

than standard strains *S. aureus* 25923 ATCC). Density of *C. albicans* 609 biofilm exceed the density of the standard strain *C. albicans* CCM 885 biofilm at 14.5%. However, dual bacteria-fungal biofilm *S. aureus* U14 + *C. albicans* 609 exceed density of biofilm *S. aureus* 25923 ATCC + *C. albicans* CCM 885 more than twice (208%). Dual-species biofilm isolated from throat healthy media, *S. aureus* 609 + *C. albicans* 609, did not differ in density from dual-species biofilm of reference cultures.

Thus, when coupled with cultivation yeast *C. albicans* *in vitro* aggressiveness of *S. aureus* clinical strain was increased. Carrier state yeast fungi, therefore, could serve as a risk factor for developing a more dense staphylococcal biofilm on the mucous membranes and worsen the course of the disease.

9.23 doi: 10.15789/2220-7619-2018-4-9.23

### MICROBIOLOGICAL MONITORING OF THE RESISTANCE OF HOSPITAL BACTERIAL FLORA WITHIN THE SYSTEM OF PREVENTION OF HEALTHCARE-ASSOCIATED INFECTIONS

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Effective implementation of disinfection activities in healthcare organizations (HCO) plays a great and, sometimes, even a critical role in the prevention of healthcare-associated infections (HAI). Formation and spread of microorganisms which are resistant to used chemical disinfectants in HCO substantially reduce the effect of disinfection measures. This, in turn, is the common reason of the high level of HAI incidence. The problem is aggravated by the development of antibiotic resistance among the strains which are resistant to DA (cross-resistance).

According to the requirements of Sanitary Regulations and Norms 2.1.3.2630-10, it is necessary to conduct monitoring of hospital bacterial flora sensitivity to disinfection agents (DA).

The assessment of sensitivity of microorganisms isolated from the objects of intrahospital environment of intensive care, intensive therapy and surgical units — 20 strains (29%), and from the pathological loci of in-patients — 50 strains (71%) resistant to various groups of antibiotics (*K. pneumonia*, *A. baumannii*, *P. aeruginosa*, *P. mirabilis*, *S. maltophilia*) — was carried out.

Testing was conducted according to the method described in Methodical Guidelines 3.5.1.3438-17 “Assessment of sensitivity to disinfection agents demonstrated by microorganisms circulating in healthcare organizations”. To compare the resistance of hospital microorganisms with that of the microorganisms from the collection which demonstrate standard resistance to DA a collection strain *P. aeruginosa* ATCC 27853 was used.

It was determined that 11 strains were resistant to cationic surface-active agents, 10 strains — to active oxygen, 6 strains — to the combination of quaternary ammonium compounds and active oxygen. 27 (38.7%) out of 70 strains of microorganisms isolated from external environment objects and patients were resistant to used DA.

The identity of resistant strains isolated from external environment and patients serves as evidence of cross-contamination and leads to the spread of resistant strains among patients which, in turn, determines the need to improve the organization of preventive activities.

9.24 doi: 10.15789/2220-7619-2018-4-9.24

### GENETIC VARIANTS OF RESISTANCE DETERMINANT TO SILVER IN EPIDEMIC STRAINS OF ACINETOBACTER BAUMANNII

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Silver-containing dressings are widely used in burns and leg ulcers for prevention and treatment infection. Heavy metal pump CzcA of RND transporters family predicted roles in the efflux both toxic cations including silver and some antibiotics from bacterial cells. Molecular epidemiology and surveillance of outbreaks for last decades indicate that the most resistant *Acinetobacter baumannii* belong to two globally disseminated clonal lineages, GC1 and GC2. Strains of GC2 are epidemic as for Far East and Indochina. Our study was designed in order to clarify an evolution of silver resistance determinant in clinical *A. baumannii*.

