



Assessing the Potential Impact of CH.1.1 and JN.1 Variants on Bangladesh's COVID-19 Situation: Should Bangladesh be Concerned?



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Dear Editor,

On March 8, 2020, the first COVID-19 patient was detected in Bangladesh. Being a resource-poor, highly densely populated country, the nation encountered significant challenges in containing the virus's spread at that time¹⁻².

Since the arrival of SARS-CoV-2 in 2019, the virus has gone through several mutations. According to the World Health Organization (WHO), there are 5 major variants of concern (VOC) of SARS-Cov-2, among which Omicron (B.1.1.529) has raised huge concern in the global community. The Omicron variant (B.1.1.529) underwent fast genomic evolution in a short period, providing five initial lineages (BA.1.1, BA.2, BA.3, BA.4, and BA.5), including the BA.2.75 lineage³.

The CH.1.1 sub-lineage, also known as "Orthrus", is a descendant of BA.2.75⁴. Since the emergence of the CH.1.1 sublineage, it has raised alarm due to the appearance of the L452R mutation in the S protein, which boosts transmissibility (similar to the Delta variant and BA.4/5 variants). Other mutations in the receptor-binding domain (RBD) allow it to evade antibodies and bind tightly to ACE2 receptors. CH.1.1 has 39 spike protein mutations in common with the Delta variation, indicating the possibility of enhanced disease severity and vaccine evasion. Studies indicated that it shows nearly complete escape from neutralization by triple-vaccinated or BA.4/5 infected sera, which demonstrates considerable immune evasion capabilities and heightens concerns despite its current low prevalence⁴⁻⁷.

On the other hand, JN.1 is a highly mutated sub-variant of BA.2.86 (also known as "Pirola") that has increased in prevalence and evolved quickly. It is presently listed as a "variant of interest." by the WHO⁸⁻⁹. JN.1 is much more transmissible than its parent strain and more resistant to antibodies due to the S: L455S mutation in the spike protein. This mutation separates JN.1 from other variants, contributing to its superior immune evasion skills and probably explaining its higher reproducing rate. It propels it to become the dominant strain in many countries, outperforming other variants⁹. In Bangladesh, the inadequate monitoring of water systems presents a significant danger, particularly given the widespread presence of the JN.1 variant, which has been efficiently identified through surveillance methods based on wastewater epidemiology¹⁰.

Furthermore, JN.1 shows considerable resistance to XBB.1.5 vaccination sera, indicating that it can potentially be a highly immune-evading mutant with negative effects on vaccine efficacy and transmission dynamics⁹.

According to Outbreak.info as of March 20, 2024, CH.1.1 gradually expanded to over 88 countries after emerging first in India in July 2022^{4,11}. The website reveals India and China having CH.1.1 prevalence below 0.5% from September 2022 to February 2023 and November 2022 to June 2023, respectively, with no cases reported in Bangladesh. Additionally, CH.1.1 has shown very low prevalence worldwide in the last six months¹¹. JN.1, on the other hand, was discovered in the United States in September 2023 and has reached at least 106 nations. JN.1's first case in Bangladesh

was reported by IEDCR in January 2024. This sub-variant is prevalent in India (37%) and China (19%), with Bangladesh notably higher at 82%, within specific timeframes from late 2023 to early 2024, according to Outbreak.info. The WHO claims that because JN.1 is immune resistant, it might spread quickly throughout Bangladesh, especially during the winter^{8,11-12}. However, limited data on mortality and hospitalization rates for the JN.1 variant in Bangladesh are available, although in the neighboring country like India, these rates were low in the case of both variants, suggesting a lower severity of the disease in the country according to the Times of India¹³⁻¹⁴.

Both CH.1.1 and JN.1 variants pose concerns regarding transmission, immune escape, and disease severity. CH.1.1, despite not being detected in Bangladesh yet, carries mutations like L452R, enhancing transmissibility and potentially increasing disease severity. Similarly, JN.1, with mutations such as S: L455S, is highly transmissible and resistant to antibodies, affecting vaccine efficacy and transmission dynamics. Both variants evade immunity from previous infection or vaccination; CH.1.1 shows nearly complete escape from neutralization by triple-vaccinated or BA.4/5 infected sera, while JN.1 resists XBB.1.5 vaccination sera, challenging vaccination efforts. Although CH.1.1 has expanded to over 88 countries, including India, its global prevalence remains relatively low. Conversely, JN.1 has spread to at least 106 nations, with significant presence in India, China, and Bangladesh. While limited data on JN.1's severity in Bangladesh exist, the lower severity observed in India may not guarantee the same outcome in Bangladesh.

Challenges such as limited or poor healthcare infrastructure and ICU capacity compromised immune systems due to previous immunizations, inadequate antiviral treatments, and poor hygiene awareness pose significant concerns in Bangladesh¹⁵. Also, with shortages of ventilators and oxygen, Bangladesh's strained healthcare system may struggle further exacerbating the situation. Limited medical expertise and high population density further increase the risk of complications from emerging variants. Therefore, to lessen the impact, enhancing healthcare capacity and vaccination coverage is crucial. Improving testing, sanitation, and public awareness along with enforcing travel restrictions, promoting safety measures, and investing in variant-specific treatments are vital steps that the country should focus on.

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