(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 doi: 10.15789/2220-7619-2018-4-3.10

EPIDEMIOLOGICAL CHARACTERISTICS OF MEASLES

A.S. Buntovskaia, S.A. Peleshok, V.N. Bolekhan

S.M. Kirov Military Medical Academy, St. Petersburg, Russia

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.

3.11 doi: 10.15789/2220-7619-2018-4-3.11

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

F. Coulibaly, E.V. Adjogoua, A. Ouattara, H. Kadjo, V. Akran, B. Kouakou, E. Kra, L. Tieoulou, H. Kouadio, F. Guidy

Pasteur Institute of Côte d'Ivoire, Abidjan, Côte d'Ivoire

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 characterizing 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 poliovirus 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.

3.12 doi: 10.15789/2220-7619-2018-4-3.12

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

J. Doté[1,2], P. Mbelesso[2,3], A. Mazitchi[1], A. Manirakiza[1], R. Mbailao[4], S. Ndjapou[4], E. Sawadogo[5], U. Binza[5], C. Manengu[6], I. Gouandjika-Vasilache[1]

[1]Institut Pasteur de Bangui, Bangui, Central African Republic; [2]Université de Bangui, Bangui, Central African Republic; [3]Neurology Departement of Hôpital de l'Amitié, Bangui, Central African Republic; [4]Department of Health and Population, Central African Republic; [5]World Health Organization Office, Bangui, Central African Republic; [6]World Health Organization regional office, Brazzaville, Republic of Congo

Central African Republic (CAR) joined the Polio Eradication Initiative (PEI) in 1996. Despite the fact that the last autochthone 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 flasks 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.

During the study period we listed 1803 notified cases of (AFP). Out of 3920 stools samples collected from AFP cases, contacts and internally displaced population, 64.4% (2524/3920) were transported at the laboratory within three days of collection and 76.4% (2997/3920) of the stool samples were considered to be adequate. We isolated 225 vaccine polioviruses, 803 non-polio enterovirus, and 51 wild polioviruses of which the last one in November 2011. ES was implemented at the week 52 of 2017 in Four (4) sites selected in Bangui. We received 46 ES samples from the implementation to the 30th of June 2018, among which we isolated 7/42 (16.6%) non-polio enterovirus. (No) Any poliovirus was not isolated in these 46 ES samples. The routine vaccine coverage was particularly low in the country with an average of 49%. The quality of SIA's is still poor and part of the CAR territory is inaccessible for security reasons.

The recurrent civil and military unrest have considerably affected the surveillance system of AFP which must be reinforced by the ES extension to the former districts that experienced wild poliovirus importation, coupled to an improvement of the routine vaccine coverage to attend the WHO standards.

3.13 doi: 10.15789/2220-7619-2018-4-3.13

CIRCULATION OF THE EPIDEMIC VARIANT OF NOROVIRUS GII.4_SYDNEY2012 IN NIZHNY NOVGOROD, RUSSIA

N.V. Epifanova, V.V. Zverev, T.A. Sashina, N.M. Khokhlova, A.Yu. Kashnikov, N.A. Novikova

Blokhina Nizhny Novgorod Research Institute of Epidemiology and Microbiology, Nizhny Novgorod, Russia

Noroviruses (NoVs) are a major cause of gastroenteritis. The epidemic process of NoV infection in the last two decades is characterized by the dominance and periodic replacement of variants belonging to genotype GII.4. Currently more than 10 epidemic variants of NoVs GII.4 identified. Dominance period of most of these variants did not exceed 2–4 years. However, the variant GII.4_ Sydney2012 prevails in many countries of the world for the last 5–6 years.

The aim of this work was to analyze the dynamics of circulation of NoVs GII.4_Sydney2012 in the territory of Nizhny Novgorod in 2013–2018.

NoVs were detected by reversed transcription polymerase chain reaction in fecal specimens obtained from patients with acute diarrhea. Genotyping of NoVs was performed by partial sequencing of the genome regions encoding capsid protein and RNA-dependent RNA polymerase using the genetic analyzer Beckman Coulter CEQ8000 (USA). The nucleotide sequences were analyzed using a web based NoV Genotyping Tool 2.0 and program MEGA6.

