BRIEF REPORT



Evaluation of a Screening Method for the Detection of Colistin-Resistant *Enterobacteriaceae* in Stool

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Emergence of mobile colistin resistance (*mcr*)-containing *Enterobacteriaceae* is a public health threat, prompting enhanced surveillance through the Centers for Disease Control and Prevention. We evaluated a selective culture medium for the isolation of *Enterobacteriaceae* with non-wild-type colistin minimum inhibitory concentrations, including those with *mcr-1* genes, in spiked stool samples.

Keywords. colistin resistance; *mcr Enterobacteriaceae*; screening.

Mobile colistin resistance (*mcr*) genes encode resistance to polymyxins, a class of antibiotics used when treatment options are limited. The *mcr* genes are plasmid-mediated, which may facilitate their transfer between bacteria, resulting in the spread of resistance. Recently, there has been an increase in the isolation of bacteria harboring *mcr* genes in humans and animals in the United States, prompting the US Centers for Disease Control and Prevention (CDC) to enhance surveillance for organisms with these genes [1].

The ability to screen clinical samples for bacteria displaying non-wild-type colistin minimum inhibitory concentrations (MICs) due to carriage of *mcr* genes would improve our understanding of this problem. Zurfluh et al. [2] reported fecal carriage rates of colistin-resistant *Enterobacteriaceae*,

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including *mcr*-containing isolates, using a selective culture medium containing colistin, vancomycin, and amphotericin B [2]. We evaluated this screening method for the detection of *Enterobacteriaceae* displaying non-wild-type colistin MICs in stool spiked with well-characterized isolates containing the *mcr*-1 gene.

METHODS

The screening medium was made using Luria-Bertani (LB) medium. In an Erlenmeyer flask, 25 g of LB and 15 g of Bacto agar powder were dissolved in 1000 mL of double distilled water (ddH2O). The solution was autoclaved on a liquid cycle at 121°C for 15 minutes and cooled in a water bath to 56°C. Once it cooled, 1 mL of colistin sulfate (stock solution 4000 mg/dL in ddH2O; Sigma-Aldrich, St. Louis, MO), 1 mL of vancomycin HCl (stock solution 10 000 mg/mL in ddH2O; Sigma-Aldrich, St. Louis, MO), and 1 mL of amphotericin B (5000 mg/mL in ddH20; Sigma-Aldrich, St. Louis, MO) were added, for final concentrations of 4, 10, and 5 mg/mL.

Nine members of the family Enterobacteriaceae were used from panels obtained from the CDC and US Food and Drug Administration (FDA) Antimicrobial Resistance Isolate Bank (AR Isolate Bank; https://www.cdc.gov/drugresistance/ resistance-bank/index.html). The presence of resistance mechanisms was established through isolate whole-genome sequencing using the ResFinder database (last updated June 2, 2016, and accessed on October 25, 2016) [3]. Seven of the isolates carried mcr-1 genes. The mechanism of colistin resistance for the remaining isolates was unknown. MICs for colistin were determined via broth microdilution by the AR Isolate Bank (Table 1). Using frozen stock (-80°C), each isolate was subcultured twice on tryptic soy agar with 5% sheep's blood (Trypticase soy agar with 5% sheep's blood [TSA with 5% SB]; Becton, Dickinson and Company, Sparks, MD) and incubated in ambient air at $35^{\circ}C \pm 2^{\circ}C$ for 18 to 24 hours before use.

Donated fecal matter capsules were used for the spiked stool samples. Donor feces were screened for stool pathogens and multidrug-resistant bacteria and packaged into capsules, as described by Youngster et al. [4]. Each capsule was kept frozen (-80°C) until use. Once each capsule was removed from the freezer, the outer capsule was manually removed, leaving the inner capsule in place. Capsules were placed in 2 mL of sterile water and mixed on a rotator until thawed.

