Table 1. Clinical characteristics and outcomes of 48 patients who received cefiderocol for gram-negative infections

Age, median (IQR)	70.5 (61-75)
Male sex, n (%)	45 (95.7%)
Charlson Comorbidity Index, age unadjusted, median (IQR)	6 (2-9)
Renal replacement therapy when cefiderocol initiated, n (%)	10 (20.8%)
Creatinine clearance >120 mL/min [1], n (%)	10 (20.8%)
Infectious syndrome(s)[2]:	
Lower respiratory tract infection, n (%)	23 (47.9%)
Urinary tract infection, n (%)	14 (29.2%)
Endovascular infection, n (%)	9 (18.8%)
Bone/joint infection, n (%)	4 (8.3%)
Other, n (%)	8 (16.7%)
Infectious organism(s)[2]:	
Pseudomonas aeruginosa, n (%)	30 (62.5%)
Enterobacterales, n (%)	17 (35.4%)
Acinetobacter baumannii, n (%)	10 (20.8%)
Stenotrophomonas maltophilia, n (%)	3 (6.3%)
Other, n (%)	2 (4.2%)
Negative cultures, n (%)	3 (6.3%)
Clinical failure, n (%)	17 (35.4%)
30-day all-cause mortality, n (%)	13 (27.1%)
90-day all-cause mortality, n (%)	22 (45.8%)
30-day microbiologic failure, n (%)	16 (33.3%)
90-day microbiologic failure, n (%)	22 (45.8%)

[1]: FDA package insert recommends increased dosing frequency (2g every 6 hours) compared with standard dosing (2g every 8 hours).
[2]: A patient may have one or more infectious syndromes and/or one or more organisms.

ocol had similar clinical and microbiological efficacy compared to the best available therapy, but the mortality rate was unexpectedly higher in the cefiderocol group. We investigated the postapproval, real-world clinical outcomes of cefiderocol therapy. **Methods:** We conducted a prospective, observational study of patients who received cefiderocol for at least 2 days within the Veterans' Health Administration (VHA) between the date of approval by the US Food and Drug Administration (FDA), November 14, 2019, and August 31, 2022. Types of infections were defined by NHSN criteria. Clinical failure was a composite outcome based on type of infection including survival (30- and 90-day mortality) and resolution of signs and symptoms of infection. Microbiologic failure was defined as culturing the same organism, as defined by the CDC NHSN, at least 7 days after the start of cefiderocol. Structured data were sourced from the VHA Corporate Data Warehouse, and each eligible episode underwent manual chart review. **Results:** During the study period, 8,763,652 patients across 132 VA medical centers received 1,142,940,842 prescriptions (not limited to antibiotics). Overall, 48 unique individuals had received cefiderocol, with 48 cefiderocol courses prescribed. Patients had a median age of 70.5 years (range, 61–75), and a median Charlson comorbidity score of 6 (range, 2–9). The most common infectious syndromes were lower respiratory tract infection in 23 (47.9%) of these 48 patients and urinary tract infection in 14 (29.2%) of these patients. The most common pathogens cultured were *P. aeruginosa* in 30 patients (62.5%), Enterobacterales in 17 patients (35.4%), and *A. baumannii* in 10 patients (20.8%). The clinical failure rate was 35.4% (17 of 48), and 15 (88.2%) of these 17 patients died within 3 days of clinical failure. The 30-day and 90-day microbiologic failure rates were 33.3% (16 of 48) and 45.8% (22 of 48), respectively. The 30-day and 90-day all-cause mortality rates were 27.1% (13 of 48) and 45.8% (22 of 48), respectively (Table 1). **Conclusions:** Our study cohort included older individuals with multiple comorbidities who were treated with cefiderocol mainly for lower respiratory tract and urinary tract infections, with *Pseudomonas aeruginosa* as the main causative pathogen. Clinical and microbiologic failure were seen in>30% of patients, and >40% of these patients died within 90 days. These data contribute to the growing body of literature on the real-world use of cefiderocol and provide outcome data on clinical failure, microbiologic failure, and mortality.

