

Subject Category: Multidrug-Resistant (MDR) Organisms

Abstract Number: SG-APUSIC1136

Multidrug-resistant organisms: Elevating issues identified by antimicrobial stewardship to improve infection control responses

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Objectives: Resistance to third-generation cephalosporins in *Escherichia coli* bacteremia is on the rise in Australia. Currently, laboratory definitions of multidrug-resistant organisms determine infection control responses. The incidence of particular extended-spectrum β -lactamase (ESBL) *E. coli* phenotype, with nonsusceptibility to both ciprofloxacin and trimethoprim-sulfamethoxazole, is increasing in the Australian Capital Territory, Australia. The increase was noted primarily through antimicrobial stewardship clinical care rather than standard infection control or microbiology processes. Clinically, patients are left with limited or no oral therapeutic options for treatment. Despite not necessarily meeting the laboratory definition of a multidrug-resistant organism, this phenotype is likely to be just as transmissible as other healthcare-associated pathogens. We sought to determine whether laboratory definitions of multidrug-resistant organisms adequately inform infection control responses. **Methods:** Using laboratory data from Australian Capital Territory (ACT) Pathology, we identified all ESBL *E. coli* bloodstream isolate episodes from 2016 to 2020. We then reviewed the antibiotic sensitivities of each isolate to identify isolates with nonsusceptibility to both ciprofloxacin and trimethoprim-sulfamethoxazole. We then compared these isolates with the multidrug-resistant organism definition used by ACT Pathology. **Results:** In total, 152 isolates were reviewed. ACT Pathology classified 35 (23.0%) of these isolates as a multidrug-resistant organisms. We identified 80 (52.6%) isolates with nonsusceptibility to both ciprofloxacin and trimethoprim-sulfamethoxazole. Of these 80 isolates, only 24 (30.0%) met the ACT Pathology definition of a multidrug-resistant organism. **Conclusions:** Multidrug-resistant organism definitions should encompass a broad range of healthcare considerations. When the laboratory defines what is important, it may not include the complete spectrum of clinical care concerns. To help combat the rise of multidrug-resistant organisms, definitions for organisms of resistance and transmissibility significance should be developed in conjunction with microbiology, infection control, and antimicrobial stewardship.

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Diagnostic and infection prevention and control (IPC) performance of rapid polymerase chain reaction (PCR) compared to conventional culture PCR methods for detecting carbapenemase-producing organisms (CPOs)

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Objectives: In this study, we compared the performance of a rapid polymerase chain reaction (PCR) method in detecting carbapenemase-producing organisms (CPOs) and its impact on infection prevention and control (IPC) measures compared with a culture PCR method. **Methods:** All patients requiring CPO screening were included. Rectal swabs were collected with double rayon swabs (Copan 139C). They were simultaneously analyzed for the presence of CPOs using rapid PCR assay (Xpert Carba-R assay, Cepheid, Sunnyvale, CA) and a culture-PCR method (ChromID CARBA-SMART, bioMerieux, Marcy-l'Étoile, France). For CARBA-SMART, only colored colonies (ie, Enterobacterales) were evaluated for CPOs according to the prevailing institutional protocol. We tracked time to CPO detection. Using CPO positivity from either the rapid PCR or the culture PCR method as the gold standard, we calculated the sensitivity and specificity of both tests. We calculated the number of epidemiologically linked contacts generated when the first test results were known. We prospectively followed the ward census to identify the putative additional number of contacts generated by the later known result. Contacts were patients who shared the same ward (with overlapping time) as the CPO patients. **Results:** Between April 2019 and June 2020, culture PCR method detected CPOs in 316 (1.3%) of 24,514 samples (*bla*OXA48, N = 211; *bla*NDM, N = 51; *bla*IMI, N = 21; *bla*IMP, N = 10; *bla*KPC, N = 9; mixed genotypes, N = 14). The rapid PCR test detected CPOs in 605 (2.5%) of 24,514 samples (*bla*OXA48, N = 266; *bla*NDM, N = 161; *bla*IMP, N = 99; *bla*VIM, N = 29; *bla*KPC, N = 15; mixed genotypes, N = 35). The sensitivity of direct PCR and culture PCR methods were 94.2% (95% CI, 92.1%–95.8%) and 43.5% (95% CI, 39.6%–47.4%), respectively. Both tests had 100% specificity. The median times to detection for the rapid PCR and culture PCR methods were 3–4 hours and 4 days, respectively. Compared with rapid PCR, the culture PCR method generated additional 7,415 contacts when it also tested positive for CPOs and an additional 23,135 contacts when it tested negative for CPOs. **Conclusions:** In our study, the rapid PCR test was more sensitive, identified CPO faster, and generated fewer epidemiologically linked contacts than the culture PCR method.

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Evaluation of a pooling strategy using Xpert Carba-R assay for screening for carbapenemase-producing organisms in rectal swabs

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Objectives: Rapid and accurate screening for carbapenemase-producing organism (CPOs) in hospitalized patients is critical for infection control and prevention. The Xpert Carba-R assay is designed for rapid detection of CPOs, but 1 assay is usually conducted for only 1 sample. We evaluated a pooling strategy for CPO screening using the Xpert Carba-R assay. **Methods:** Swab sets containing 2 swabs were collected from 415 unique patients at Peking University People's Hospital. One swab was used for the pooling test, in which 5 swabs from different patients were mixed in 1 sample treatment solution. The prevalence of CPOs in the hospital (5.3%) predicted that 5:1 pooling was most economical. As the reference method, the other swab was tested by culture using sequencing. **Results:** Of 415 samples, 383 were CPO negative using the pooling test strategy and 31 were positive. All samples that were negative by pooling were negative by culture and sequencing. Among the 31 positive samples identified by the pooling strategy, 26 were positive by culture and sequencing (including 24