To determine the limit of detection (LOD) of the medium for *Enterobacteriaceae* with a colistin MIC \geq 4, serial 10-fold dilutions of an inoculum with an optical density of 0.5 McFarland (approximately 10⁸ colony-forming unit [CFU]/mL) of AR Isolate Bank *Escherichia coli* 0346 and *Klebsiella pneumoniae* 0125 were

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Table 1. Isolate Detection for LB Medium With Colistin, Vancomycin, Amphotericin B in Stool Spiked With Enterobacteriaceae With Elevated MICs to Colistin

AR Isolate Bank No.	Species	Colistin MIC, µg/mLª	Mechanism of Colistin Resistance	Isolate Detected at $10^2 \mbox{ and } 10^3 \mbox{ CFU/mL}$
AR-Bank 0346	E. coli	4/>4	mcr-1	Y
AR-Bank 0349	E. coli	2-4/2	mcr-1	Y
AR-Bank 0350	E. coli	4/4	mcr-1	Y
AR-Bank 0493	E. coli	8/>4	mcr-1	Y
AR-Bank 0494	E. coli	8/>4	mcr-1	Y
AR-Bank 0495	E. coli	4/4	mcr-1	Y
AR-Bank 0496	Salmonella enteritidis	8/>4	mcr-1	Y
AR-Bank 0040	K. pneumoniae	4/>4	Unknown	Y
AR-Bank 0125	K. pneumoniae	>4/4	Unknown	Y

Abbreviations: CDC, Centers for Disease Control and Prevention; CFU, colony-forming unit; CLSI, Clinical and Laboratory Standards Institute; FDA, Food and Drug Administration; LB, Luria-Bertani; MIC, minimum inhibitory concentration.

^aMIC performed by the CDC and FDA Antimicrobial Resistance Isolate Bank/MIC performed via broth microdilution per CLSI guidelines on isolate identified in stool.

prepared; 100 μ L of each dilution was pipetted into 900 μ L of thawed donated fecal matter, and 0.5 mL of each spiked stool was placed in 4.5 mL of an Enterobacteriaceae enrichment broth (EE broth; Hardy Diagnostics, Santa Maria, CA) and incubated at 35°C \pm 2°C [2]. After 24 hours of incubation, 10 µL of the spiked EE broth was inoculated onto the selective medium and incubated in ambient air at 35°C ± 2°C for 48 hours. 0.5 mL of nonspiked thawed donor fecal matter was placed in 4.5 mL of EE broth, incubated, and subcultured on the selective medium as a negative control. All unique colonies were subcultured to TSA with 5% SB and MacConkey II agar (MAC; Becton, Dickinson and Company, Sparks, MD) and were identified using the Vitek MS system, version 2.0, in vitro diagnostic database (bioMérieux, Durham, NC). MICs to colistin, amikacin, gentamicin, tobramycin, aztreonam, cefepime, cefotaxime, ceftazidime, ciprofloxacin, levofloxacin, ertapenem, imipenem, meropenem, and trimethoprim-sulfamethoxazole were determined for all isolates. Broth microdilution was performed using the Sensititre Vizion system (ThermoFisher Scientific, Waltham, MA) according to Clinical and Laboratory Standards Institute (CLSI) guidelines [5]. Results were compared with MICs reported for these drugs by the AR Isolate Bank for accurate identification of the spiked organisms [5].

To determine the sensitivity of the screening medium for detection of *Enterobacteriaceae* with a colistin MIC \geq 4, thawed donated fecal matter was spiked with 1 of the 9 isolates and serially diluted to final concentrations of 10² or 10³ CFU/mL (Table 1). Each spiked stool was processed as described above, and nonspiked thawed donor fecal matter was used as a negative control. All unique colonies, subcultured to TSB with 5% SB and MAC, underwent organism identification and susceptibility testing for accurate identification of all organisms.

