KPC-3–Producing *Serratia marcescens* Outbreak between Acute and Long-Term Care Facilities, Florida, USA

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We describe an outbreak caused by *Serratia marcescens* carrying blaKPC-3 that was sourced to a long-term care facility in Florida, USA. Whole-genome sequencing and plasmid profiling showed involvement of 3 clonal lineages of *S. marcescens* and 2 blaKPC-3-carrying plasmids. Determining the resistance mechanism is critical for timely implementation of infection control measures.

*Serratia marcescens* has been linked to healthcare-associated outbreaks, particularly after use of colistin, which is intrinsically resistant to polymyxins (1,2). Outbreaks of carbapenemase-producing *Enterobacteriaceae* (CPE) in long-term care facilities (LTCF) have been well described (3,4); outbreaks of the closely related carbapenemase-producing (CP)–*S. marcescens* are unusual. We describe an outbreak in 2 hospitals in Florida, USA, of *S. marcescens* producing *Klebsiella pneumoniae* carbapenemase (KPC). Subsequent investigation identified a local LTCF as the source.

The Study

In June 2018, a 382-bed hospital that is part of a large hospital health system network in Miami, Florida, identified an increase of CP–*S. marcescens*. A retrospective search for more cases included all patients admitted to any facility in the 4-hospital network during October 2017–June 2018 using the automatic surveillance system (VigiLanz; VigiLanz Corporation, https://vigilanzcorp.com) with interface to the electronic medical record (EMR).

We defined cases as patients with carbapenem-resistant *S. marcescens* by Clinical and Laboratory Standards Institute (CLSI) breakpoints (5) isolated from any source, including clinical or surveillance cultures, during October 2017–December 2018. Based on Centers for Disease Control and Prevention guidelines, community-onset events (CO) were those cases identified ≤3 days after hospital admission; hospital-onset (HO) were those for which the specimens were collected >4 days after hospital admission (6).

In response to the outbreak, and in addition to interventions in place to prevent hospital-acquired infections (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/26/11/20-2203-App1.pdf), all possible cases were prospectively identified upon admission to any of the network facilities via automatic surveillance system. Transfer forms and regular communication with the local Department of Health (DOH) notified hospitals when a known case-patient was transferred from the LTCF. All patients admitted from the source LTCF were placed in contact precautions at admission and screened for CPE. If positive, patients were placed in enhanced contact precautions (Appendix Table 1) for the duration of their stay. Miami-Dade DOH provided infection prevention and control education and support to the LTCF.

We performed matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry (bioMérieux, https://www.biomerieux-diagnositics.com) and Biofire BCID panel (bioMérieux) for bacterial identification. We conducted susceptibility testing using Vitek2 (bioMérieux) following CLSI guidelines. We tested carbapenemase production with CarbaNP test (Hardy Diagnostics,
We subjected 1 isolate per patient to whole-genome sequencing on NextSeq500 (Illumina, https://www.illumina.com). We assembled sequences by SPAdes version 3.13 (https://github.com/aablab/spades) and annotated them by prokka version 1.14 (https://github.com/tseemann/prokka). Snippy version 4.4.0 (https://github.com/tseemann/snippy) was used to identify SNPs. We used ResFinder 3.2 (https://cge.cbs.dtu.dk/services/ResFinder) and PlasmidFinder 2.0 (https://cge.cbs.dtu.dk/services/PlasmidFinder) to identify antimicrobial resistance genes and plasmid replicons. We generated a SNP phylogenetic tree with RAxML version 8.2.11 (https://github.com/stamatak/standard-RAXML) and visualized it using Interactive Tree of Life (iTOL) version 5 (https://itol.embl.de) (7). We sequenced isolates 505 and 514 using the MinION platform (Oxford Science Park, UK, https://nanoporetech.com/products/minion) to define the bla<sub>KPC</sub>-harboring plasmids. We used Unicycler version 0.4.8-β (https://github.com/rrwick/Unicycler) for hybrid assembly of Illumina and MinION reads; we confirmed the presence of identified plasmids by aligning Illumina reads to the identified plasmid sequences.

We purified plasmids by alkaline-lysis method and used them to transform Escherichia coli TOP10 by electroporation (8). We selected transformants harboring bla<sub>KPC-3</sub> on lysogenic agar with ampicillin, and confirmed acquisition of plasmids by PCR. The plasmids were extracted from the E. coli transformants, digested (EcoRI or HindIII), and run on 0.7% gel to obtain restriction patterns.

