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EPIDEMIOLOGICAL ANALYSIS OF MEASLES OUTBREAK IN GUINEA 2017–2018

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With the end of the largest ever known epidemic outbreak of Ebola in Guinea, since the beginning of 2016, comprehensive disease surveillance and response are under way. The five most common diseases, chosen according to their frequency in recent years, are monitored. These are viral hemorrhagic fevers, including Ebola and Yellow fever, cholera, meningitis, measles and poliomyelitis. Monitoring cases of measles shows that since the beginning of 2016 and despite the response organized in February 2016, confirmed cases are still being registered, and this occurs in several health districts.

The purpose of this paper was to describe the epidemiological profile of measles cases during the epidemic in 2016 and 2017. And also to study the results of the evaluation and the survey of immunization coverage in the framework of measles vaccination.

With the method of descriptive analysis, we developed a basic early warning system, a laboratory database and a national response plan

In 2016 (from 27 to 52 weeks of the year), 1304 suspected cases of measles were recorded, of which the blood was collected from 382 patients, which was 29.3%. Of these, 379 (99, 2%) were admitted to the laboratory, among them 193 (50.9%) were positive (IgM+ = 189, indeterminate = 4).

In 2017 (from 1 to 9 weeks), 2.133 suspected cases of measles were recorded, blood was withdrawn from 549 patients (25.73%). The laboratory received 443 samples (80.69) and 163 (36.8%) were positive. Confirmed cases of measles continue to be recorded, despite the ongoing vaccination and campaign to fight the disease in the outbreaks. This epidemic affected 17 prefectures in the country from 38. 73% of children is under the age of 5. There is no difference between the sexes (F = 50%, M = 50%). Coverage of vaccinations is 21 and 44%, respectively, in cases of confirmation and without measles, with a total vaccination coverage of 35%. 40% of cases of unconfirmed measles have IgM+ to rubella. Mortality is low due to lack of information. Determining the cause of the persistence of measles will help to stop the epidemic.

3.33 doi: 10.15789/2220-7619-2018-4-3.33 ASSESSMENT OF THE RISK OF MEASLES INFECTION IN HOSPITAL

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There is no unambiguous assessment of the current epidemiological situation on measles. On the one hand, there is a decrease in morbidity, on the other — an increase in the number of seronegative women of childbearing age, thus affecting the measles incidence among the young children.

Assess the risk of measles infection in pregnant women, parturient women and newborns, as well as the need for serological examination of newborns aimed at the following anti-epidemic measures became possible with the introduction of infection in the hospital (maternity hospital). A total of 104 patients were examined in the laboratory. Blood serum was obtained from pregnant women (29), parturient women (46) and newborns (29) on the 2nd day when the measles case in the obstetric ward was revealed. The diagnosis of measles was confirmed by the ELISA (IgM) and PCR. The specific IgG antibodies were detected using the Anti-Measles Viruses ELISA (IgG) test system, Euroimmun (Germany).

In the study the seronegatives among the pregnant women consisted 31.0%, and among the parturient women 34.8%. In blood serum of the newborns IgG were detected in 21 patients (72.4%). Taking into account that among the examined persons were 22 mother-child couples, it was possible to confirm the presence of maternal immunity. Thus, in the sera of 6 infants IgG antibodies were not detected and their mothers were also seronegative. At the same time in the sera of the other 16 infants from the seropositive mothers IgG antibodies were detected. The IgG titers varied from 0.2 to 3.0 IU/ml the mean value consisted (0.70 ± 0.45) IU/mL for infants and (0.60 ± 0.35) IU/mL for their mothers.

The data obtained show that in case of the risk of spreading the measles infection and deciding whether to perform a procedure for determining the specific IgG in the newborn's sera, it is more appropriate to carry out a serological examination of the parturient women due to the identity of the content of measles antibodies in the sera of infants and their mothers.