RESULTS

AR Isolate Bank *E. coli* 0346 and *K. pneumoniae* 0125 were successfully isolated at concentrations of 10^2 CFU/mL and above

on all of the selective medium after 48 hours of incubation. Other organisms identified included *Serratia* and *Hafnia* spp., which have intrinsic resistance to colistin, and *Enterobacter* spp. and *Clostridium paraputrificum*, both of which have the potential for non-wild-type colistin MICs [2, 5–7]. No *E. coli* or *K. pneumoniae* were isolated from the nonspiked thawed donated fecal matter sample.

Using an LOD of 10^2 CFU/mL, donated fecal matter was then spiked with 1 of the 9 isolates at a concentration of 10^2 and 10^3 CFU/mL and cultured using the methods described above. All 9 organisms were isolated from the selective medium after 48 hours of incubation at concentrations of 10^2 and 10^3 CFU/mL (Table 1). Serratia fonticola was also isolated. No strains of *E. coli, K. pneumoniae,* or Salmonella enteritidis were isolated from the medium inoculated with the nonspiked thawed donated fecal matter sample. The sensitivity of this screening medium was 100%.

DISCUSSION

The emergence of plasmid-mediated resistance to colistin in *Enterobacteriaceae* through acquisition of *mcr* genes is a public health concern. Screening algorithms to identify clinical isolates that may carry these resistance genes are needed. Our results show that the selective culture method described by Zurfluh et al. [2] can detect *Enterobacteriaceae* with non-wild-type colistin MICs, including those with known *mcr* genes, at low concentrations in spiked stool obtained from healthy, asymptomatic adults.

No large studies exist evaluating the concentration of *mcr*bearing bacteria in the stool of colonized patients, and the limited data examining this have conflicting results. Dona et al. identified *mcr*-1-bearing *E. coli* in the stool of 2 asymptomatic subjects at approximately the LOD of a real-time polymerase chain reaction (PCR) assay for the detection of *mcr*-1-bearing bacteria (10 g DNA copies/reaction), indicating that concentrations of *mcr*-1-bearing *Enterobacteriaceae* in the stool of colonized patients could be quite low [8]. Conversely, Nijhuis et al. reported the identification of an *mcr*-1-bearing *E. coli* in a surveillance stool specimen well below the cycle threshold for the LOD of a real-time PCR assay (3–30 CFU/reaction), indicating the presence of this organism at a fairly high concentration [9]. If we examine data regarding the concentration of other bacteria known to colonize the gastrointestinal track of humans, such as vancomycinresistant *Enterococci* (VRE), concentrations of this organism in the stool of colonized patients range from 10^{2.5} to 10^{8.1} CFU/mL [10]. Extrapolating this information to *mcr*-bearing bacteria in the stool of colonized patients, this screening method could reliably detect these organisms.

Our study has limitations. First, only 9 isolates were used for the evaluation of this screening medium and method. This number was based on the availability of well-characterized strains from the AR Isolate Bank. Many MICs to colistin for isolates containing other mcr genes have been reported to be high enough to overcome the concentration of colistin in this medium; a formal evaluation of isolates with other mcr genes should be performed [1, 11-14]. Second, this screening method is capable of isolating Enterobacteriaceae with non-wild-type colistin MICs, but it does not distinguish between mcr- and nonmcr-mediated colistin resistance mechanisms. Confirmatory methods to detect the presence of mcr genes, such as PCR, are required; this can be done through the CDC's AR Lab Network [15]. Third, the specificity of this medium for the detection of non-wild-type colistin MICs was not specifically addressed. However, the growth of nonspiked Enterobacteriaceae was limited to those with intrinsic resistance or the potential for nonwild-type phenotypes to colistin. Despite this, formal evaluation is needed. Finally, the screening method was evaluated using spiked stool from asymptomatic adults; further study, particularly in subjects who are potential carriers of Enterobacteriaceae with non-wild-type colistin MICs, is needed.

In conclusion, the selective culture method of Zurfluh et al. [2] is valid for detecting *Enterobacteriaceae* with non-wild-type phenotypes to colistin, including those with known *mcr-1* mutations in human stool. The ease of the screening method makes it an appropriate initial screening tool for most clinical laboratories.

