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Impact of PCR Testing for *Clostridium difficile* on Incident Rates and Potential on Public Reporting: Is the Playing Field Level?

To the Editor—Healthcare-associated infections are a challenge to the healthcare field that pose an impact on the outcomes of patients. Preventive measures are implemented at most healthcare institutions to minimize the risks of acquiring healthcare-associated infections.[1] *Clostridium difficile* is a fastidious anaerobic organism that is primarily responsible for antibiotic-associated colitis and accounts for about one-quarter of nosocomial antibiotic-associated diarrhea.[2] In response to a recognized increase in disease activity and severity, the Ohio Department of Health made *C. difficile* infection (CDI) a reportable disease in 2006,[3] and it was reinstated under the revised House Bill 197 in August 2010. While the benefits to transparency are numerous, the downside is that rates will be used for interhospital comparison, despite lack of adjustment for case mix.[4] The intersection of public reporting for CDI in Ohio and the advent of testing based on polymerase chain reaction (PCR) adds another layer of complexity. On October 19, 2010, the Cleveland Clinic changed testing from enzyme immunoassay to a PCR test for *C. difficile* detection. We sought to compare our CDI rates before and after the institution of PCR-based testing and evaluate the effect this will have on our mandate for public reporting.

TABLE 1. Results of Testing of Consecutive Stool Samples for *Clostridium difficile* Using Enzyme Immunoassay (EIA) Toxin and Polymerase Chain Reaction (PCR) during a 3-Month Period

	EIA	PCR	*P*
No. of lab specimens	2,579	2,534	
Mean no. (%) positive	167 (6.5)	382 (15.1)	<.001
CDI rates[a]	4.9	10.3	<.001

NOTE. EIA toxin used before October 19, 2010, and PCR used after. CDI, *Clostridium difficile* infection.
[a] Cases per 10,000 patient-days.

CDI surveillance is performed prospectively at the Cleveland Clinic by infection preventionists. Cases are ascertained by daily review of lab reports of patients with positive stool tests for *C. difficile*, and chart review establishes the presence and onset of symptoms. Before October 19, 2010, testing was performed by enzyme immunoassay detection of toxins A and B (Wampole), and after this date, the testing methodology was changed to PCR (BD Genehom). Query of the microbiology information systems was done to compare the results of testing for CDI, using consecutive stool samples during a 3-month period before and after the change. A telephone survey of 11 other Ohio hospitals was conducted to determine whether PCR testing for CDI had been implemented at their institution.

The prevalence of positive tests for CDI increased significantly from 6.5% of 2,579 stools tested to 15.1% of 2,534 stools tested after introduction of PCR testing ($P < .001$). The rate of CDI also increased significantly (from 4.9 per 10,000 patient-days to 10.3; Table 1). There was no identified *C. difficile* cluster after implementation of PCR testing to account for the increased percent positives observed. None of the 11 hospitals in Ohio contacted had introduced PCR testing for CDI during this time. There was a significant increase in the number and rates of CDI after the introduction of PCR testing that was unexplained by other reasons and not unexpected. Decisions about choice of diagnostic platform for CDI testing are complex and should not be driven by need for publicly reporting rates. However, public display of CDI rates are an implicit comparison of quality of care provided. In the case of CDI, identifying test methods should be included.

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Nosocomial Infections in Tbilisi, Georgia: A Retrospective Study of Microbiological Data from 4 Major Tertiary Care Hospitals

To the Editor—Healthcare-associated infections (HAIs) are important and ever-increasing public health problems worldwide. These infections are associated with increased morbidity, length of stay, mortality, and costs.[1-3] The problem is somewhat underrecognized in the country of Georgia.[4] There are relatively scarce statistical data available regarding the epidemiology of nosocomial infections and the prevalence of infection due to multidrug-resistant (MDR) organisms in the region. During the past decade, several small-scale studies have tried to address the problem and clearly showed a significant burden of HAIs and high prevalence of MDR infections in Georgia.[5-8]

The goal of our study was to evaluate the epidemiology of nosocomial pathogens and their resistance patterns at 4 major tertiary care centers in Tbilisi, Georgia. A 3-year retrospective descriptive analysis of microbiological data collected during the period 2007–2010 from 4 major tertiary health care centers in Tbilisi, Georgia, was performed. All microbiology specimens were Gram stained and cultured at the same referral microbiology laboratory. Identification of the bacterial pathogens was performed with an automated system for identification and susceptibility tests (VITEK; bioMérieux). Antibiotic susceptibility testing was performed with the disk diffusion method or by using an automated method (VITEK; bioMérieux). Stool samples were assessed for *Clostridium difficile* with enzyme-linked immunosorbent assay for A and B toxin.

A total of 3,452 available clinical samples were included in the study, and positive findings were documented for 1,607 cultures (46.6%). The most commonly isolated microorganisms included *Klebsiella pneumonia* (in 26.5% of samples), *Pseudomonas aeruginosa* (15.2%), *Candida albicans* (12.3%), *Staphylococcus aureus* (9%), *Escherichia coli* (7.6%), and *Acinetobacter baumannii* (5.1%). The susceptibility patterns of gram-negative rods (GNRs) to the most commonly used antibiotics are shown in Table 1. Among 95 GNR isolates tested for the presence of extended-spectrum β-lactamase (ESBL), 33.7% were found to be ESBL carriers. Extensive resistance to different groups of antibiotics was found among GNRs, including resistance to carbapenems. Only 29% and 11.9% of *Pseudomonas* and *Acinetobacter* isolates, respectively, were susceptible to imipenem. The vast majority of GNRs showed susceptibility to colistin, but we identified 8 colistin-resistant isolates, which included *P. aeruginosa*, *K. pneumoniae*, *Proteus* species, and *E. coli*. The most common gram-positive cocci (GPC) recovered were *S. aureus*, *Staphylococcus epidermidis*,

TABLE 1. Antibiotic Susceptibility of Selected Bacterial Pathogens

	Susceptibility to antibiotics, %							
Bacterial pathogen	AMK	CEPH-3	CFT	CFP	CIP	PIP/TAZ	IMP	FOSPH
Klebsiella pneumoniae	45.1	60.7	57.2	59.1	69.1	60.7	76.8	57.0
Pseudomonas aeruginosa	20.4	0	13.1	12.5	22.6	20.0	29.0	31.5
Escherichia coli	59.0	50.0	53.4	52.5	40.4	44.9	89.4	63.4
Acinetobacter baumannii	10.1	0	1.8	7.0	4.8	13.7	11.9	23.3
Enterobacter aerogenes	39.1	4.2	19.4	20.6	21.0	20.3	39.1	49.1
Proteus mirabilis	46.4	42.9	48.3	42.9	48.3	53.8	51.7	61.1
Klebsiella oxytoca	39.3	55.6	69.6	60.7	64.3	57.1	100.0	64.0
Enterobacter cloacae	54.5	42.9	36.4	42.9	59.1	55.0	71.4	66.7

NOTE. AMK, amikacin; CEPH-3, third-generation cephalosporins other then ceftazidime; CFT, ceftazidime; CFP, cefepime; CIP, ciprofloxacin; FOSPH, fosphomycin; IMP, imipenem; PIP/TAZ, piperacillin-tazobactam.