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Investigation of *Clostridium difficile* antigen, toxin A+B and toxin genes in cases of hospital acquired diarrhea

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Background: This study aimed to identify the toxin production and toxin gene profiles of *Clostridium difficile* species through investigation of *C.difficile* antigen glutamate dehydrogenase, toxinA + B and toxin genes in the stool samples of cases of hospital acquired enteritis.

Methods & Materials: Eighty-three patients between 2012-2013 were included in the study. Data of the patients were reached through screening the computerized operating system of the hospital and patient files.

Results: Risk factors such as presence of malignancy, chronic diseases, chemotherapy, radiotherapy and immunosuppression were present in the majority of the patients (Table). *C.difficile* antigen was found to be positive in 5 patients using membrane enzyme immunoassay. ToxinA + B positivity was not found in any patients with membrane EIA. Toxin-B gene positivity was found in 3 out of 5 patients with *C.difficile* antigen positivity with real-time polymerase chain reaction method. Binary toxin gene positivity and single base deletion in nucleotide 117 of the tcdC gene were found in no patients. In conclusion, *C.difficile* infection was identified in 3 patients and *C.difficile* colonization with non-toxigenic species was determined in 2 patients. The incidence of hospital originated CDI was calculated to be 0,10/10,000 patient admission days and 0,06/10,000 patient presentation.

Table Epidemiological data of the patients

	Epidemiological data	Number (%)
Clinic	Internal	74 (%90,2)
	Surgical	5 (%6,1)
	ICU*	3 (%3,7)
Antibiotic usage	1 antibiotic	23 (%40,4)
	2 antibiotic	24 (%42,1)
	≥3 antibiotic	10 (%17,5)
Chemotherapy	No	46 (%56,1)
	Yes	36 (%43,9)
Radiotherapy	No	80 (%97,6)
	Yes	2 (%2,4)
Chronic disease	No	51 (%62,2)
	Yes	31 (%37,8)
Malignancy	No	43 (%52,4)
	Yes	39 (%47,6)

* Intensive Care Unite

Conclusion: CDI is seen in varying rates in different hospitals and countries. In addition, the test methods and kits used conditions of transport, storage, examination of the samples and the epidemiological characteristics of the patients might influence the CDI rates. We believe that the antibiotic usage policies and infection control precautions that are in practice in our hospital for a long time are closely related with the low rates of CDI's seen in this study. GDH screening with EIA method in patients with probable infectious enteritis and verification by PCR in patients with GDH positivity is considered as a quick, effective and reliable method.

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Dynamics of detection of MBL-producing nosomial strains of *P. aeruginosa* in Kazakhstan's hospitals for the period of 2009-2013 years

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Background: The problem of nosocomial infections caused by P.aeruginosa is very urgent. Especially at production of metallo-β-lactamases by P. aeruginosa strains, which are the cause of inefficiency of antibiotic treatment, including therapy by carbapenems. Aim was to study of the dynamics of detecting of P.aeruginosa MBL-producing strains in the Kazakhstan for 2009-2013.

Methods & Materials: The material was obtained during multicenter study on monitoring of the stability of nosocomial P. aeruginosa, isolated in hospitals of Central Kazakhstan. The design: multicenter prospective microbiological study of many years. It was determined the sensitivity to antibiotics of 900 nosocomial P. aeruginosa, isolated in the period January 2009-September 2013 in hospitals of Central Kazakhstan. The isolates were identified by time-of-flight mass-spectrometry MALDI-TOF (Bruker Daltoniks). The interpretation of antibiotic susceptibility was performed according to CLSI 2007/2012. MBL production had been identified phenotypically by double discs method with EDTA. The detection of main resistance genes with carbapenemase activity was performed by PCR in real time.

Results: The proportion of P. aeruginosa MBL-producing strains in 2009 was 3,94% (n = 254, 95% CI 1,55-6,33%), in 2010–12,99% (n = 254, 95% CI 8,86-17,13%), in 2011–3,45% (n = 87, 95% CI–0,39-7,28%), in 2012–16,13% (n = 217, 95% CI 11,24-21,02%), in 2013–9,09% (n = 88, 95% CI 3,08-15,10%). It was revealed the significant increase of the proportion of P. aeruginosa MBL-producing strains in 2010 and 2012 in comparison with the other years (Chi-square value is from 19,676 to 41,841; $p < 0,0001$). All the isolates produced carbapenemases of bla_{VIM2} molecular class. According to MLVA analysis all the isolates belong to the same clonal complex. MLST-typing showed that all the strains belong to st235 clonal group.

Conclusion: The study of the dynamics of detecting of P. aeruginosa MBL-producing strains in Kazakhstan in 2009-2013 showed the circulating of MBL-producers of bla_{VIM2} molecular class, which according to MLVA-analysis relate to the same clonal complex. According to the results of MLST-typing the strains belong to st235 clonal group. In 2010 and 2012 it was registered the significant increase in the proportion of P. aeruginosa MBL-producers.

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