samples it was detected G-genotype in 182 cases (86,7%) and P-genotype in 176 cases (83,8%). P-genotype and G-genotype were not identified in 3,3% and 4,3% of samples, respectively. In 5,7% of samples both genotypes were not identified. It was shown that during each epidemic season from 2006 to 2009 in Ukraine G1P[8] was the dominant genotype, which varied from 30% to 80% of all positive samples. The second most distributed genotype was G4P[8] (40%), third - genotype G3P[8] (25%), and the fourth - G2P[8] (11%). During the epidemic period 2006-2009 in Kiev, for the first time genotype G9P[8] was identified in 5% of cases. Thereafter it was found seldom during 2007, then appeared in rare cases. In some clinical samples multiple genotypes were identified: G1P[8] + G3; G1P[8] + G2; G3P[8] + G4. Genetic variant G2P[4] was the cause of rare cases of diarrhoea during the studied period. For the first time the features of rotavirus group A circulation in Ukraine among children under 5 years old were shown. The obtained data of the major rotavirus genotypes has a great importance in deciding the implementation of specific prevention of rotavirus diarrhoea in Ukraine.

Investigation of Antibiotic Resistance in Enterobacteriaceae, Acinetobacter and Candida Species

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An increased level of hospital infections resistance and emergence of new resistance mechanisms in the conditions of widespread antibiotics use makes serious demands to the quality of laboratory diagnostics and organization of microbiological monitoring. The objective of the research: to determine the frequency of the resistant to antibiotics strains of Enterobacteriaceae, Acinetobacter and Candida species; with the help of phenotypic methods to identify the production of extended-spectrum b-lactamases (ESBL) of different classes and other enzymes and mechanisms providing resistance. Material for the investigation was presented with 102 strains of K. pneumoniae, E. coli, A.baumannii and Candida spp., selected from the patients with different pathology treated in therapeutic departments. The determination of selected isolates was performed with the help of disk-diffusion method according to the recommendations of Clinical and Laboratory Standards Institute (CLSI). For identification and results control of the sensitivity identification an automatic system Vitek 2 (Bio Merieux) was used. 27% of the Enterobacteriaceae and Acinetobacter strains showed resistance to penicillins, 3d and 4th generations of cephalosporins and sensitivity to cephamycins what confirms the production of ESBL belonging to molecular class A. 16,7% of the same bacteria were resistant to 3d and 4th generations of cephalosporins, cephamycins, so to reveal ESBL of C AmpC type. 8,3% of the strains that appeared to be Acinetobacter baumannii, produced carbapenemases and in this regard were characterized by a high resistance level to 3d and 4th generations of cephalosporins and carbapenems. 16,7% of the strains produced penicillinases and 2,1%- cephalosporinases. Aminoglycoside-modifying enzymes were found in 33,3% cases. Resistance to ftorchinolones was equal to ciprofloxacin, norfloxacin and ofloxacin and was noticed in 38, 5% of the tested strains. Candida species were more resistant to azole antifungal drugs (50% of fluconazole-resistant strains) then to polyens (20, 3% nystatin-resistant) according to disk-diffusion method. The results of Candida resistance obtained from disk-diffusion method were not confirmed by the following Vitek study that can be explained by the absence of CLSI disk-diffusion method recommendations for non-albicans strains.