During October 2017–December 2018, a total of 14 patients with CP–S. marcescens were identified in our hospitals (Figure 1); all patients resided at a neighboring LTCF (Table 1). Five cases (36%) were HO, but 4 were detected ≤15 days after admission and did not coincide in location or time with the other cases. Transmission within the hospital was not suspected; those patients were possibly colonized at admission but undetected due to low sensitivity of AST protocols. The fifth patient had long length-of-stay and previous bloodstream infection (BSI) with KPC-producing Klebsiella pneumoniae.

Ten patients had ≥1 rectal AST; all were negative. Twelve patients had ≥1 tracheal aspirate AST; 2 were positive for CP–S. marcescens (susceptibilities in Table 2; Appendix Table 2). Ten cases had clinical infections by CP–S. marcescens including pneumonia (n = 9) and bloodstream infection (n = 4). Most cases were treated empirically with piperacillin/tazobactam, ceftazidime, and vancomycin. Targeted treatments included ceftazidime/avibactam. Four cases were colonized without signs or symptoms of CP–S. marcescens infection during hospital admission. Three patients died (21% in-hospital mortality); these deaths were not associated with infection by CP–S. marcescens.

During June 2018–January 2019, the 67 notifications of admissions from the source LTCF were related to 30 individual patients. In 7 cases (23%), CP–S. marcescens was present at admission.

We performed molecular testing on 12 isolates, 1 per patient. Core genome analysis demonstrated the presence of 3 clonal lineages of bla<sub>KPC-3</sub>-carrying...
S. marcescens involving >1 patient, and 1 outlier (Figure 2). Eleven isolates belonging to the 3 lineages shared a 43-kb FII-type bla<sub>KPC-3</sub>-harboring plasmid, which had >99% sequence identity with pKPC-Kp46 plasmid previously described in K. pneumoniae (GenBank accession no. KX348146.1) (9); confirmation was by an identical plasmid restriction profile. Lineage 1 isolates shared a 19-kb ColRNAI-type bla<sub>KPC-3</sub>-harboring plasmid, 99% identical to previously reported pNJST258C2 from K. pneumoniae (GenBank accession no. CP006919.1), except for the absence of the transposable element containing aminoglycoside resistance genes <i>aacA1</i> and <i>aacA4</i> (10). The outlying isolate, 520, only contained a pNJST258C2-like bla<sub>KPC-3</sub>-harboring plasmid identical to that found in lineage 1. The bla<sub>KPC-3</sub> sequence was identical between the 2 plasmids and was located on <i>Tn4401b</i>-like elements, which were identical except for a 70-bp deletion in <i>tnpA</i> leading to frameshift and premature stop in the pNJST258C2-like plasmid. This deletion did not seem to affect KPC expression; isolate 520, carrying only the pNJST258C2-like plasmid, was still resistant to carbapenems. In addition to bla<sub>KPC-3</sub> the pKPC-Kp46-like plasmid contained bla<sub>TEM</sub>Δ<sub>bla<sub>oxa-9</sub></sub> and <i>qnrB19</i>. The pNJST258C2-like plasmid did not contain additional antimicrobial resistance genes; however, it contained an operon encoding production of colicin, an antimicrobial substance that is lethal against related strains that lack it (11). Isolate 520 was from the patient with a history of KPC-producing K. pneumoniae, suggesting that the bla<sub>KPC-3</sub>-harboring plasmid was transferred to <i>S. marcescens</i> in the patient in a separate event from the infection of the other 11 cases.

**Conclusions**

Use of an automatic surveillance system enabled retrospective and prospective detection of cases and identification of their common exposure in an LTCF on the basis of shared address. Prospective identification of residents of the source LTCF enabled screening at point of entry and implementation of interventions to prevent hospital transmission. Direct communication between the infection control department and the LTCF was difficult and relied upon the local DOH to share information about known cases. Unfortunately, a regional registry of patients with CPE is not available in Florida (12,13).

The pKPC-KP4-like plasmid shared among the 3 clonal lineages involved in the outbreak, and the pNJST258C2-like plasmid, shared between lineage 1 and the outlier isolate, were the vehicles of bla<sub>KPC-3</sub> in this polyclonal outbreak. However, it is unclear why lineage 1 isolates contained both bla<sub>KPC-3</sub>-harboring plasmids. It is possible that in addition to antimicrobial resistance, factors such as colicin production facilitated dissemination within the LTCF.

