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NEW VARIANTS OF THE SARS-COV-2 VIRUS AND THEIR IMPACT ON THE EPIDEMIC PROCESS

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Introduction. Worldwide, as of April 18, 2021, 140,322,903 confirmed cases of COVID-19 were registered, including 3,003,794 deaths. [1] Since the beginning of the pandemic, as of April 18, 1,946,510 confirmed cases of COVID-19 have been recorded in Ukraine, including 39,786 deaths. The number of active patients is 424,645 people [2].

Viral populations that exist in nature are well adapted to external conditions and may not undergo significant changes for a long time. However, when these conditions change, the restructuring of the hereditary structure becomes necessary for the survival of the population.

Viruses are constantly changing as a result of mutations, and variations of the SARS-CoV-2 virus are observed all over the world due to the processes of evolution and adaptation [3].

The aim of the work is to review mutations SARS-CoV-2 and their impact on the epidemic process. Outlining the necessary directions of development and prospects for improving the system of surveillance for COVID-19.

Methods. The work used a bibliosemantic method and a systematic review of individual studies and published data. The materials of the research were publications in foreign scientific journals.

Results. Cases of pneumonia of unknown etiology were first reported in late December 2019 in Wuhan, Hubei Province, People's Republic of China. A new type of coronavirus was isolated on January 7, 2020. [4].

SARS-CoV-2 is a single-stranded RNA-containing strain of the genus beta-coronavirus, with a compact genome length of 29,903 nucleotides [5].

Shortly after the SARS-CoV-2 virus was discovered in China, researchers began analyzing samples and publishing genetic codes online [6].

More than 450,000 SARS-CoV-2 genomes have already been sequenced worldwide [7].

The diversity of viruses and their genetic diversity is largely due to mutations and changes in structure. All viruses, including SARS-CoV-2, subsequently change. There are hundreds of variants of this virus in the world.

Although most emerging mutations will not significantly affect the spread of the virus, some mutations or combinations of mutations may confer a selective advantage on the virus, such as increased transmissibility or the ability to evade the host immune response. [3]

A variant of SARS-CoV-2 with the D614G mutation in a gene encoding a spiny protein appeared in late January or early February 2020, and within a few months the D614G mutation replaced the original SARS-CoV-2 strain identified in China by June 2020. has become the dominant form of the virus circulating around the world. Studies of human respiratory cells and animal models have shown that compared to the original strain of the virus, the strain with the D614G mutation enhances infectivity and transmission. [8]

Apart from this, several new options appeared last year, in particular: in the UK, known as 20I / 501Y.V1, VOC 202012/01, or B.1.1.7; in South Africa, known as 20H / 501Y.V2 or B.1.351 (this variant has some mutations with B.1.1.7); in Brazil, known as P.1, which was first detected in four travelers from Brazil who were tested during a routine survey at Haneda Airport outside Tokyo, Japan. This variant has 17 unique mutations, including three in the spike protein receptor-binding domain. [9]

Variant SARS-CoV-2 VOC 202012/01 contains 23 nucleotide substitutions and has no phylogenetic link with the SARS-CoV-2 virus circulating in the United Kingdom at the time of detection of this variant. Preliminary results of epidemiological, phylogenetic, clinical studies and modeling indicate increased transmissibility of SARS-CoV-2 VOC 202012/01 [8]. However, previous studies also show that in the United Kingdom there are no changes in the severity of the disease (measured by the duration of hospitalization and 28-day mortality) or recurrent infections in patients infected with this variant, compared with patients infected with other SARS-CoV-2 viruses circulating in the United Kingdom [10].

Regarding the variant that appeared in South Africa, genomic data show that the 501Y.V2 variant rapidly displaces other lines circulating in South Africa, and previous studies have suggested that this variant is associated with a higher viral load, which may indicate increased transmissibility, but this is the subject of further study [8].

As of the beginning of April, the circulation of a strain of British origin was recorded in 21 regions of Ukraine, and in the Poltava region – of South African origin [11].

Scientists are working to learn more about the options, to better understand how easily they can be transmitted, and about the effectiveness of approved vaccines.

The GISAID initiative facilitates the rapid exchange of data on all influenza viruses and coronaviruses, which causes COVID-19. These include the genetic sequence and relevant clinical and epidemiological data related to human viruses, as well as geographical and species-specific data related to avian and other animal viruses, to help researchers understand how viruses develop and spread during epidemics and pandemics. [12]

Early exchange of SARS-CoV-2 genome sequences allowed the rapid development of molecular diagnostic tests, which increased global preparedness and facilitated the development of pandemic response measures. Rapid large-scale sequencing of the viral genome helps to understand the dynamics of viral epidemics and assess the effectiveness of control measures [13].

Conclusions. The identification of variants of the virus and their subsequent characteristics allows us to study: their ability to spread faster among humans, the ability to cause severe forms of the disease, the ability to avoid detection by special diagnostic tests for viruses, to assess the ability to avoid natural or vaccine-induced immunity.

Monitoring and regular analysis of available data on SARS-CoV-2 genetic sequences is very important to support response and control measures.

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