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ORIGINAL ARTICLE

Infectious Disease

Methicillin-resistant *Staphylococcus aureus* and *Pseudomonas aeruginosa* community acquired pneumonia: Prevalence and locally derived risk factors in a single hospital system

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Abstract

Objectives: Current American Thoracic Society/Infectious Disease Society of America (ATS/IDSA) community-acquired pneumonia (CAP) guidelines expand the CAP definition to include infections occurring in patients with recent health care exposure. The guidelines now recommend that hospital systems determine their own local prevalence and predictors of *Pseudomonas aeruginosa* and methicillin-resistant *Staphylococcus aureus* (MRSA) among patients satisfying this new broader CAP definition. We sought to carry out these recommendations in our system, focusing on the emergency department, where CAP diagnosis and initial empiric antibiotic selection usually ooccur.

Methods: We performed a retrospective cohort study of patients admitted with CAP through any of 3 EDs in our hospital system in Northern California between November 2019 and October 2021. Inclusion criteria included an ED admission diagnosis of pneumonia or sepsis, fever or hypothermia, leukocytosis or leukopenia, and consistent chest imaging result. SARS-CoV-2-positive cases were excluded. We abstracted variables historically associated with *P. aeruginosa* and MRSA. Outcome measures were prevalence of *P. aeruginosa* and MRSA in the overall clinically defined cohort and among microbiologically confirmed cases and predictors of *P. aeruginosa* or MRSA isolation,

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as determined by univariate logistic regression, bootstrapped least absolute shrinkage and selection operator, and random forest analyses. Additionally, we describe the iterative process used and challenges encountered in carrying out the new ATS/IDSA guideline recommendations.

Results: There were 1133 unique patients who satisfied our definition of clinically defined CAP, of whom 109 (9.6%) had a bacterial pathogen isolated. There were 24 *P. aeruginosa* isolates and 11 MRSA isolates in 33 patients. Thus, the prevalence *P. aeruginosa* and MRSA was 2.9% in the overall CAP cohort, but 30.3% in the microbiologically confirmed cohort. The most important predictors of either *P. aeruginosa* or MRSA isolation were tracheostomy (odds ratio [OR] 22.08; 95% confidence interval [CI] 10.39–46.96) and gastrostomy tube (OR 14.7; 95% CI 7.14–30.26). Challenges included determining the suspected infection type in patients admitted simply for "sepsis"; interpreting dictated radiology reports; determining functional status, presence of indwelling lines and tubes, and long-term care facility residence from the electronic health record; and correctly attributing culture results to pneumonia.

Conclusion: Prevalence of MRSA and *P. aeruginosa* was low among patients admitted in our medical system with CAP – now broadly defined – but high among those with a microbiologically confirmed bacterial etiology. Our locally derived predictors of MRSA and *P. aeruginosa* can be used to aid our emergency physicians in empiric antibiotic selection for CAP. Findings from this project might inform efforts at other institutions.

KEYWORDS
antimicrobial resistance, antimicrobial stewardship, community acquired pneumonia, emergency department

1 | INTRODUCTION

1.1 | Background

Community-acquired pneumonia (CAP) is the third most common reason for hospitalization in the United States and the leading cause of sepsis and death from infection. The increasing prevalence of drug-resistant pathogens in CAP has presented a therapeutic challenge for decades. For this reason, in 2005 the American Thoracic Society and Infectious Disease Society of America (ATS/IDSA) developed a new community onset pneumonia category, health care-associated pneumonia (HCAP), to identify patients at high risk of infection with antimicrobial resistant pathogens. HCAP was defined, in essence, by the following patient characteristics: residence in a long-term care facility (LTCF), recent hospitalization or receipt of dialysis, chemotherapy or home infusion therapy or wound care. Initial empiric use of broad-spectrum antibiotics (with activity against multidrug-resistant [MDR] gram-negative pathogens, particularly *P. aeruginosa*, and methicillin-resistant *Staphylococcus aureus* [MRSA]) was recommended for pneumonia cases satisfying the definition of HCAP.[1]

