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

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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

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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

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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 technics suitable for the characterization of enteroviruses in different types of samples. By specifically targeting enterovirus genomes, these technics 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

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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

are epidemic rises of the incidence of influenza and acute respiratory viral infections. In St. Petersburg, in 2018 the epidemic reached its peak in the 7th week (February), when the epidemic threshold was exceeded, the maximum number of cases was registered during the 11th week (16 365 patients on 12.03.18), then after the 15th week the number of cases was below the epidemic threshold. The average daily number of cases of influenza and respiratory viral infections in January was 5270, in February it was 8127, in March — 9018, in April — 6330. The highest incidence was among children 3–6 years of age. In total, more than 20 000 patients were hospitalized from the beginning of the year till May, among whom 20% were adults. Among children, The majority of hospitalized children (55.3%) were the children under the age of two.

In January-May 2018 the laboratory received 111 nasopharyngeal samples from patients of St. Petersburg hospitals 18–70 years of age. Samples were examined by real-time PCR using test systems from "InterLabService", Moscow, 50 samples proved to be positive of the influenza virus and 7 samples — to other respiratory viruses (rhinoviruses, adenoviruses). In 20 samples out of 50 RNA of virus of influenza B was detected, which makes 40%, the samples with RNA of influenza A(H3N2) virus constituted 24%, in 14.0% of the samples we identified RNA of virus of influenza A(H1N1) while in 22.0% of samples we did not identify RNA of the influenza virus. From the positive in PCR samples we isolated 26 strains of influenza viruses by two passages on the culture of MDCK cells. The typing of isolates with diagnostic sera to reference and epidemic strains of influenza viruses showed that in February-March 2018 all three serotypes of the influenza virus circulated in St. Petersburg. In 50% of cases we identified viruses of influenza B of the Yamagata Line, antigenic related to the strain B/Phuket/3073/13; 30.8% of isolates belonged to serotype A (H3N2) and were antigenic related to the strain A/HK/4801/14, and 19.2% of isolates were closely related to the strain A(H1N1)pdm09. During this epidemic rise we did not find influenza viruses of the Victorian Line which prevailed in circulation for many previous years.

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MEASLES AND RUBELLA IN NORTH-WEST REGION OF RUSSIA AT THE STAGE OF ELIMINATION

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The WHO strategic plan to eliminate measles, rubella and congenital rubella is aimed to the global elimination of these infections by 2020. The National program to eliminate measles and rubella is developed and carried out in Russia. In this study, ELISA test was used to detect the IgM and IgG antibodies to measles virus (MV) and rubella virus (RV) in blood serum samples from patients suspected to have the MV infection.

Within the last decade in the North-West Region (NWR) of Russia the highest measles incidence was registered in 2012 (1.11 per 100 000). In the following years the measles morbidity declined to even none of measles cases in 2016 and then 3 measles cases were registered in 2017. Molecular genetic studies of the biological material from patients with measles revealed the D8 genotype, MVs/Frankfurt Main. In January-June, 2018 the measles incidence significantly increased — 24 cases were notified on 5 territories of NWR of Russia. In St. Petersburg 17 measles cases were laboratory confirmed in this period: 5 of 17 cases were revealed in the City Hospital and 2 cases were the contacts with this epidemiological focus. The epidemic cluster of 3 cases was notified in St. Petersburg among patients from the Republic of Moldova. The B3 genotype, Kabul MeaNS-4298 was genetically confirmed.

Rubella incidence in NWR of Russia remains at low level: one family focus of 2 rubella cases was notified on one territory in 2016 and no cases were registered in 2017. In the first half of 2018 three rubella cases were laboratory confirmed in St. Petersburg and Leningrad Oblast'. Besides, 13 blood serum samples from pregnant women suspected to have the RV infection were studied. The lack of the specific IgM antibodies to RV, high levels of the IgG antibodies titers of high avidity were revealed by ELISA in serum samples of all examined pregnant women thus evidencing the absence of the acute RV infection.

The presented data on low measles and rubella morbidity in 2016–2017 and the absence of the local MV circulation within more than 12 years period evidenced the possibility of certifying the NWR of Russia for the absence of the endemic MV circulation. However the worsening of the epidemic situation on measles was observed in NWR as well as in Russia as a whole in the first half of 2018.

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EVOLUTION OF THE VP1 REGION TYPE 2 VACCINE-DERIVED POLIOVIRUS SHEDDING FROM AN IMMUNOCOMPROMISED ALGERIAN CHILD

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Both live attenuated oral poliomyelitis virus vaccines (OPV) and inactivated poliomyelitis virus vaccines (IPV) are effective in providing individual protection against poliomyelitis and have been used widely. However, in rare incidences the attenuated virus used in OPV reverts to neurovirulence results in transmissible vaccine-derived poliovirus (VDPV) strains. Here, we describe the accumulation of mutations in gene coding the VP1 protein of Sabin 2 Poliovirus (PV), suggested a prolonged replication of the vaccine, occurring in an infant with severe combined immunodeficiency.

The analyses of stool specimens were conducted from 2011 to 2012 in a 6-month-old boy, with severe combined immunodeficiency. Viral isolation is carried out according to the standard methods recommended by the WHO. Extracts were cultured on human rhabdomyosarcoma cell line (RD), and mouse L cells expressing the human PV receptor (L20B). All isolates routinely characterized by VP1 sequencing. Analysis of the full nucleotide VP1 region was performed.

The 12 samples were positive for PV. The rRT-PCR confirms the vaccine-like. 10 isolates of type 2 exhibit significant nucleotide variations in the VP1 protein and were collinear with the Sabin 2 strain.

A detailed molecular analysis VP1 region showed accumulates mutations. The substitution Ile143Thr which restores the consensus residue for the prototype wild type 2 PV strains is found in all type 2 polioviruses isolates.

Polio eradication requires not only complete absence of circulating wild PV but also absence of VDPV the emergence of genetically divergent vaccine-derived polioviruses