Multiple-resistant strains from different geographic locations were selected. List of strains included *A. baumannii* AYE (GC1, epidemic in France for past years) and strains of GC2: ACICU isolated in an outbreak (Italy), sturdy-biofilm forming 1656-2 (South Korea), LY9 and BJ5 recovered in Southern and Northern China hospitals, consequently and strain of sequence-type ST2 (Institut Pasteur typing scheme) endemic in Perm in 2010–2011. Sequences of *czcA* were retrieved from GenBank database for *in silico* comparative analysis using BLAST.

Surprisingly, *czcA* gene on chromosomes of *A. baumannii* GC1 and GC2 spread over the world is presented as two prevailing alleles only (allele 1 in AYE, ACICU, 1656-2 and allele 2 in LY9, BJ5 and Perm). Even di- and multinucleotide variants on positions 213–215 ACC or TTT, 897–898 TG or AC, 945–948 CCGT or TAAA and 951–952 AG or TA have been related to distinct allele (nucleotide numbers from start codon ATG).

The important mechanism of *A. baumannii* survival under silver presence is expressed in an extreme decrease in the genetic heterogeneity of encoding sequence.

*This study was supported by the Federal research programme under state registration number 01201353247.*

9.25 doi: 10.15789/2220-7619-2018-4-9.25

### COMMENSAL STRAINS OF ESCHERICHIA COLI AND BETA-LACTAM RESISTANCE

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According to the World Health Organization, the antimicrobial resistance (AMR) remains a huge worldwide problem of our time which we yet have to overcome. One of the ways to contain the antibiotic resistance is to monitor a circulation of resistant strains of microorganisms, as well as genes that determine the AMR. Studies in recent years have shown a high level of resistance in *Klebsiella pneumoniae* and *Escherichia coli*, the causative agents of nosocomial and community-acquired infections. However, resistant strains also may be a part of gastrointestinal microbiota in healthy individuals.

Antimicrobial susceptibility of 511 commensal *E. coli* strains isolated from faeces of children in age groups from 1 month to 17 years old living in St. Petersburg to 9 groups of antibiotics have been studied by disco-diffusion method. The resistance mechanisms among strains insusceptible

to beta-lactams have been studied by PCR with electrophoretic detection with specific primers to beta-lactamase encoding genes.

39.3% of isolated strains were resistant to 1 and more classes of antimicrobials, while 16.6% of isolates were characterized by multiple resistance (resistant to 3 or more classes of antibiotics). Resistant and multiresistant strains were isolated equally often from children of all age groups. 29.5% of the strains were not susceptible to ampicillin, while 11.2% were insensitive to cephalosporins. It was established that the resistance mechanism to ampicillin is associated with the production of beta-lactamase molecular classes of TEM, SHV and OXA; to cephalosporins — CTX-M, TEM, SHV and AmpC. The most common genes are beta-lactamases of molecular class TEM (22.7%) and CTX-M (9.6%). Simultaneous production of several beta-lactamases was found in 8.4% of strains. *E. coli* strains producing beta-lactamases, unlike strains that do not produce them, are statistically significantly more often resistant to other groups of antibiotics (quinolones, aminoglycosides, chloramphenicol, tetracycline).

The results indicate that colonization of an intestine by resistant strains of *Enterobacteriaceae* starts in early childhood. In the context of the widespread use of antibiotics in medicine, veterinary, agriculture and food industry, such strains persist for a long time in the microbiota of children and adults, making them potential sources of resistance determinants for enteropathogens causing the acute intestinal and septic infections.

**9.26** doi: 10.15789/2220-7619-2018-4-9.26

#### **VIRULENCE GENES AND PHYLOGENETIC GROUPS OF COMMENSAL STRAINS OF *ESCHERICHIA COLI***

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The species *Escherichia coli* (*E. coli*) is globally distributed. Representatives of the species live in the distal intestine of almost every person on the planet, as well as in the intestines of mammals, amphibians and birds, participating in the biotransformation of nutrients and the synthesis of biologically active molecules. Among the non-pathogenic members of the species various pathotypes are found, which cause diseases of intestinal tract (enteropathogenic *E. coli* (EPEC), enterohemorrhagic *E. coli* (EHEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), enteroaggregative *E. coli* (EAggEC)) and extraintestinal infections (uropathogenic *E. coli* (UPEC), meningitis-associated *E. coli* (MNEC)). They are characterized by a variety of virulence factors. Studies of the evolution of intraspecific diversity revealed seven phylogenetic groups, four of which are the main (A, B1, B2, D).