Subsequent studies have found that the ATS/IDSA HCAP criteria are poor at predicting the isolation of drug resistant pathogens.[2] Although adoption of the HCAP concept into US practice resulted in greater use of broad-spectrum antibiotics for CAP, pneumonia outcomes did not improve.[3,4] Therefore, the latest ATS/IDSA CAP guidelines abandon the concept of HCAP, expanding the CAP definition to encompass patients with recent health care exposure or from a LTCF.[5] The new guidelines recommend that empiric treatment for MRSA and *P. aeruginosa* be based, where possible, on locally validated risk factors for infection with these pathogens. The new guidelines propose, "clinicians need to obtain local data on whether MRSA or *P. aeruginosa* is prevalent in patients with CAP and what the risk factors for infection are at a local (ie, hospital or catchment area) level." Obtaining local prevalence and risk factor data is also consistent with the IDSA recommendation that antibiotic stewardship programs should implement facility-specific clinical practice guidelines.[6]

1.2 | Importance

We are not aware of any published experience to date of a health care system specifically implementing the new ATS/IDSA recommendations. We chose to focus on the emergency department, because initial pneumonia diagnosis, risk stratification, and empiric antibiotic selection in the ED tend to determine subsequent inpatient antibiotic

therapy ("antibiotic inertia") and have a significant impact on overall antibiotic use.[6–9]

1.3 | Goals of this investigation

We sought to (1) determine the prevalence of MRSA and *P. aeruginosa* CAP in our hospital system; (2) identify locally valid predictors of MRSA and *P. aeruginosa* isolation in culture; and (3) describe the iterative process, and associated challenges, of carrying out the ATS/IDSA recommendations.

The Bottom Line

Among emergency department patients admitted for community acquired pneumonia in this system, the presence of tracheostomy or gastrostomy tubes were predictive of methicillin-resistant *Staphylococcus aureus* (MRSA) or *Pseudomonas aeruginosa* as the causative organisms.

2 | METHODS

2.1 | Study design and setting

This was a retrospective cohort study based primarily on computerized query of the electronic health record (EHR), supplemented by manual chart review. It was undertaken in a 3-hospital health care system, located in urban Northern California, with a combined annual ED census of 130,000 patients, including a 169-bed academic, safety net trauma center, a 68-bed community hospital serving a predominantly LTCF population and a 63-bed community hospital with attached 35-bed subacute care facility. The initial intended study period was 1 year, beginning November 1, 2019, but because of changes in census and respiratory infection patterns related to the COVID pandemic, was extended to 2 years, ending October 31, 2021. The study was approved by our health system investigational review committee.

2.2 | Selection of participants

Cohort 1, clinically defined CAP, was composed of all patients admitted through the ED satisfying the following a priori inclusion criteria (met within 48 hours of ED arrival): ED or admission diagnosis of "pneumonia" or "sepsis"; chest X-ray or computed tomography report consistent with pneumonia; WBC) >12,000 or <4000/μL, or temperature >100.4 F or <96.8 F. We chose to include the admission diagnosis of sepsis because emergency physicians (EPs) often decide to admit and assign a diagnosis once sepsis is evident, without refining the diagnosis further in the EHR. A priori exclusion criteria were: CD4 count <500/μL; age <18 years; receiving chemotherapy, radiation therapy, or history of organ transplant. Only the first hospitalization during the study period was included. Subsequently, we chose to exclude patients with any of the following: a COVID-19 diagnosis or positive SARS-CoV-2 test; a radiology report judged not definitive for pneumonia (by manual review of radiology results); a diagnosis of sepsis only (at ED admission and during first 48 hours) without a hospital discharge diagnosis of pneumonia; or a clear primary source of infection other than CAP (eg, abscess, endocarditis; discovered during chart review).

