

in 2017. Study of susceptibility of *E. coli* showed that resistant to antibiotics strains prevailed (61.8%) and the ratio of such strains increased almost two-fold in 2017 (72.1%) from 2016 (43.2%). Most isolates were resistant to ampicillin and inhibitor-protected penicillins such as amoxicillin/clavulanate (61.0%). Proportion of such strains increased almost two-fold in 2017 (72.2%) from 2016 (40.9%). Resistant to fluoroquinolones, cephalosporins were 3.2% and 2.4% strains, more than 20 times less. All of them were isolated in 2016. Isolates resistant to two preparations at the same time were most frequent (58.5%). The proportion of multidrug resistant cultures was low (2.4%). There were only 3 isolates resistant to ampicillin, inhibitor-protected penicillins, fluoroquinolones and cephalosporins.

Number of strains of diarrheagenic *E. coli* increased two-fold in 2017 compared with 2016, most of them were EIEC O144 and ETEC O25. Antibiotic-resistant cultures prevailed. Multidrug resistant strains were rare. All strains were susceptible to carbapenems, most of them — to fluoroquinolones and cephalosporins.

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### MOLECULAR ANALYSIS OF PATHOGENS OF PARTICULARLY DANGEROUS BACTERIAL INFECTIONS: FROM THEORY TO PRACTICE

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The modern period of development of medical and biological science is characterized by significant successes in the field of structural analysis of microorganisms and wide technological possibilities of obtaining living objects with given properties. A new scientific trend has emerged — synthetic biology. One of the urgent goals is the application of molecular methods in the practice of epidemiological analysis, to determine the source of infection and the pathways of the spread of the microbial pathogen, to assess its virulence and other properties.

At the present time, considerable material has been accumulated on the genetics of pathogens of anthrax, plague, cholera, brucellosis and other extremely dangerous microorganisms. The algorithms of PCR analysis have been developed in determining the epidemiological significance of isolate strains and their taxonomic features. There is experience of genotyping using MLVA, MLST, SNP and other methods, as well as the analysis of the complete genomic sequence (WGS).

Taking into account the levels of strain analysis (diagnosis of infection or epidemiological analysis), the following current research areas can be identified:

- Detection and identification: application of nucleic acid amplification methods for the differentiation of living and dead cells; introduction of multiplex (multifactor) PCR analysis technologies; creation (completion) of databases of mass spectra of microorganisms; introduction of methods of direct mass-spectrometric analysis of clinical material.
- Molecular typing: the creation of sequential (optimal) genotyping algorithms for each species; application of protein profiling methods for typing pathogens.
- Application of information systems, epidemiological analysis: creation of own databases of full-genomic sequencing; genomic profiling of pathogens in specific areas; creation of complex software products using the data of geographical information systems and predictive modeling.

As a result, an algorithm for bioinformational analysis should be developed for the epidemiological investigation

of outbreaks (cases) of infectious diseases, including those caused by new (atypical) genetic variants of pathogens of especially dangerous infections.

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### DIFFERENTIATION OF *KLEBSIELLA* spp. STRAINS FOR SENSITIVITY TO ANTIBIOTICS USING MASS SPECTROMETRY ANALYSIS MALDI-TOF

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*Klebsiella* spp. strains are frequent causative agents of health care-related infections. Those strains especially dangerous if they circulate in hospitals. They are usually antibiotic-resistant. Therefore, information about the sensitivity of the isolated strain is necessary in the shortest time for proper etiological treatment.

The aim of our study was to assess the possibility of using mass spectrometry analysis (MALDI-TOF) for the rapid prediction of a selected *Klebsiella* spp. strain resistance.

The study used 195 strains of *Klebsiella* spp. isolated in various medical centers of St. Petersburg. All strains were identified by MALDI-TOF. Antibiotic sensitivity was studied by the disco-diffusion method in accordance with the recommendations of EUCAST 8.0. We used 19 antibiotics from 5 classes for testing strains: aminoglycosides, beta-lactams, beta-lactams of extended spectrum, quinolones and carbapenems.

A hierarchical clustering of spectra was made using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) to determine the relationship between clusters. We used Pearson correlation coefficient between variable values of peak intensity in spectral profiles as a measure of the distance between individual mass spectra. We identified 2 significant difference in the spectrum of the cluster. One cluster included spectra of strains resistant to all studied classes of antibiotics, second cluster — strains sensitive to them (Distance Level — 0.65). It was also found that all strains included in the clusters, which differ from others by Distance Level more than 0.2, have the same profile of antibiotic resistance.

As a result of this work, we have formed profiles of phenotypic resistance of *Klebsiella* spp. strains to 19 antibiotics and 5 classes. The prospect of using the results of the study is a significant reduction in the study of biological material from the patient. Thus, simultaneously with the identification of *Klebsiella* spp. strains by MALDI-TOF it is possible to predict the sensitivity of the isolated strain to different classes of antibiotics or even to one of them. This will allow timely recognition of resistant strains of *Klebsiella* spp and prescribe adequate etiological therapy, which will significantly improve the quality of treatment of patients and will prevent the spread of resistant strains of bacteria in the medical establishments.

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### PATHOGENIC POTENTIAL OF COMMENSAL *ESCHERICHIA COLI* ISOLATED FROM ADULTS IN SAINT PETERSBURG

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*Escherichia coli* is one constitute a component of the natural microbiota of warm-blooded animals including humans. At the same time commensal *E.coli* is a dynamic population and in some cases is capable to cause ex-