COVID-19 variants and its overview.

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Abstract

The virus that causes COVID-19, SARS-CoV-2, has had a significant impact on human health worldwide; infecting a large number of people; causing severe disease and associated long-term health sequelae; leading to death and excess mortality, especially among older and vulnerable populations; disrupting routine health services; disrupting travel, trade, education and many other social functions; more generally, it has a detrimental effect on the physical and mental health of people.

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Introduction

The WHO has received many reports of unusual public health incidents, likely due to variants of SARS-CoV-2, since the beginning of the COVID-19 pandemic. The WHO periodically evaluates whether SARS-CoV-2 variants contribute to changes in transmissibility, clinical appearance and severity, or whether they affect countermeasures, including diagnostics, therapies and vaccines.

Interest and concern have been posed by previous reports of the D614G mutation and recent reports of virus variants from the Kingdom of Denmark, the United Kingdom of Great Britain and Northern Ireland, and the Republic of South Africa about the effects of viral changes.

In late January or early February 2020, a version of SARS-CoV-2 with a D614G substitution in the gene encoding the spike protein appeared. The D614G mutation replaced the initial SARS-CoV-2 strain found in China over a span of several months and became the dominant form of the virus circulating globally by June 2020. Studies in human respiratory cells and animal models have shown that the strain with D614G replacement has improved infectivity and transmission relative to the initial virus strain. D614G replacement SARS-CoV-2 virus does not cause more serious disease or change the efficacy of current laboratory diagnostics, therapeutics, vaccines, and preventive measures for public health.

A SARS-CoV-2 variant associated with infection among farmed mink and subsequently transmitted to humans was reported in North Jutland, Denmark, in August and September 2020. The variant, referred to by the Danish authorities as the 'Cluster 5' variant, has a combination of mutations not previously observed. Due to preliminary studies conducted in Denmark, there is concern that this variant may lead to decreased human neutralisation of the virus, potentially reducing the length and period of immune defence after natural infection or vaccination. Studies are underway to test human neutralisation of viruses with this variant. To date, after thorough investigation and surveillance, only 12 human cases of the Cluster 5 variant were detected by the Danish authorities in September 2020, and it does not seem to have spread widely.

The authorities of the United Kingdom reported to the WHO on 14 December 2020 a variant referred to by the United Kingdom as SARS-CoV-2 VOC 202012/01 (Variant of Concern, year 2020, month 12, and variant 01). This version comprises 23 substitutions of nucleotides and is not phylogenetically related to the SARS-CoV-2 virus circulating in the United Kingdom at the time of discovery of the variant. It is unknown where and how SARS-CoV-2 VOC 202012/01 originated. Initially, SARS-CoV-2 VOC 202012/01 emerged in South East England, but started replacing other virus lines in this geographic region and London within a few weeks. As of 26 December 2020, from routine sampling and genomic research carried out throughout the United Kingdom, SARS-CoV-2 VOC 202012/01 was identified. Preliminary epidemiological, modelling, phylogenetic and clinical studies indicate an increased transmissibility of SARS-CoV-2 VOC 202012/01.

Epidemiological and virological studies are being performed by the authorities in the affected countries to further assess the transmissibility, seriousness, risk of reinfection, and the antibody response to new variants. Since one of the mutations (N501Y) contained in the receptor-binding domain is found in both the SARS-CoV-2 VOC 202012/01 and 501Y.V2 variants, the authorities are investigating the neutralisation. Since one of the mutations (N501Y) found in both the SARS-CoV-2 VOC 202012/01 and 501Y.V2 variants is in the receptor binding domain, the authorities are investigating the neutralisation activity of sera against these variants from recovered and vaccinated patients to determine whether there is any impact on the performance of the vaccine. Such studies are underway.