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Identifying patients at high risk for carbapenem-resistant Enterobacterales carriage upon admission to acute-care hospitals

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Background: Prompt identification of patients colonized or infected with carbapenem-resistant Enterobacterales (CRE) upon admission can help ensure rapid initiation of infection prevention measures and may reduce intrafacility transmission of CRE. The Chicago CDC Prevention Epicenters Program previously created a CRE prediction model using state-wide public health data (doi: 10.1093/ofid/ofz483). We evaluated how well a similar model performed using data from a single academic healthcare system in Atlanta, Georgia, and we sought to determine whether including additional variables improved performance. **Methods:** We performed a case–control study using electronic medical record data. We defined cases as adult encounters to acute-care hospitals in a 4-hospital academic healthcare system from January 1, 2014, to December 31, 2021, with CRE identified from a clinical culture within the first 3 hospital days. Only the first qualifying encounter per patient was included. We frequency matched cases to control admissions (no CRE identified) from the same hospital and year. Using multivariable logistic regression, we compared 2 models. The "public health model" included 4 variables from the Chicago Epicenters model (age, number of hospitalizations in the prior 365 days, mean length of stay in hospitalizations in the prior 365 days, and hospital admission with an infection diagnosis in the prior 365 days). The "healthcare

Table 1: Key Characteristics of Cases and Controls and Results from Univariable Analyses

	Cases (n=105)	Controls (n=441,460)	Unadjusted odds ratio	95% CI
Age (years), median (IQR)	66 (57–74)	60 (44–72)	1.02	1.01–1.03
Male sex, n (%)	57 (54)	196,174 (44)	1.49	1.01–2.18
Race and ethnicity, n (%)				
Non-Hispanic Black	39 (37)	187,429 (43)	1.19	0.77–1.84
Non-Hispanic White	41 (39)	165,868 (38)	1.36	0.83–2.25
Other[a]	25 (24)	88,163 (20)	ref	
Hospitalizations in the prior 365 days, median (IQR)	1 (0–3)	0 (0–1)	1.15	1.09–1.21
Mean (SD) LOS (days) in hospitalizations from prior 365 days	14.2 (12.3)	6.9 (7.7)	1.01	1.01–1.02
Prior infection diagnosis[b], n (%)	48 (46)	44,331 (10)	7.54	5.14–11.08
Prior admission to an ICU[b], n (%)	24 (23)	17,198 (4)	7.31	4.63–11.53
Prior malignancy diagnosis[b], n (%)	15 (14)	22,257 (5)	3.14	1.82–5.43
Elixhauser score, median (IQR)	6 (5–9)	4 (2–6)	1.29	1.22–1.37
Inpatient antibiotic DOT in the prior 365 days, median (IQR)	27 (14–47)	12 (4–30)	1.57	1.31–1.89

Abbreviations: CI, confidence interval; IQR, interquartile range; SD, standard deviation; LOS, length of stay; ICU, intensive care unit; DOT, days of therapy
a. Includes Hispanic, Asian, Native Hawaiian or Other Pacific Islander, American Indian or Alaskan Native, Multiple Races, and Unknowns
b. Within the prior 365 days from current admission

Table 2. Comparison of the Two Logistic Regression Models Predicting CRE Carriage on Admission

	Public Health Model		Healthcare System Model	
	aOR	95% CI	aOR	95% CI
Prior infection diagnosis[a]	5.56	3.32–9.34	3.21	1.79–5.77
Hospitalizations in the prior 365 days	1.14	1.04–1.24	0.99	0.85–1.16
Age	1.01	1.00–1.03	1.01	1.00–1.03
Mean LOS (days) in hospitalizations from prior 365 days	1.01	1.01–1.02	1.01	1.00–1.02
Prior admission to an ICU[a]			2.48	1.43–4.31
Prior malignancy diagnosis[a]			1.70	0.92–3.13
Elixhauser score			1.10	1.01–1.21
Inpatient antibiotic DOT in prior 365 days[b]			1.49	1.14–1.93
AUC	***0.76***		***0.79***	

