

Conflicts of interest. All authors report no conflicts of interest relevant to this article.

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The 501.V2 and B.1.1.7 variants of coronavirus disease 2019 (COVID-19): A new time-bomb in the making?

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To the Editor—The second wave of coronavirus disease 2019 (COVID-19) has been incessantly causing catastrophe across the world. According to the World Health Organization (WHO), the total numbers of confirmed cases and deaths as of December 20, 2020, were 75,110,651 and 1,680,395, respectively.¹ America is leading, with the highest number of cases, followed by Europe, Southeast Asia, the Eastern Mediterranean, Africa, and the Western Pacific. Although many countries have loosened lockdowns and travel restrictions, the crisis is not yet over. Many emerging economies were already facing feeble growth before the crisis; the COVID-19 shock introduced difficult obstacles and devastated these economies.² This plight has highlighted the need for immediate action to cushion the pandemic's health and economic repercussions, protect susceptible populations, and set the stage for a lasting recovery.²

Apparently, severe acute respiratory coronavirus virus 2 (SARS-CoV-2) brings a new challenge to the world with every new day. Genomic scientists in South Africa noticed a particular variant of SARS-CoV-2 in the samples collected over the past 2 months and named it the 501.V2 variant.³ The distinguishing feature of this variant is that it has several mutations in the parts that allow it to attach to human cells, which is a target of antibody therapies and vaccines. Preliminary analysis of the swabs revealed faster spread associated with high viral load. One of the mutations is N501Y, which occurs in the genetic sequence that codes for viral spike protein that binds to the human ACE-2 receptor.⁴ This mutation is most likely associated with a faster spread in other countries like Britain and Australia.³ The 3 leading vaccines are producing

antibodies against many regions of the spike protein. It has been predicted that a single mutation in the spike protein will not cause the failure of the vaccine. England's Health Secretary Matt Hancock said, "If this new viral strain causes vaccine failure or reinfection, then that case would be treated as a high priority for genetic sequencing."⁴

Another variant, B.1.1.7, was detected by the evolution working group of the World Health Organization (WHO) with UK medical authorities. This strain has been detected in the Netherlands, Denmark, and Australia, and it is predicted to affect the pandemic.⁵ Two major concerns related to this variant are the unprecedented number of mutations and the speed of spread. Scientists say that 23 letters in the viral genetic code have been changed, of which 17 might cause behavioral changes in the entry into and propagation of human cells. Computer modeling of this strain suggests that it is 70% more transmissible than other SARS-CoV-2 strains. These characteristics enable this new strain to supplant other strains of SARS-CoV-2. However, there is uncertainty regarding the course of illness, the severity of disease in the people infected with B.1.1.7 strain, and the effectiveness of vaccines under development against it.⁵

These new mutant strains are presenting a new global threat in the COVID-19 pandemic. By December 9, 2020, the 501.V2 strain occupied 62% of London, 59% of eastern England, and 43% of the southeastern region of the England.⁶ Due to fear of this new COVID-19 strain, countries like Italy, Belgium, France, and the Netherlands have banned flights to and from the United Kingdom. Saudi Arabia has also suspended its international commercial flights recently. This ban has also been applied to the passengers coming through land and seaport, but it has not been applied to the imports, commodities, and supply chains from countries where the mutated virus has not appeared.⁶

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The origin of this new variant is unknown. Regular COVID-19 tests cannot detect viral mutations. Variants can be identified when all 30,000 letters of viral genetic code in each sample are determined using specialized sequencing techniques.⁵ Britain's robust surveillance system detected the new strain before other nations. However, it remains likely that these variants are present in other regions of the world and have not been detected yet. Testing of the new variant will take weeks, but there is no expectation regarding the changes in the severity of disease or resistance to vaccination.⁴ More coordinated regional or global efforts on genetic sequencing are needed to monitor the COVID-19 variants and to curb their transmission through vaccines or antibody therapies.

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