## Genetic Characterization and Epidemiological Overview of Circulating Influenza Viruses A/H3N2 and A/H1N1pdm09 in Georgia

Seasonal influenza viruses such as A/H3N2 and A/H1N1pdm09 pose significant public health challenges due to frequent mutations and the emergence of new strains. Genetic analysis and epidemiological surveillance are crucial in elucidating the evolutionary dynamics of influenza viruses, as specific mutations can impact transmission potential, disease severity, and the effectiveness of vaccines and antiviral treatments. Therefore, the primary objective of this study is to conduct a phyloepidemiological analysis of A/H3N2 and A/H1N1pdm09 influenza viruses identified in Georgia over five influenza seasons spanning from 2019 to 2024.

Influenza virus RNAs were sequenced using Illumina's MiSeq and MiSeq DX platforms via next-generation sequencing. Samples were prepared with the Nextera XT Illumina kit. High-coverage genomes were deposited into the International Influenza Virus Genome Database (GISAID). Phylogenetic trees were constructed using the Molecular Evolutionary Genetics Analysis (MEGA) software.

During the influenza seasons from 2019 to 2024, a total of 14,984 samples collected from influenza reference laboratories in Tbilisi, Kutaisi, and Batumi were examined. Among these, there were 1,485 laboratory-confirmed cases of influenza A. The A/H3N2 virus predominated during the 2019-2020, 2021-2022, and 2022-2023 seasons, while the A/H1N1pdm09 virus was predominant in 2023-2024.

Genomic profiling of influenza viruses revealed diverse strains circulating in Georgia, consistent with trends in the European region. These strains exhibited multiple mutations compared to vaccine strains, with none showing the H275Y mutation in the NA gene, which confers reduced sensitivity to antiviral drugs.

This study underscores the ongoing genetic variability of influenza viruses. Sharing phyloepidemiological data from Georgia is critical for understanding viral

transmission dynamics and informing global influenza prevention and control strategies.