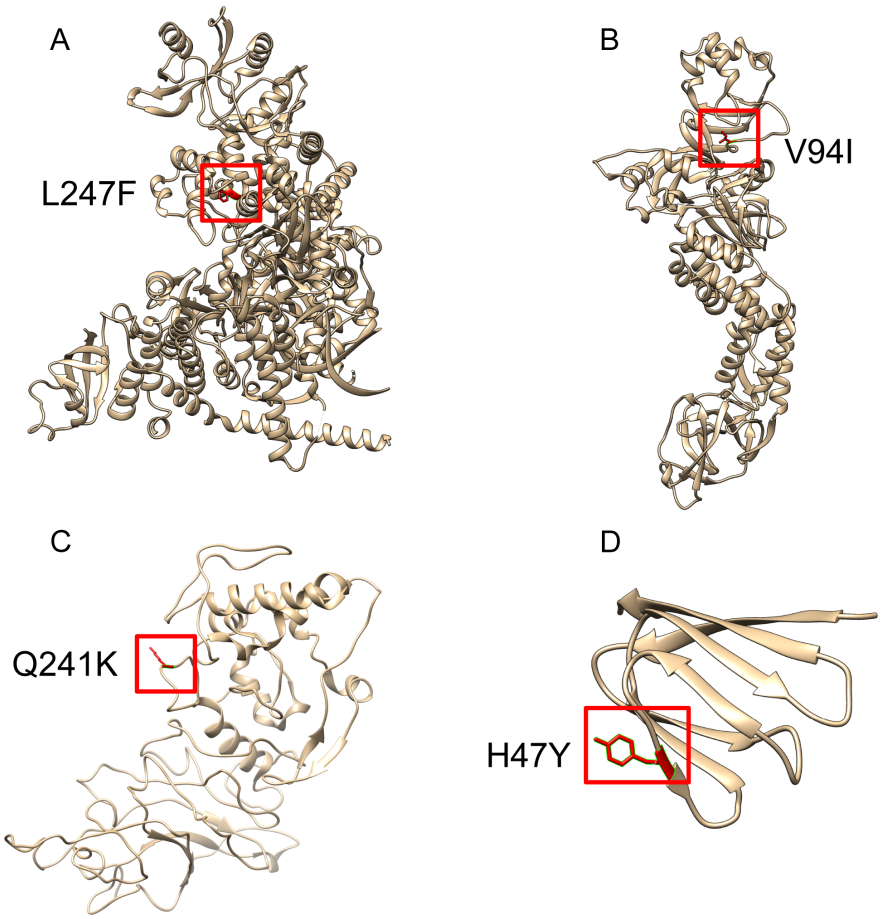


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