Notes

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Disclaimer. The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Potential conflicts of interest. J.A.B. has received research support from Zeus Scientific, Immunetics, Alere, DiaSorin, bioMerieux, the Bay Area Lyme Foundation, the Lyme Disease Biobank Foundation, and the National Institute of Allergy and Infectious Diseases (Award 1R21AI119457-01) for other research projects and has served as a consultant to DiaSorin and T2 Biosystems. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References

- Centers for Disease Control and Prevention. About *mcr* genes, an emerging threat. https://www.cdc.gov/drugresistance/biggest-threats/tracking/mcr.html. Accessed March 13, 2018.
- Zurfluh K, Stephan R, Widmer A, et al. Screening for fecal carriage of MCRproducing Enterobacteriaceae in healthy humans and primary care patients. Antimicrob Resist Infect Control 2017; 6:28.
- Food and Drug Administration and the Centers for Disease Control and Prevention. CDC and FDA Antibiotic Resistance Isolate Bank. Accessed October 25, 2016.
- Youngster I, Sauk J, Pindar C, et al. Fecal microbiota transplant for relapsing *Clostridium difficile* infection using a frozen inoculum from unrelated donors: a randomized, open-label, controlled pilot study. Clin Infect Dis 2014; 58:1515–22.
- Clinical and Laboratory Standards Institute. Performance Standards for Antimicrobial Susceptibility Testing. CLSI Supplement M100. 28th ed. Wayne, PA: Clinical and Laboratory Standards Institute; 2018.
- Jayol A, Poirel L, Dortet L, Nordmann P. National survey of colistin resistance among carbapenemase-producing *Enterobacteriaceae* and outbreak caused by colistin-resistant OXA-48-producing *Klebsiella pneumoniae*, France, 2014. Euro Surveill 2016; 21(37).
- Jayol A, Saly M, Nordmann P, et al. *Hafnia*, an enterobacterial genus naturally resistant to colistin revealed by three susceptibility testing methods. J Antimicrob Chemother 2017; 72:2507–11.
- Donà V, Bernasconi OJ, Kasraian S, et al. A SYBR* Green-based real-time PCR method for improved detection of *mcr*-1-mediated colistin resistance in human stool samples. J Glob Antimicrob Resist 2017; 9:57–60.
- Nijhuis RH, Veldman KT, Schelfaut J, et al. Detection of the plasmid-mediated colistin-resistance gene mcr-1 in clinical isolates and stool specimens obtained from hospitalized patients using a newly developed real-time PCR assay. J Antimicrob Chemother 2016; 71:2344–6.
- D'Agata EMC, Gautam S, Green WK, Tang Y-W. High rate of false-negative results of the rectal swab culture method in detection of gastrointestinal colonization with vancomycin-resistant *Enterococci*. Clin Infect Dis 2002; 34:164–72.
- Xavier BB, Lammens C, Ruhal R, et al. Identification of a novel plasmid-mediated colistin-resistance gene, *mcr-2*, in *Escherichia coli*, Belgium, June 2016. Euro Surveill 2016; 21(27).
- Wise MG, Estabrook MA, Sahm DF, et al. Prevalence of *mcr*-type genes among colistin-resistant *Enterobacteriaceae* collected in 2014–2016 as part of the INFORM global surveillance program. PLoS One 2018; 13:e0195281.
- Wang X, Wang Y, Zhou Y, et al. Emergence of a novel mobile colistin resistance gene, *mcr-8*, in NDM-producing *Klebsiella pneumoniae*. Emerg Microbes Infect 2018; 7(1):122.
- Roer L, Hansen F, Stegger M, et al. Novel *mcr-3* variant, encoding mobile colistin resistance, in an ST131 *Escherichia coli* isolate from bloodstream infection, Denmark, 2014. Eurosurveillance 2017; 22(31).
- Centers for Disease Control and Prevention. About CDC's antibiotic resistance lab network. Accessed April 16, 2019.