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.

3.8

doi: 10.15789/2220-7619-2018-4-3.8

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

M. Bichurina[1], N. Zheleznova[1], E. Timofeeva[2]

[1]St. Petersburg Pasteur Institute, St. Petersburg, Russia;
[2]St. Petersburg Administration of Federal Service for Surveillance on Consumer Rights Protection and Human Wellbeing, St. Petersburg, Russia

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.

3.9

doi: 10.15789/2220-7619-2018-4-3.9

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

D. Boulahbal-Anes[1], S. Chikhaoui[1], S. Bouraoude[1], A. Chouchane[1], M.-L. Joffret[2], F. Delpeyroux[2], M. Seghier[1]

[1]Laboratoire National de Référence OMS pour la Surveillance de la Poliomyélite, Institut Pasteur d’Algérie, Dély-Brahim, Algeria; [2]Institut Pasteur, Paris, France

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