The aim of the study was to determine the phylogenetic profile of the population of *E. coli* commensal strains, to identify genetic determinants of known virulence factors and to compare their prevalence in the genomes of *Escherichia* in different phylogenetic groups.

511 strains of *Escherichia coli* isolated in 2012–2014 were studied. Strains were isolated from children faeces in age groups from 1 month to 17 years old living in St. Petersburg, without diarrhea and urinary tract infections, and studied with the PCR using electrophoretic detection with specific primers to genes encoding virulence factors and markers of phylogenetic groups.

The studied population of *E. coli* was represented by strains of phylogroup A — 33%; B1 — 7%; B2 — 34%; D — 26%. The genome of commensal strains contains virulence genes of EPEC (2.5%), EAggEC (4.5%). Strains with EPEC

virulence genes are more common in phylogenetic group B1 (18.9%), whilst strains with EAggEC virulence genes are more common in phylogroup D (12.4%). Virulence genes of EHEC, ETEC, EIEC were not identified. The genome of commensal strains contains some genes of UPEC virulence (*hlyB* — 20.9%; *cnf* — 17.4%; *pap* — 29.5%; *sfa* — 19.8%; *aer* — 20.0%). Genes of toxins (*hlyB*, *cnf*) and adhesins (*pap*, *sfa*) are encountered more frequently, with statistical significance, in strains of phylogenetic group B2.

The study showed that genes encoding virulence factors for some pathotypes of *E. coli* are also found in the genomes of the commensal *E. coli* strains and the probability of their detection among representatives of different phylogroups is inconsistent.

**9.27** doi: 10.15789/2220-7619-2018-4-9.27

#### **THE SEROPREVALENCE *H. PYLORI* INFECTION IN DIFFERENT GEOGRAPHICAL REGIONS**

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*H. pylori* colonizes more than 50% of humans worldwide. It causes unnoticed chronic gastritis in all carriers and represents a major risk factor for peptic ulcer disease and gastric cancer. It is known that a higher prevalence of *H. pylori* infection will lead to a higher overall prevalence of upper gastrointestinal disease. However the form of such disease may be dictated by socioeconomic and environmental factors as well as the habits and traditions of the people living in different geographical regions.

The aim of our work was to study the seroprevalence infection caused by toxigenic *H. pylori* strains among residents of different geographical regions.

We examined residents of the North-West region of the Russian Federation, Central Asia, Guinea and North Vietnam. Age of the examined was from 20 to 50 years. IgG screening for *H. pylori* and *Cag A* *H. pylori* antibodies was performed using ELISA method with test-system produced DRG (Germany), Biohit (Finland).

In the inhabitants of the North-West region of the Russian Federation, the seroprevalence of infection caused by toxigenic *H. pylori* strains was 55.59±1.2%. The lowest was the infection of *H. pylori* in North Vietnam — 43.75±8.7%. The highest percentage of *H. pylori* infection was found in Guinea and Central Asia — 85.11±5.2% and 84.00±3.7%, respectively.

An uneven prevalence of infection caused by toxigenic *H. pylori* strains was found among residents of different geographical regions. An increasing process of migration of the population can lead to the spread of infection and the exchange of *H. pylori* strains, specific for the particular regions. This suggests the necessity for further epidemiological studies of *H. pylori* infection in different geographical regions.

**9.28** doi: 10.15789/2220-7619-2018-4-9.28

#### **INFLUENCE OF CHOLESTEROL ON THE GROWTH OF *STAPHYLOCOCCUS* spp.**

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The aim of research was investigation of the effect of cholesterol (C) on the growth kinetics of *Staphylococcus aureus* and *S. epidermidis*.

We used *S. aureus* and *S. epidermidis* from ATCC collection, which were cultured in meat-peptone broth with