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Phylogenetic analysis of influenza viruses of the seasons 2016-2018 in Ukraine

Content

Background

The phylogenetic analyses of influenza viruses allow to performing the comparison between viruses and monitoring the evolution in a frame of territory. Influenza viruses have high level of mutations caused by errors of polymerase.

The aim of our work was to analyze variability of influenza viruses type B which were isolated during 2016-2018 years and to construct of phylogenetic trees.

Materials

Nasal-throat swabs taken from influenza-affected patients from different regions of Ukraine, collected during 2016-2018 years, were used in the study. Samples were analyzed using real-time polymerase chain reaction (RT-PCR). Influenza viruses were isolated in MDCK and MDCK-SIAT cell culture. The sequences of influenza viruses from other countries were received from web-site GISAID using BLAST analysis. Sequences were aligned using ClustalW algorithm. Phylogenetic analysis was performed using MEGA 7 software.

Results

All recently circulating viruses from Ukraine analyzed carried HA genes that fell into genetic group 1A, the B/Brisbane/60/2008 genetic group, the vast majority falling into a genetic group defined by two HA1 amino acid substitutions. Despite the appeared new clusters with deletions in 162-164 HA1 in different countries, we not detected it in Ukrainian isolates (B/Kyiv/367/2017, B/Kharkiv/372/2017, B/Kyiv/375/2017 and B/Kyiv/46/2018).

Conclusions

The phylogenetic analyzes of Ukrainian influenza viruses of 2016-2018 seasons of B/Victoria linage was done. A large number of unique amino acid substitutions were observed by sequencing in influenza viruses sequences HA and NA gene, which had not affect the antigenic or other functional regions.

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