**Figure 1.** Epidemic curve of carbapenemase-producing <i>Serratia marcescens</i> infections by month in 2 hospitals of a large healthcare system in Miami, Florida, USA, 2018. Asterisk (*) indicates the implementation of new interventions in response to the outbreak. CO, community-onset; HO, hospital-onset.

| Month | Total no. of cases |
|-------|-------------------|
| Jan   | 1                 |
| Feb   | 5                 |
| Mar   | 1                 |
| Apr   | 1                 |
| May   | 1                 |
| Jun   | 1                 |
| Jul   | 1                 |
| Aug   | 1                 |
| Sep   | 1                 |
| Oct   | 1                 |
| Nov   | 1                 |

**Table 2.** Susceptibility profiles of KPC-producing <i>Serratia marcescens</i> isolates, Miami, Florida, USA.*

| Drug   | Total no. isolates tested | % Susceptible | % Intermediate | % Resistant |
|--------|---------------------------|---------------|----------------|------------|
| ATM    | 14                        | 0             | 0              | 14 (100)   |
| CFZ    | 14                        | 0             | 0              | 14 (100)   |
| FEP    | 14                        | 0             | 0              | 14 (100)   |
| CAZ    | 14                        | 0             | 0              | 14 (100)   |
| CRO    | 14                        | 0             | 0              | 14 (100)   |
| LVX    | 14                        | 5 (36)        | 1 (7)          | 8 (57)     |
| MEM    | 14                        | 0             | 0              | 14 (100)   |
| AMK    | 14                        | 14 (100)      | 0              | 0          |
| GEN    | 14                        | 0             | 13 (93)        | 1 (7)      |
| TOB    | 14                        | 0             | 0              | 14 (100)   |
| SX7    | 14                        | 14 (100)      | 0              | 0          |
| TET    | 14                        | 2 (14)        | 8 (57)         | 4 (28)     |
| TGC    | 12                        | 12 (100)      | 0              | 0          |
| CZA    | 3                         | 3 (100)       | 0              | 0          |

*AMK, amikacin; ATM, aztreonam; CAZ, ceftazidime; CFZ, cefazolin; CRO, ceftriaxone; CZA, ceftazidime/avibactam; FEP, cefepime; GEN, gentamicin; LVX, levofloxacin; MEM, meropenem; SX7, trimethoprim/sulfamethoxazole; TET, tetracycline; TGC, tigecycline; TOB, tobramycin.
In summary, our investigation of this CP–S. marcescens outbreak in 2 hospitals in Florida identified a local LTCF as the source. Early identification, communication, and implementation of preventive measures within healthcare facilities and cooperation with local public health authorities are pivotal in preventing transmission of multidrug-resistant organisms among vulnerable populations.

Acknowledgments
We thank Daniel R. Evans for his assistance with MinION sequencing and Marissa P. Griffith for bioinformatics support.

A.I. was supported through Physician Scientist Incubator Program at the University of Pittsburgh, sponsored by the Burrows Wellcome Fund. Y.D. was supported by research grants from the National Institutes of Health (grant nos. R01AI104895, R21AI135522, and R21AI151362).

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**Appendix**

**Appendix Table 1.** Interventions to prevent spread of KPC-producing *Serratia marcescens* bacteria in healthcare facilities, Florida, USA

| Bundle of interventions to prevent hospital-acquired infections (HAI) in place before outbreak of *Serratia marcescens* carrying *bla*KPC within a large healthcare network in Miami, Florida |
|---|
| **Daily bathing with chlorhexidine gluconate foam, nasal decolonization with alcohol-based nasal sanitizer, and daily distribution of alcohol-based wipes for patients' hand hygiene for all adults in all units.** |
| **AST for CPE carriage in perirectal swab and tracheal aspirate (vented patient) upon admission and weekly thereafter to all adult ICU patients.** |
| **Enhanced contact precautions for patients infected or colonized with any CPE.** |
| **Environmental cleaning monitoring with UV powder.** |

Elements of enhanced contact precautions for CPE patients

- Private room setting.
- Dedicated patient care equipment.
- Different color-coded isolation sign at the patient’s room entrance.
- Patient’s room cleaning with bleach-based products twice a day.
- Disposable gowns and gloves for contact isolation.
- Patient and family/visitor education.
- Staff cohorting.

AST, active surveillance testing; CPE, carbapenemase-producing Enterobacteriales; ICU, intensive care unit; UV, ultraviolet.

**Appendix Table 2.** Susceptibility testing of CZA against 3 *Serratia marcescens* carrying *bla*KPC-3 from an outbreak in Miami, Florida

| Isolate   | E-test MIC | Comments             |
|-----------|------------|----------------------|
| ATCC 25922| 0.032      | Both plasmid         |
| S-505     | 0.5        | KP46 plasmid only    |
| S-514     | 0.5        | NJST258 plasmid only |
| S-520     | 0.047      | NJST258 plasmid only |

CZA, ceftazidime/avibactam. CZA MIC in isolates with 2 plasmids is not any higher than that of single plasmid, which was expected. CZA resistance usually requires KPC mutations; none were present in the isolates. The variation seen between S-520 and S-505 and S-514 was probably driven not by KPC, but by other β-lactamases, porins, or efflux. The isolates were quite distinct from each other.