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GENETIC DRIFT SARS-COV-2 STRAINS MUTATIONS AMONG UKRAINIAN POPULATION

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Objectives. The goal of investigation: assess the prevalence of mutations SarS-CoV-2 genome among the population of Ukraine. COVID-19 was declared a public health emergency of international concern. Genomic sequencing of SarS-CoV-2 structure of the virus allows to detect transmission chains, track contacts and identify new strain variants, namely variants of concern (VOC) and variants of interest (VOI), which are responsible for increasing the transmission of the virus, the formation of immune evasion and reducing the susceptibility of vaccinated individuals to infection with new strains. However, the analysis of the spread of mutations in the SarS-CoV-2 genome in Ukraine remains completely unexplored.

Materials and methods. Data on COVID-19 epidemiology trends of cases of infection and death in Ukraine were obtained on the open platform Google Public Data. Analysis of meta-data of all SARS-CoV-2 genomes from Ukrainian population (n = 534) submitted to the GISAID database was performed from 2020 to 2021. The analysis include data about the type and subline of the genome identified GISAID database. Genome evolution analysis was performed on the Nextstrain web platform. Statistical analysis.

Results. Ukraine ranks 8th among all European countries in terms of prevalence (n=3,696,468) and mortality (n=97,088) from COVID-19. It was revealed 3 peak increases in new daily cases of morbidity and mortality. The strain GRY ("Alpha") was circulated from 01 to 06.2021 with 3 maximal peaks of spread. Currently dominated the strain GK ("Delta"), which has 4 peaks of growth. Since from 12.2021, the first cases of the GRA virus strain ("Omicron") have been registered in Ukraine.

Conclusions. It was shown high levels of Alpha, Gamma and Delta strains of Sars-CoV-2 virus mutations during 2020-2021 among Ukrainian population. Currently, the Omicron strain poses a new potential threat. The emergence of new strains in the country coincided with a new peak of COVID-19.