

# Phyloepidemiology and adaptive evolution of SARS-CoV2 during the first and second wave of COVID-19 in India

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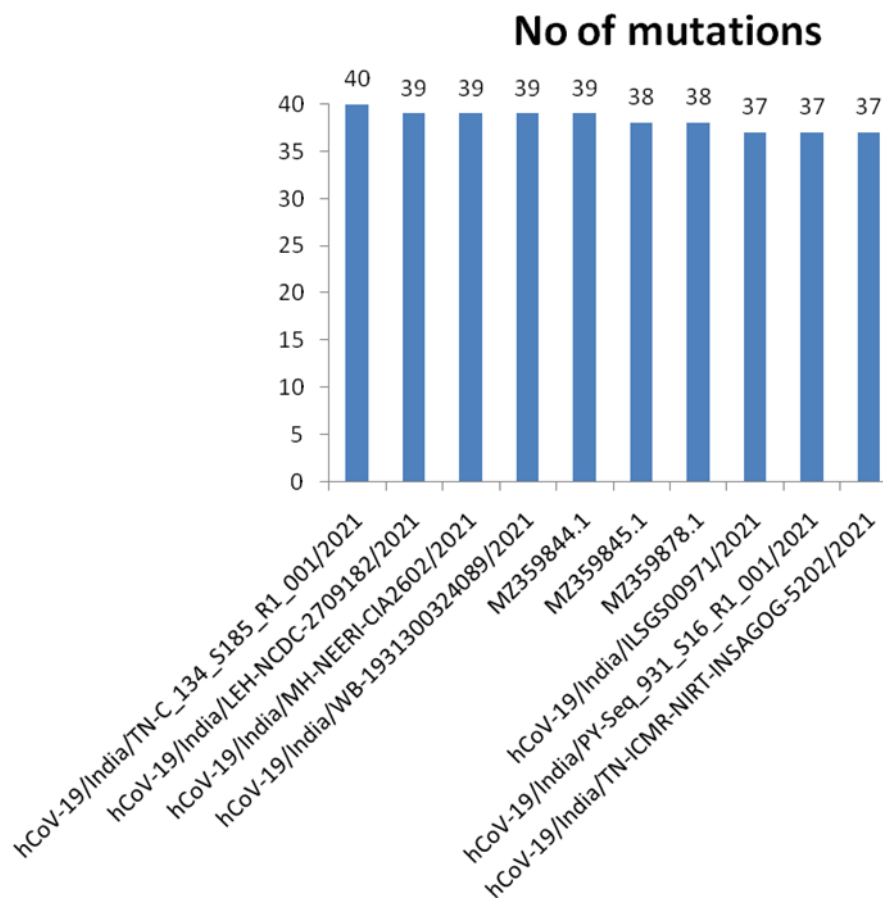
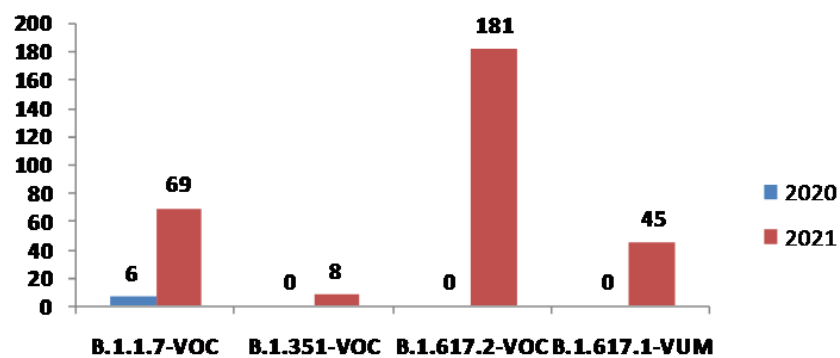
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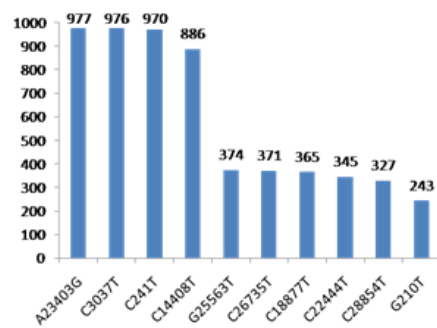
## Abstract

This study was conducted to know the various circulating lineages of SARS-CoV-2, prevalent mutations in lineages, and selective pressure analysis on the genome of SARS-CoV-2 during the first and second wave of the COVID-19 pandemic in India. For this purpose total of 1451 sequences from June 2020-June 2021 spanning from various regions of India were downloaded from NCBI and GISAID. The sequences were blasted using the Pangolin COVID-19 lineage assigner. Total, forty-one lineages were found to be circulating in India during this one year. Thirty-five lineages were circulating during the first wave and twenty lineages were circulating during the second wave out of which six were new lineages. During the first wave, in 2020 only one Variant Of Concern (Alpha) was found and during the second wave in 2021 three variants of concern (Alpha, Beta, and Delta) were in circulation. One Variant Under Monitoring was also prevalent during the second wave. The most frequent mutations observed were S: D614G, NSP3: F106F, NSP 12b: P314L, ORF3a: Q57H, M: Y71Y, NSP14:C279C, S: D294D, N: S194L. Interestingly, the ten most mutated samples belonged to Delta variant of B.1.617.2 lineage and all were found in the second wave which justifies the severity of the second wave. Five mutations L452R, T478K, E484Q, N501Y, and D614G in the spike protein responsible for increased transmissibility and reduction in neutralization by convalescent sera were majorly prevalent during second wave out of which D614G, L452R, and T478K were present at prevalence rate of 88.25%, 21.04%, and 16.80%, respectively. The major selection was purifying selection, however, few sites in the NSP2, NSP3, NSP13, S protein, ORF3a, and ORF9 evolved under positive selection. We hereby also report six novel mutations, three in NSP2 (P129A, V381A, V381F), one in NSP3 (P822S), and one in S protein (Q23R) evolving under positive selection pressure.

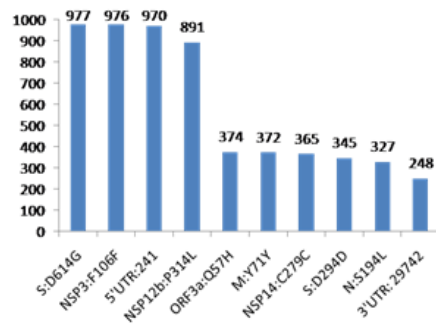
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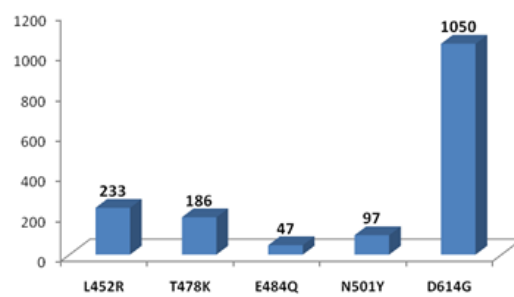




(3a.)



(3b.)



(3c.)