Abbreviations: aOR, adjusted odds ratio; CI, confidence interval; LOS, length of stay; ICU, intensive care unit; DOT, days of therapy
a. Within the prior 365 days from current admission
b. This variable was log transformed

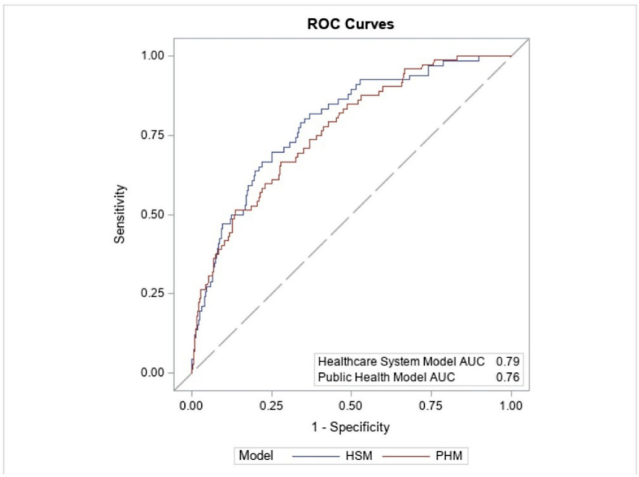

Figure 3: Receiver operating curves for the Public Health Model (shown in red) and the Healthcare System Model (shown in blue)

system model" added 4 additional variables (admission to the ICU in the prior 365 days, malignancy diagnosis, Elixhauser score and inpatient antibiotic days of therapy in the prior 365 days) to the public health model. We used billing codes to determine Elixhauser score, malignancy status, and recent infection diagnoses. We compared model performance using the area under the receiver operating curve (AUC). **Results:** We identified 105 cases and 441,460 controls (Table 1). CRE was most frequently identified in urine cultures (46%). All 4 variables included in the public health model and the 4 additional variables in the healthcare system model were all significantly associated with being a case in unadjusted analyses (Table 1). The AUC for the public health model was 0.76, and the AUC for the healthcare system model was 0.79 (Table 2; Fig. 1). In both models, a prior admission with an infection diagnosis was the most significant risk factor. **Conclusions:** A modified CRE prediction model developed using public health data and focused on prior healthcare exposures performed reasonably well when applied to a different academic healthcare system. The addition of variables accessible in large healthcare networks did not meaningfully improve model discrimination.

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Surveillance of healthcare-onset clinical cultures using whole-genome sequencing reveals hidden nosocomial transmission

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Background: Traditional hospital outbreak-detection methods are typically limited to select multidrug-resistant pathogens in a single unit, which can miss transmission of many medically important healthcare-transmissible pathogens. Whole-genome sequencing (WGS) enables comprehensive genomic resolution for accurate identification of clonal transmission. Previously, lack of scalability limited the use of WGS for hospital surveillance. **Methods:** We conducted prospective surveillance of select bacteria from all inpatient clinical cultures plus all bacteria from clinical cultures from ICUs and oncology units at the University of California Irvine (UCI) Clinical Microbiology Laboratory from September 2021 to February 2022. Due to pandemic stressors, this pilot test was a prelude to a real-time demonstration project. Its goal was to demonstrate the efficiency and scalability of the WGS platform when receiving samples monthly and analyzing results quarterly without the intent for real-time response. Bacterial isolates slated for discard were collected weekly and sent monthly to Day Zero Diagnostics for sequencing. In total, 1,036 samples from 926 patients were analyzed for genomic relatedness, a