3.34 doi: 10.15789/2220-7619-2018-4-3.34 DEVELOPMENT OF PROTOTYPE OF UNIVERSAL INFLUENZA VACCINE BASED ON LIVE ATTENUATED INFLUENZA VACCINE VIRAL VECTOR

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Human influenza viruses are respiratory pathogens that cause annual epidemics and occasionally serious pandemic outbreaks. Seasonal influenza vaccination is the most effective way to control the spread of the disease; however it remains to be ineffective against pandemic influenza viruses due to the antigen mismatch. Therefore, the development of new universal vaccine with broad and durable effect is important issue for medical care. The extracellular domain of M2 protein (M2e) is highly conserved among all influenza A viruses and is widely used for generating broadly-reactive influenza vaccines. A new strategy of induction M2e-specific antibody is the expression of M2e tandem repeats in hemagglutinin (HA) molecule of live attenuated influenza vaccine (LAIV) used as viral vector. Recombinant LAIV viruses with chimeric HA proteins were generated by the means of reverse genetics. For that purpose BsmBI restriction site was inserted between signal peptide and HA1 subunit of HA genes of A/Switzerland/9715293/2013 (H3N2), A/Anhui/1/2013 (H7N9) or A/South Africa/3626/2013 (H1N1). Subsequently, four M2e tandem repeats were cloned into the inserted BsmBI cloning site. Recombinant LAIV viruses based on A/Leningrad/134/17/57 backbone were rescued by electroporation of Vero cells using Neon Transfection System (Invitrogen). All the LAIV-4M2e viruses actively replicated in eggs and preserved the temperature sensitive and cold-adapted phenotypes typical for LAIV viruses. Infectious virus titers were determined in eggs and MDCK cells incubated at different temperatures. Protective efficacy of new recombinant LAIVs against a panel of various influenza viruses was assessed in BALB/c mouse model. In addition, the recombinant LAIVs were attenuated for mice. These data indicate that the 4M2e insertion did not affect LAIV virus replication characteristics. The expression of M2e epitopes by the recombinant viruses was confirmed by ELISA with M2especific antibody 14C2 (ab5416). The results of immunogenicity and cross-protective efficacy of the new LAIV-4M2e viruses will be presented.

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CIRCULATION OF COXSACKIEVIRUS A IN HAND-FOOT-MOUTH DISEASE IN SOUTHERN VIETNAM, 2015–2016

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Hand, food and mouth disease (HFMD), a common contagious disease that usually affects children, is normally mild but can have life-threatening manifestation. It can be caused by enteroviruses, particularly Coxsackieviruses (CA) and human enterovirus 71 (EV71) with highly variable clinical manifestation.

In 2011–2014, EV71 and CA16 were responsible for the HFMD outbreak in South Vietnam. However, CA6 and CA 10 were observed increased dramatically from 2015–2017. In 3 years, 1488 cases were detected positive for enterovirus from 3277 HFMD cases, the results are the more frequently presented serotypes as 908 EV-71 (61%) and 580 other EV none EV71 (39%).

The HFMD cases which were detected as other EV positive, had been sequenced and serotyped with results: CA6 (196.34%), CA10 (75.13%), CA16 (146.25%) and CA2.4, 5.8, 9; CB3.4, 5; ECHO6.9, 11.16, 25.30... (163, 28%).

Furthermore, serotype of CA 6, CA 10 replacement every year.

CA10 increased in 2016 and the presence of CA10 were 68% (69/102) in the group of Enterovirus non EV71. Our study demonstrates variety of enterovirus genotypes as viral pathogens in causing HFMD in Southern Vietnam. CA10 and CA6 were co-circulating together with EV-71 and CV-A16 in recent years.

