GENETIC SIGNIFICANCE AND MONITORING OF CIRCULATING VARIANTS OF THE SARS-CoV-2 VIRUS IN THE REPUBLIC OF MOLDOVA

Svetlana COLAC

National Agency for Public Health, Chisinau, Republic of Moldova

Corresponding author: Svetlana Colac, e-mail: colac.svetlana92@gmail.com

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Introduction. COVID-19 is an infectious disease caused by the SARS-CoV-2 coronavirus, first reported in December 2019 in Wuhan, China. During the COVID-19 pandemic, more than 763 million confirmed cases of the SARS-CoV-2 coronavirus and over 6.9 million deaths were recorded worldwide (as of WHO data on April 23, 2023). The first confirmed case of COVID-19 in the Republic of Moldova was registered on March 7, 2020. The SARS-CoV-2 virus exhibits high mutability, leading to changes in its virulence and antigenic structure, which in turn pose challenges for diagnosis and treatment. Coronaviruses can display genetic variability due to mutations in the viral genome during replication. This study involves a phylogenetic analysis of circulating variants of the SARS-CoV-2 virus, with a focus on samples collected in the Republic of Moldova.

Aim. The aim of this study is to assess the genetic significance and monitor circulating variants of the SARS-CoV-2 virus in the Republic of Moldova to enhance epidemiological surveillance measures and the response to COVID-19.

Material and methods. A retrospective descriptive study was conducted in the virology laboratory of the National Agency for Public Health. The study analyzed 416 biological samples collected from COVID-19 patients with confirmed SARS-CoV-2 virus presence through molecular biology techniques (PCR). Genetic variant identification and mutation type determination were performed through fragment sequencing using the Ion Torrent Genexus tool and the Pangolin and GISAID programs.

Results. In 2022, a total of 416 biological samples were sequenced based on clinical, epidemiological, and laboratory diagnostic criteria. The results of sequencing revealed that the Omicron variant was identified in 413 biological samples, while the Delta variant was found in 3 samples. Analysis of the data suggests that the Omicron variant of the SARS-CoV-2 virus emerged at the beginning of 2022 and replaced the previously dominant Delta variant. Sequencing data also revealed that in early January 2022, isolated cases of the Delta variant (2 cases AY.122 and one case AY.4.2.3) were detected. The Omicron variant underwent significant genetic changes throughout 2022. Thus, four distinct periods of genome change of the SARS-CoV-2 virus can be distinguished: the first period (January – March) marked the predominance of BA.1 with its descendants (BA.1.1, BA.1.1.1, BA.1.1.13, BA.1.15, BA.1.17 etc.), the second period (March – June) saw the prevalence of the BA.2 sublineage with its descendants (BA.2.3, BA.2.75.2, BA.2.9, BA.2.12.1 and BA.2.14), the third period (June – October) saw the predominance of BA.4/ BA.5 with descendants, and the fourth period featured the predominance of various sublineages – BQ.1*, BN.1*, CC.1*, XBB.1.5 with its descendants.

Conclusions. This study revealed that the Omicron variant of the SARS-CoV-2 virus was in circulation in the Republic of Moldova in 2022 and replaced the previously dominant Delta variant. Genome sequencing of SARS-CoV-2 has become an essential tool for public health surveillance systems.