From July 2013 to June 2018 7018 children under 14 years hospitalized in the infectious diseases hospital of Nizhny Novgorod were examined. NoVs were detected in 17.5% of cases, the genotype was determined for 189 isolates. Distribution of genotypes: GII.2 — 19.0%, GII.3 — 1.6%, GII.4 — 45.5%, GII.6 — 20.6%, GII.7 — 0.5%, GII. 13 — 1.1%, GII.14 — 0.5%, GII.17 — 10.6%.

Variant GII.4_Sydney2012 predominated in all years, with the exception of 2014–15 season, when its share in the spectrum of NoVs genotypes decreased to 9.8%, and the genotype GII.6 came out on top. In autumn 2016 there was a sharp increase in the frequency of NoVs detection, which coincided with the replacement of previously circulating recombinants GII.Pe-GII.4_Sydney2012 to recombinants GII.P16-GII.4_Sydney2012. The share of the latter was 60.0% in 2016–17 and 55.3% in 2017–18.

Phylogenetic analysis of recombinants showed the presence of clusters corresponding to the specificity of the polymerase, with the absence of significant differences in the capsid protein.

Thus, the prolonged circulation of NoVs GII.4_Sydney2012 may be associated with the acquisition of genes of non-structural proteins that provide virus with selective advantages. However, the impact of minor changes in the capsid protein on the antigenicity of the virus and its ability for successful spreading can not be ruled out.

3.14 doi: 10.15789/2220-7619-2018-4-3.14

INFLUENCE OF VAGINAL MICROBIOTA ON THE ACTIVITY OF HUMAN PAPILLOMAVIRUS

D.K. Ermolenko, A.V. Zakrevskaya, L.B. Kulyashova, N.G. Roshchina

St. Petersburg Paster Institute, St. Petersburg, Russia

The prevalence increases in women with cervical pathology in proportion to the severity of the lesion and reaches about 90% in the contingent with a third degree of cervical intraepithelial neoplasia and invasive cervical cancer. The severity of these changes depends not only on the duration of the persistence of pathogens, but also on their activity. This determines the need to identify the factors influencing on viral activity.

Therefore, the aim of this study was to compare the viral load of pathogens in women with bacterial vaginosis and with vaginal normocenosis.

40 women aged 23–32 were selected for the study. Diagnosis of bacterial vaginosis was based on microscopy, genetic study (polymerase chain reaction in real time, PCR-RT) of the vaginal discharge and clinical features. Control group consisted of 40 patients aged 25–34 without disorders of vaginal microbiota. HPV of phylogenetic groups A5, A6, A7 and A9, most often affecting the epithelium of urogenital tract and the perianal zone and low oncogenic risk of type 6 and type 11, were identified by PCR-RT.

HPV of low oncogenic risk of type 6 and type 11 were not detected in any of the patients. Clinically, the infection manifested as small papillary formations in the vagina and vulvae 23 (57.5%) patients from control group and 28 (70%) from study group. In 5 (12.5%) patients from control group and 9 (22.5%%) from study group changes were revealed only in colposcopy as planar formations in the thickness of the mucous membrane of the vaginal part of the cervix. The presence of flat warts correlated with mild dysplasia of 1 steppe revealed by cytological study. The viral load evaluation demonstrated that it was significantly higher in study group than in the control group (lg 5.24±0.18 and log 4.30±0.26 respectively, $p < 0.001$).

The results suggest that the presence of bacterial vaginosis in patients with concomitant papillomavirus infection (PVI) of the urogenital tract can support and stimulate the activity of HPV, which contributes to more frequent formation of manifest forms of viral infection in such patients. This indicates the need to assess the microbiota of the genital tract in all patients with an identified oncogenic HPV with an obligatory correction when finding violations. This should be considered as a main part of therapeutic measures in the therapy of PVI of the urogenital tract in women.