Cohort 2 was composed of the subset of cohort 1 with microbiologically confirmed CAP, defined a priori as having a respiratory or blood culture that grew any of the following pathogens: *S. pneumoniae*, *S. aureus*, *H. influenzae*, *M. pneumoniae (serum IgG/IgM)*, *E. coli*, *K. pneumoniae*, other *Enterobacterales species*, *P. aeruginosa*, *L. pneumophila (urine antigen test)*. Subsequently, 2 investigators (R.M., M.L., an infectious disease [ID] specialist and ID pharmacist) manually reviewed culture results and EHR records of cohort 2 patients, identifying and excluding those with culture isolates unlikely attributable to pneumonia (eg, blood culture contamination, respiratory colonization, bacteremia from a non-pneumonia source); patients with the same pathogen in blood and urine culture were all excluded. They also rated the connection between culture isolate and pneumonia as definite or probable. Cohort 3 was composed of the subset of cohort 2 patients whose culture grew MRSA and/or *P. aeruginosa*. Figure 1 summarizes the iterative process used to assemble the 3 cohorts.

2.3 | Data collection

An investigator (A.S.) with data analytics experience, clinical informatics board certification, and Epic (Verona, WI, our EHR vendor) certification in clinical data modeling identified cases and collected data by structured query language (SQL) query of the Epic Clarity database. Data were imported into an Excel file and deidentified. The query identified inclusion and exclusion criteria using key words, for example, diagnosis field containing "pneumonia" or "sepsis" or chest imaging report containing "infiltrate" or "consolidation," and so on. *International Classification of Diseases, Tenth Revision* codes were not used for case identification. Microbiological data linked to culture orders were collected electronically by SQL query.

Candidate predictor variables potentially associated with MRSA or *P. aeruginosa* included most elements of the HCAP definition and additional predictors found to be associated with MRSA and *P. aeruginosa* pneumonia in prior studies.[1,2,5,10–12] Predictor variables are defined and described in Supplement Table S1. Variables were ascertained primarily electronically by SQL query except residence in a LTCF. Additionally, ascertainment of tracheostomy and gastrostomy tube and peripherally inserted central catheter and central line data was supplemented by brief manual EHR abstraction, as these nursing documentation fields in the EHR were not consistently populated. We were unable to reliably ascertain functional status or chronic wound care from the EHR.

