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STUDY ON HERD IMMUNITY AGAINST INFLUENZA VIRUS AMONG THE POPULATION OF ALMATY REGION IN 2017–2018

A.M. Baimukhametova, T.I. Glebova, N.S. Ongarbayeva, M.G. Shamenova, N.T. Saktaganov, S.B. Baiseit, G.V. Lukmanova, N.G. Klivleyeva

LLP Scientific Production Center for Microbiology and Virology, Almaty, Kazakhstan

Influenza is one of the infections registered on all continents. Despite the obvious scientific achievements pertaining to anti-epidemic measures, ARVI and influenza still present a major problem in medicine. Timely diagnosis of the causative agents for influenza and acute respiratory infections in humans allows for adjusting the treatment regimen and determining the correct vaccination tactics and choosing the appropriate vaccine variant during the interepidemic period. The arsenal of diagnostic methods still preserves serological techniques, which ensure the detection of specific antibodies in the blood in the disease dynamics and provide indirect evidence of the influenza virus circulation among humans.

The purpose of this study was to carry out serological analysis of the circulation of influenza A and B viruses in the 2017–2018 epidemic season. The level of antibodies specific for the influenza virus hemagglutinins in blood serum was determined in the hemagglutination inhibition assay (HAI) and enzyme immunoassay (EIA).

60 serums collected from patients diagnosed with ARVI, influenza, ARD, and pneumonia in health care facilities located in the Almaty region during the 2017–2018 epidemic period were used for serological studies. EIA data showed that antibodies in 23.3% of cases (14 serums) were detected in high titers (1:80–1:320) against the A/H3N2 virus serosubtype, in 18.3% (11 samples) against influenza A/H1N1 viruses, and in 1.6% (1 sample) against the causative agent of influenza type B virus.

Antibodies against influenza virus were detected by HAI assay in 31.6% of cases (19 samples), of which 16.6% (10 samples) were classified as A/H1N1 subtype and 13.3% (8 samples) as A/H3N2 subtype. Antibodies against influenza type B virus were found in 1.6% (1 sample).

The results from serological studies of serums thereby indicate that in the 2017–2018 epidemic season the simultaneous circulation of influenza A (H1N1 and H3N2) and B viruses was observed in the Almaty region.

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CIRCULATION OF INFLUENZA VIRUSES AMONG HUMANS AND SWINE IN THE REGIONS OF NORTHERN AND WESTERN KAZAKHSTAN IN 2017–2018

S.B. Baiseit, N.S. Ongarbayeva, M.K. Kalkozhayeva, M.G. Shamenova, N.T. Saktaganov, G.V. Lukmanova, N.G. Klivleyeva

LLP Scientific Production Center for Microbiology and Virology, Almaty, Kazakhstan

The influenza viruses of genus A are unique among the agents of infectious diseases in both humans and a large number of mammals (horses, swine, whales, seals, etc.) and birds (Lvov D.K., 1987; Webster R.G. et al., 1992). To predict the influenza epidemics and timely preventive measures, an important stage consists in tracking the spread of the infection in various regions of the world, including the Republic of Kazakhstan.

The aims and objectives were to examine the circulation of influenza viruses among humans and swine in the regions of Northern and Western Kazakhstan in 2017–2018.

In the 2017–2018 epidemic and inter-epidemic periods 274 nasopharyngeal swabs were collected in the Northern and Western Kazakhstan: 94 human and 180 swine samples from livestock farms.

Primary screening of nasopharyngeal swabs was performed in real-time polymerase chain reaction (RT-PCR) using AmpliSens reagent kits (Moscow, Russia).

Primary screening in RT-PCR of 94 biological samples collected from humans showed the presence of genetic material of the influenza virus in 32 swabs (34.04% of the total number of samples examined). Influenza type A virus RNA was detected in 19 samples (20.21%), influenza type B virus RNA in 13 samples (13.83%). Subtyping of influenza type A positive samples revealed influenza A/H1 virus RNA in 3 samples (3.19%), A/H3 virus RNA in 16 samples (17.02%).

RT-PCR screening of biological materials obtained from swine showed the presence of influenza virus RNA in 28 swabs (15.56% of the total number). A/H1 virus RNA was detected in 26 samples (14.44%), A/H3 virus RNA in two samples (1.11%).

The results from the primary screening of nasopharyngeal swabs collected from humans and swine in RT-PCR indicate the co-circulation of A/H1N1 and A/H3N2 influenza viruses in humans and swine during the period 2017–2018 in the regions of Northern and Western Kazakhstan. In this regard, the monitoring of the spread of infection among humans and swine, as well as timely diagnosis of the infectious agent and prevention of the disease are extremely important.

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CHARACTERIZATION OF ENTEROVIRUSES BY NEXT-GENERATION SEQUENCING

M. Bessaud, M.-L. Joffret, P. Polston, E. Achouri, F. Delpeyroux

Institut Pasteur, Paris, France

Next generation sequencing methods constitute a powerful tool for the study of viruses. By allowing concomitant sequencing of millions of DNA fragments, they allow rapid sequencing of a great number of samples and in-depth characterization of minority genomic variants.

Our laboratory has developed different techniques suitable for the characterization of enteroviruses in different types of samples. By specifically targeting enterovirus genomes, these techniques reduce the number of reads from non-virus origin: thus, more than 90% of the reads that are generated through sequencing are relevant.

However, generating full-length genomic sequences remains a challenge in case of samples containing complex mixtures of viruses, particularly when mixed viruses share common sequences because of recombination. We are currently trying to address this limitation.

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EPIDEMIC RISE OF INFLUENZA IN ST. PETERSBURG IN JANUARY-MARCH 2018

M.A. Bichurina¹, P.A. Petrova², A.A. Go¹, I.G. Chkhyndzheriya³, L.V. Voloshchuk¹, M.M. Pisareva², N.I. Konovalova²

¹St. Petersburg Pasteur Institute, St. Petersburg, Russia;

²Smorodintsev Research Institute of Influenza, St. Petersburg, Russia;

³Federal Service on Customers' Rights Protection and Human Well-Being Surveillance, St. Petersburg, Russia

Influenza and acute respiratory viral infections remain one of the most urgent medical and socio-economic problems. Almost every year in autumn and winter there