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B.1.617.2: do you know all about it?

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Abstract

In December, 2019, a series of pneumonia cases of unknown cause emerged in Wuhan, Hubei, China, with clinical presentations greatly resembling viral pneumonia. Deep sequencing analysis from lower respiratory tract samples indicated a novel coronavirus, virus formerly called as the “Wuhan virus” and provisionally designated as novel coronavirus “2019-nCoV” by WHO & was identified as being responsible for this outbreak. **Globally**, as of 23 April 2021, there have been **144,099,374 confirmed cases** of COVID-19, including **3,061,912 deaths**, reported to WHO. The global spread of SARS-CoV-2 has resulted in tens of thousands of mutations in the native strain within a short time. The D614G mutation in the viral S-protein is now the most prevalent globally. However, it may be noted that the D614 prevalent epidemics are still prevalent in many locations when G614 first began to appear. The D614G mutant virus is not associated with increased mortality or clinical severity but is more transmissible among hosts and associated with a higher viral load. This study was conducted by circulating an online questionnaire among people of different age groups and professions. The results were assessed according to the option selected by participants, each question was provided with multiple choice options.

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