3.36 doi: 10.15789/2220-7619-2018-4-3.36 EPIDEMIOLOGY OF ADENOVIRAL INFECTION IN ST. PETERSBURG

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The modern methods of laboratory diagnostic for different virus significantly expanded etiological spectrum of acute gastroenteritis. Along with wide spread rota- and noroviral gastroenteritis, a large amount of cases with adenoviral etiology is registered. According to the published data, the adenoviral acute intestinal infections constitute from 1 till 15% of all diarrheal diseases and depends on the region.

The purpose of this study was to find the prevalence of adenoviral acute intestinal diseases in St. Petersburg, to estimate the significance of this problem, find the risk groups and other epidemiological features.

We used the official data from St. Petersburg center for registration of infectious and parasitic diseases in 2016–2017. Epidemiological investigation of 344 cases of adenoviral infection was performed by standard contact investigation. Molecular diagnostics was performed using PCR based tests. The incidence level of adenoviral infection in St. Petersburg in 2016 was 4.1 per 100 000; in 2017 — 2.4 per 100 000. Adenoviral infection was registered in 90.0% in hospital patients, because of using high technology laboratory methods. Findings among outpatients were rare and were only in depth examination. From 2016–2017 adenoviral infection was found in 34 (9.8%) outpatients only. Adenoviral gastroenteritis was registered in all districts of our city, in 2016 more frequently in Viborgsky, Central and Primorsky districts of St. Petersburg; in 2017 more frequently in Kalininsky, Primorsky and Krasnogvardeisky districts. All the patients with this infection were recovered.

Monthly trend showed autumn-winter seasonality, in summer the incidence decreased. Analysis of the age structure of adenoviral infection showed that 60% cases were in the age group from 0 to 14 years. In children from 0 to 2 years old -30% cases were registered, from 3 to 6 -24.4%. The incidence level in the age group from 0 to 2 was 24.1 per 100 000 in 2017 (6 times increase from common level of this infection); in children from 3 to 6-18 per 100 000 (4 times increase from common level of this infection). We found the same tendency in 2016. Adenoviral infection is also registered among people of active age (in the age group 20-29 we found 12.9% cases; 30-39-7.1); in the elderly patients we found decreasing trend. It was only 3.2% cases of adenoviral infection in patients after 60. Diagnostic investigations on the etiology of acute intestinal infections were organized on different agents simultaneously. So 38% cases in this investigation were with associations of adenovirus with over etiologic viral and bacterial agents. Viral-viral associations were in 54% of all mixed cases. More frequently associative epidemic foci were forming with adenovirus and rotavirus (32%); adenovirus and norovirus (16%); with over viruses -6% cases. The part of viral-bacterial associations in the adenoviral foci was 43% (33 cases). Among bacterial agents adenovirus more frequently associated with Escherichia, Campylobacter, opportunistic flora, rarely with Klebsiella and Yersinia associations with 3 etiologic agents was found in 4% cases. Two patients had adeno-, roto- and norovirus at the same time. We also found epidemic foci with mixed adenovirus, rotavirus and campylobacter infections. All mixed cases were found in hospital patients. Mixed infections had more serious clinic without specific clinical manifestation, and additional laboratory methods were required for identification.

This investigation showed significance of the problem of adenoviral infection in St. Petersburg; children from 0 to 2 years old were found to be a risk group for this disease. Autumn-winter seasonality was found. Epidemiological specific feature of adenoviral infection is forming mixed foci with other (viral and/or bacterial) etiologic agents in 38% cases.

3.37 doi: 10.15789/2220-7619-2018-4-3.37 CHALLENGES FOR POLIO ERADICATION. RISK

OF RE-EMERGENCY OF INFECTION IN POLIO FREE COUNTRIES

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The risk of importation of wild polioviruses (WPV) into polio-free countries remains till poliomyelitis is eradicated. Other risks of Polio Eradication Initiative are: circulating vaccine-derived polioviruses (VDPV) with nucleotide substitutions and recombinant profile; appearance of vaccine associated paralytic poliomyelitis (VAPP) and escape of polioviruses from polio vaccines.