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.

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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.

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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.

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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