

Phenotypic and genotypic analysis of influenza viruses susceptibility to antivirals during the 2017-2018 epidemic season in Russian Federation.

Content

Being constantly evolving influenza viruses can develop the resistance to the most common used antivirals, such as neuraminidase inhibitors. In this study we show the results of phenotypic and genotypic analysis of influenza A and B viruses isolated in the 2017-2018 season in Russia susceptibility to the neuraminidase inhibitors oseltamivir and zanamivir and M2 proton channel inhibitor rimantadine.

The total 404 influenza viruses were studied to determine 50% inhibitory concentration (IC50) using fluorescent assay (MUNANA), 176 belonged to A(H1N1)pdm09 subtype, 84 –A(H3N2), 142 were influenza B/Yamagata lineage and 2 were B/Victoria lineage.

Only one strain of A(H1N1)pdm09 subtype had shown highly reduced inhibition (HRI) to oseltamivir, confirmed by presence of H275Y aminoacid substitution in the neuraminidase gene. Also, one of influenza B strains (Yamagata lineage) had shown reduced inhibition (RI) to oseltamivir. The overall frequency of influenza viruses resistant to neuraminidase inhibitors was 0,5%, similar to what has been observed in recent global studies.

The total 260 influenza A viruses tested demonstrated resistance to rimantadine.

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