ed. The interpretation of results we accomplished according to criterions of Committee on antibiograms of French Microbiological Society.

There were identified the following pathogen bacteria: *Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis, Pseudamonas aeruginosa, Salmonella* sp., g. *Shigella* sp., *Staphylococcus aureus, Streptococcus* sp., *Streptococcus β-hemoliticus*. It was established that resistance to different antibiotics isn't the same for different bacteria. Occurring everywhere resistance to antibiotics in medical institutions of Conakry is conditioned by following causes: anarchy use of these drugs by population and by unreasonable physician recommendations. One uses antibiotics often without physician prescriptions, its sale is not controlled, the storage conditions are not kept, one use expired medicines. It increases the bacteria resistance. As an example the sharp down of susceptibility to tetracycline is conditioned by its wide distribution on the Guinean medicine market on obtainable prices. One uses this drug for self treatment.

Our study showed the wide development of resistance of pathogenic bacteria to antibiotics in Guinea by reason of its easy accessibility on medicine market. It's necessary the monitoring of antibiotics use with permanent control of the susceptibility of pathogenic bacteria to them. One must control the quality of antibiotics incoming on the market. These drugs should be used only by physician prescription or of other medical personnel having rights to do it. It is necessary the wide national, regional and international collaboration for this problem resolution.

9.4 doi: 10.15789/2220-7619-2018-4-9.4

MICROBIOLOGICAL ASPECTS OF PURULENT SEPTIC INFECTIONS BREAKOUT INVESTIGATION IN KHABAROVSK CITY

A.P. Bondarenko[1], V.A. Shmylenko[1], O.E. Trotsenko[1], T.A. Zaitseva[1], L.V. Chekan[2]

[1]Khabarovsk Research Institute of Epidemiology and Microbiology, Khabarovsk, Russia; [2]State Research Center for Applied Microbiology and Biotechnology, Obolensk, Russia

The aim of the study — to conduct an etiological interpretation of purulent-septic infection cases registered in August-September of 2017 among newborns in the maternity hospital of Khabarovsk city. A total of 8 cases of different diseases were registered (nosocomial pneumonia, urinary tract infection, omphalitis, subcutaneous whitlow, conjunctivitis).

A microbiological examination of newborns and medical staff of the maternity hospital followed by phenotypical and molecular-biologic evaluation of the isolated strains was performed. Cultures of *Staphylococcus aureus* and *Klebsiella pneumoniae* were isolated from different sites of infection from children and personnel. Vitek-2 Compact and MALDI-TOF Biotyper analyzers were used to identify the bacterial strains. The antibiotic sensitivity of the isolated strains was evaluated by disc diffusion method to 22 drugs.

S. aureus isolated from 3 children (oral pharynx, whitlow) and 13 employees did not belong to the multiresistant MRSA strains. Two groups of *K. pneumoniae* isolated from 3 newborns (oral pharynx, sputum, omphalitis) and from 7 staff members (urine, oral pharynx) differed from each other by antibiotic sensitivity. The strains isolated from newborns were producers of β-lactamase (typical feature for nosocomial strains) and were susceptible to 4 antibacterial drugs out of 22 evaluated. All strains isolated from the personnel were susceptible to the most of the antibiotic drugs. The RAPD-PCR confirmed the difference between two groups of *K. pneumoniae* strains. All strains isolated from the newborns were typed as genovariant A when those isolated from personnel belonged to different types (B, C, D, E).

The phenotypical and molecular-biological survey of *K. pneumoniae* strains isolated during the period of purulent-septic infections breakout in the maternity hospital of the Khabarovsk city indicates on the difference between two identified bacterial strains. It highlights the fact that during the breakout there were two independent epidemic foci of *K. pneumoniae* infection among newborns and medical staff.

9.5 doi: 10.15789/2220-7619-2018-4-9.5

SEROVAR SPECIFIC ANTIMICROBIAL SUSCEPTIBILITY OF SALMONELLA

S.A. Egorova

St. Petersburg Pasteur Institute, St. Petersburg, Russia

Antimicrobial susceptibility of 564 *Salmonella* strains isolated in 2014–2017 in St. Petersburg from the patients with gastroenteritis was studied. Three leading serovars — *S.* Enteritidis, *S.* Typhimurium and *S.* Infantis accounted for 89.4% of strains (78.9; 5.9 and 4.6%, respectively). Other serovars were represented by single strains. 79.4% of *Salmonella* were resistant to at least 1 antimicrobial group: *S.* Enteritidis — 86.3; *S.* Typhimurium — 63.6; *S.* Infantis — 88.5%.

S. Enteritidis is characterized by high level of resistance to fluoroquinolones (75.0%) and nitrofurans (70.0%). Beta-lactam resistance was noted to ampicillin (2.7%) and extended spectrum cephalosporins (1.8%). Resistance to other antimicrobial groups ranged from 0.4 (aminoglycosides) to 8.8% (tetracyclines). Multidrug resistance (3 and more groups) was unusual for this serovar and was found in 10.8%.

In *S.* Typhimurium resistance to many antimicrobial groups was noted: tetracycline (45.5%), ampicillin (39.4), aminoglycosides (21.2), trimethoprim/sulfamethoxazole (21.2), fluoroquinolones (18.2). This serovar is characterized by the highest proportion of beta-lactam resistance: ampicillin (39.4) and extended spectrum cephalosporins (9.1). Multidrug resistance was found in every fourth strain of this serovar.

S. Infantis were characterized by very high proportion of the resistance to fluoroquinolones, nitrofurans, tetracyclines and trimethoprim/sulfametoxazole (88.5; 80.8; 80.8 and 61.5%, respectively). This serovar was characterized by multidrug resistance: almost 8 out of 10 strains. At the same time, resistance to extended spectrum cephalosporins and chloramphenicol has not been noted.

Rarely isolated serovars were characterized by lower proportion of antimicrobial resistance (31.7%): resistance did not exceed 20.0% (quinolones) and ranged from 1.7 (extended spectrum cephalosporins and aminoglycosides) to 15.0 (nitrofurans). Multidrug resistance was observed in 10.0%.

So, in *Salmonella* isolated in St. Petersburg in 2014–2017, the resistance to drugs of choice for the treatment of light and medium-severe salmonellosis (nitrofurans), as well as complicated and severe forms of salmonellosis (fluoroquinolones) is very high. This is typical for the leading serovar *S.* Enteritidis, causing up to 80% of cases of salmonellosis. The use of these antimicrobials should be accompanied by a mandatory antimicrobial susceptibility testing for timely correction of the treatment.