

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

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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 noti-

fied 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

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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

(iVDPVs) during prolonged infection in persons with primary immunodeficiency disorders seems to be one probable source of poliovirus infection and these individuals are a potential reservoir for infection in which the virus can evolve into neurovirulent forms and become transmissible circulating vaccine-derived PV.

3.10

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EPIDEMIOLOGICAL CHARACTERISTICS OF MEASLES

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Tremendous progress has been made to decrease childhood death caused by measles. Before the introduction of measles vaccine in 1963 major epidemics occurred every 2–3 years and caused 2.6 million deaths per year. In 2012 the WHO endorsed a plan to eliminate measles by 2020. The aim of this study was to reveal epidemiological characteristics and trends of measles.

Measles is a highly contagious airborne infectious disease caused by the measles virus. Although the impressive achievements in eliminating measles with a low record in 2016 with 5273 cases in Europe region it affected 21 315 people and caused 35 deaths in 2017. There were reported about 4400 cases in Italy from January to August 2017 with median age 27 years, 88% of the cases were unvaccinated. Over 41 000 people in Europe have been infected in 2018 with at least 37 deaths. Over 23 000 people affected in Ukraine but the highest number of deaths 14 was reported by Serbia. Also a large number of cases were registered in Italy, France, and Georgia, Serbia and Moldova. There were 5004 confirmed measles cases, including 68 deaths, reported in the American region this year with 3545 cases and 62 deaths in Venezuela and 1237 cases, 6 deaths in Brazil.

Russian Federation reported about 1717 infections in children and adults this year (127 cases for the same time in 2017). Overall, there were increasing from 178 cases in 2016 to 721 last year. The most affected areas were the Republic of Dagestan (3.3 cases per 100 000), Moscow (2.7 cases per 100 000) and the Chechen Republic (2.3 cases per 100 000). Almost 9 of 10 of the affected people were not vaccinated. Ratio adults to children about 6:4. The majority of cases were caused by genotype “Dublin B-3” that is endemic for the Europe. There were several household outbreaks of measles as a recent case in Chita with 15 members of one family infected.

This situation caused by declining vaccination rates. To prevent outbreaks, at least 95% immunization coverage in every country; timely detection of all suspected cases and provide laboratory conformation; strengthen epidemiological surveillance in border areas and vaccination one month ahead of a trip to any of the European countries the WHO list; adequate intra-hospital management to avoid nosocomial transmission.

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INTRATYPIC DIFFERENTIATION OF POLIOVIRUSES IN THE INTER-POLIO LABORATORY OF THE INSTITUT PASTEUR OF COTE D'IVOIRE IN 2002–2017: WHAT EVOLUTION?

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Laboratory analysis of cases of acute flaccid paralysis is one component of the four polio eradication strategies. This analysis consisted in isolating the viruses and charac-

terizing them by the technique of intra-typical differentiation (ITD). This study proposed to take stock of the evolution of the different techniques of ITD used from 2002 to 2011.

The stools are treated with chloroform and inoculated to L20B and RD cells. The identification of isolated viruses and their characterization was carried out by evolutionary methods: seroneutralization typing with an antibody pool, conventional RT-PCR coupled with an enzyme-linked immunosorbent assay (Elisa) and finally real-time PCR. From 2002 to 2006, the identification of 370 strains of poliovirus was made by serum neutralization. It identified 258 polio type 1, 102 polio type 2 and 206 type 3. The wild or vaccine nature was determined in South Africa. From 2007 to 2010: 492 strains identified by conventional RT-PCR/ELISA were given: 256 wild polio (241 PV1, 15 PV3) and 259 polio-virus type vaccines, with dual reactions limiting the separation of virus mixtures of different type. From 2011 to 2016, 1034 strains of poliovirus tested by real-time PCR showed 300 wild-type PV3, 02 VDPV2 and many vaccine strains type 1, 2, and 3 or mixed serotypes with readily available results and The possibility of processing several samples especially with the advent of version 5.0 since October 2016.

The evolution of the techniques of differentiation allowed the increase of the capacities of the laboratory and the reliability of the results. Adaptation to new techniques (sequencing) is essential to continue to offer better services.

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EPIDEMIOLOGICAL MONITORING OF POLIOMYELITIS IN THE CENTRAL AFRICAN REPUBLIC FROM 2004 TO 2017 AND IMPLEMENTATION OF POLIOVIRUS ENVIRONMENTAL SURVEILLANCE IN BANGUI IN 2017

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Central African Republic (CAR) joined the Polio Eradication Initiative (PEI) in 1996. Despite the fact that the last autochthonous wild poliovirus was isolated in 2000, the country experienced several episodes of wild poliovirus importations between 2003–2011. Nevertheless, since 2003 CAR is ongoing numerous political-military crisis that affects the health system including the PEI performance.

The aims of the study were the analysis of key performance indicators of active acute flaccid paralysis (AFP) surveillance in CAR from 2004 to 2017 (14 years period) and to describe the introduction of Poliovirus Environmental Surveillance (ES) in Bangui, the capital of CAR.

We conducted a retrospective analysis of data available at the Institut Pasteur de Bangui, the Department of Health and Population and WHO to evaluate the polio eradication program in CAR from 2004 to 2017. The rationale, steps and first results of Poliovirus Environmental Surveillance implementation are described.