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Clindamycin Resistant clone of C. difficile PCR ribotype 027 in Europe

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Clindamycin resistance varied between isolates from unrelated institutions. Isolates from 2 healthcare settings were susceptible to clindamycin (n = 11; MIC\textsubscript{90} ≤ 0.5 mg/L). However, clindamycin-resistant PCR 027 isolates (n = 96; MIC\textsubscript{90} > 256 mg/L) were identified in the other 5 healthcare institutions. All clindamycin-resistant PCR 027 isolates were positive for the erm\textsubscript{B} gene, encoding the macrolide-lincosamide-streptogramin-B genotype.

A subset of clindamycin-sensitive and -resistant Irish 027 strains isolated throughout 2006 (n = 22) were further characterized by using a recently described MLVA protocol (3). Six clindamycin-susceptible isolates were selected from 2 healthcare settings. One hospital conducted active routine laboratory surveillance and molecular genotyping (n = 3). The second hospital submitted only random isolates (n = 3) for typing during a C. difficile outbreak. Sixteen clindamycin-resistant PCR 027 isolates were also included in the MLVA. Resistant isolates were selected from 5 healthcare settings. These included isolates from 2 C. difficile outbreaks with ongoing laboratory surveillance (n = 5, n = 6, respectively); a third hospital with ongoing laboratory surveillance (n = 3) and 2 hospitals that each submitted fecal samples from patients with severe cases of C. difficile disease (n = 1). The Stoke-Mandeville control strain R20291 was included for comparison.

MLVA determined that all strains within the clindamycin-resistant cluster were closely related and were single- or double-locus variants with a maximum 5 summed tandem-repeat difference (STRD). In contrast, the closest relationship between the clindamycin-resistant and the clindamycin-sensitive clusters was a triple-locus variant with an STRD of 17.

The nonrelated reference strain of the Stoke-Mandeville outbreak (R20291) differed considerably from all Irish isolates but was more related to the clindamycin-sensitive cluster than to the clindamycin-resistant cluster (Figure). We thus linked a defined genetic marker with the clindamycin-resistant phenotype in C. difficile PCR-027. MLVA could clearly differentiate clindamycin-resistant and -susceptible isolates from the same geographic region and subgrouped them into 2 distinct clusters (Figure).

Although high-level resistance to fluoroquinolone antimicrobial agents has been well documented in PCR 027 (1,6), resistance to clindamycin is rare. Subsequently, clindamycin has been considered as a “protective” antimicrobial agent for the development of CDAD in an epidemiologic survey in the Netherlands (8). Currently, resistance to this agent in NAP 1/PCR 027 has been restricted to the United States. McDonald and colleagues reported that 19 (79%) of 24 NAP 1 isolates were classified as less susceptible (MIC 4 mg/L) or resistant (MIC ≥ 8 mg/L) to clindamycin when Clinical and Laboratory Standards Institute criteria were used (2). Unfortunately, MIC values were not reported, and the corresponding resistance genes were not investigated. In contrast, Canadian studies to date have not reported clindamycin resistance in this strain type. The MIC\textsubscript{90} of Canadian NAP 1 isolates for clindamycin was 4 mg/L (9,10). Although outbreaks and sporadic cases of PCR 027 have been identified in several European countries, to date no clindamycin-resistant clone has been reported.

Detection of clindamycin-resistant C. difficile PCR 027 strains is an important and worrying development. Resistance to this antimicrobial agent increases the risk for CDAD in patients, and its use may be an important factor contributing to the persistence and spread of PCR 027. A similar feature has already been observed when fluoroquinolones and cephalosporins are prescribed. Clindamycin-resistant PCR
027 probably reflects the emergence of a new clone because MLVA clearly differentiates between clindamycin-susceptible and -resistant isolates.

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Increasing Incidence of Clostridium difficile–associated Disease, Singapore

To the Editor: Clostridium difficile–associated disease (CDAD) has increased in incidence across North America and Europe (1). Recent reports document the emergence of an epidemic strain of C. difficile, NAP1/BI/027, associated with increased virulence (2,3). However, less information is available regarding CDAD epidemiology in Asia. We examined the incidence of C. difficile among hospitalized patients in Singapore from 2001 through 2006 and conducted a case–control study to evaluate risk factors for testing positive for C. difficile toxin (CDT) in our population.

Tan Tock Seng Hospital (TTSH) is a 1,200-bed, acute-care general hospital in Singapore that serves an urban population of 4 million. We calculated CDAD incidence using the number of patients testing positive for CDT per 10,000 patient days from 2001 through 2006. We used this calculation because CDT testing would have been ordered for clinical indications. CDT testing was performed by using the same ELISA (Premier Toxins A&B; Meridian Bioscience, Inc., Cincinnati, OH, USA) throughout the entire period of investigation.

Case-patients and controls were selected from patients hospitalized at TTSH from January 1 through December 31, 2004. Microbiology laboratory records were used to define 3 groups. Case-patients were defined as CDT-positive inpatients (group 1). Two sets of negative controls were defined: the first (group 2) consisted of patients who tested negative for CDT. However, because false-negatives could nullify differences between groups 1 and 2, we defined a second set of negative controls (group 3) from among 18,000 inpatients not tested for CDT.