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Biological Sciences

Detection of the SARS-COV-2 virus variant B 1.1 in the Republic of Kazakhstan

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Introduction. Coronaviruses (Coronaviridae, CoV) are a family of RNA viruses containing single-stranded positive RNA as genetic material, measuring up to 33.5 t.p.o in length and the diameter of the virion is up to 140 nm. Coronaviruses cause respiratory, hepatic, and neurological diseases in humans, some species of animals and birds.

Until 2020, only six strains of 2 genus of coronaviruses were known to cause respiratory diseases in humans. In December 2019, an outbreak of a new type of severe acute respiratory syndrome coronavirus occurred in the city of Wuhan, People's Republic of China (PRC). As a result of epidemiological studies conducted by the Chinese Center for Disease Control and Prevention (CDC China) using the NGS method from samples, a new type of coronavirus was identified, which was named SARS-COV-2.

Over the past 2 years, a significant number of mutations have been identified that led to the evolution of the virus and various variants. According to the Global Initiative on Sharing Avian Influenza Data (GISAID) database (www.gisaid.org), currently there are 12 different clades of the SARS-COV-2 virus in the world.

Variant B.1.1 of the SARS-CoV-2 virus was first detected in February 2020 and has spread worldwide. Variant B.1.1 has several mutations, including 1 single nucleotide change in ORF1b protein, 1 single nucleotide change in S protein, 1 change in ORF8 protein, 2 single nucleotide mutations in N protein.

The aim of this study is to sequence the S gene of variant B.1.1 SARS-CoV-2 virus circulating on the territory of the Republic of Kazakhstan (RK).

Materials and methods. Clinical samples were obtained from the branch of the Scientific and Practical Center for Sanitary and Epidemiological Expertise and Monitoring of the RSE at the National Center for Public Health of the Ministry of Health of the Republic of Kazakhstan.

To achieve the goal of the work, molecular genetic studies and methods were used, such as virus isolation, RT-PCR, PCR, gel electrophoresis, purification of PCR products and sequencing.

Results and discussion. As a result of real-time PCR studies with the SARS-CoV-2 Fluorescent PCR Kit (Maccura Biotechnology Co., Ltd, China), the resulting test sample showed a positive result for COVID-19. Specific primers were selected based on the S gene of the reference strain Wuhan-Hu-1([NC 045512.2](#)) the SARS-CoV-2 virus. According to the results of sequencing of the S gene, about 12 single-nucleotide mutations were found. The results obtained indicate that the mutational variability of the S gene is different from the original strain that originated in Wuhan.

Conclusion. Genetic analysis of the nucleotide sequence of the studied samples showed many mutations. According to the results of the conducted studies, the ubiquitous distribution of strains of the "B 1.1" variant was established on the territory of the Republic of Kazakhstan.

The work was carried out within the framework of the grant project AP09058338 "*Study of antiviral activity of drugs in relation to the SARS-COV-2 virus in vitro and molecular epidemiological analysis of circulating COVID-19 strains*".



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