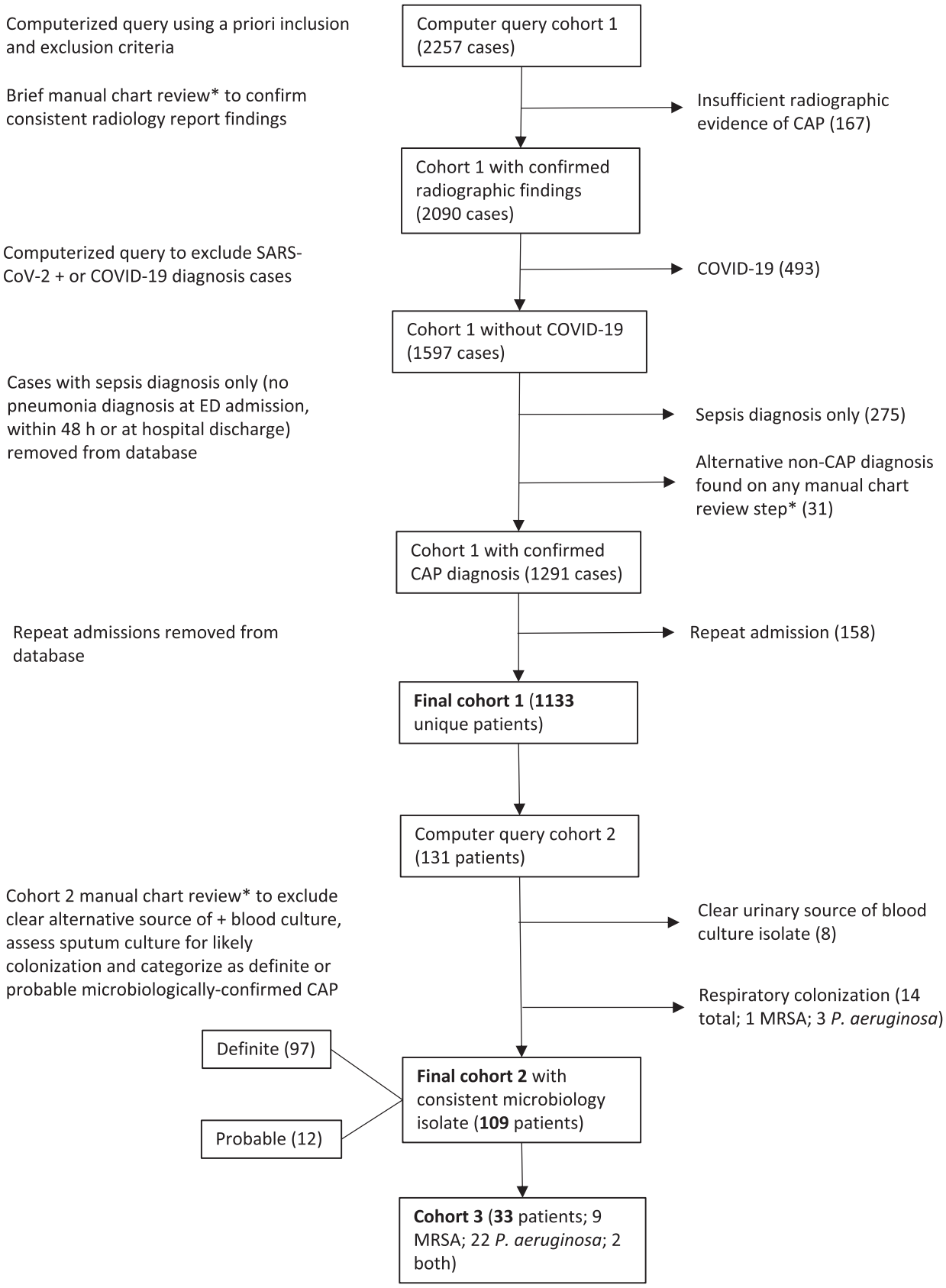

FIGURE 1 Iterative process of cohort assembly (strengthening the reporting of observational studies in epidemiology flow diagram) and prevalence results. CAP, community-acquired pneumonia; ED, emergency department; MRSA, methicillin-resistant *Staphylococcuscus aureus*.* Cases where pneumonia was judged not to be present during any chart review step (radiology review, microbiology review or manual abstraction for predictor variables) were removed from Cohort 1.

2.4 | Outcome measures

Prevalence of MRSA and *P. aeruginosa* was determined both among the entire clinically defined CAP population (cohort 1) and among the microbiologically confirmed cohort 2. Predictor variables associated with isolation of MRSA or *P. aeruginosa* were determined as described herein. We describe the iterative process required to carry out the ATS/IDSA recommendations in the methods section and in Figure 1.

2.5 | Analysis

Associations between candidate predictor variables and isolation of MRSA or *P. aeruginosa* were estimated using univariate logistic regression where the binary outcome was regressed on each candidate predictor separately. Odds ratios (ORs) are presented as point estimates with 95% confidence intervals (CIs). In addition, we performed bootstrapped least absolute shrinkage and selection operator (LASSO)[13] and random forest[14] analyses, including all candidate predictors, to rank and select the most important variables.

3 | RESULTS

During the 2-year study period, from November 2019 through October 2021, 1133 individual patients met our CAP definition, of whom 109 (9.6%) had microbiologically confirmed bacterial CAP. Table 1 shows basic demographic and clinical characteristics of the overall cohort 1. Table 2 shows the microbiology results. There were 33 patients with CAP caused by MRSA or *P. aeruginosa*, which represents 2.9% of our overall, clinically defined CAP cohort, and 30.3% of the microbiologically confirmed CAP cohort. Figure 1 shows the iterative process used to assemble the 3 cohorts and arrive at our prevalence results.

Table 3 shows results of the univariate regression analysis for each candidate predictor variable. Those showing evidence of an association with either MRSA or *P. aeruginosa* were tracheostomy (OR 22.08; 95% CI 10.39–46.96), gastrostomy tube (OR 14.70; 95% CI 7.14–30.26), LTCF residence (OR 12.75; 95% CI 5.21–31.19), central line (OR 6.05; 95% CI 2.36–15.09), ICU admission by 48 hours (OR 4.61; 95% CI 2.21–9.61); age ≥ 65 years (OR 4.01; 95% CI 1.64–9.78), initial ICU admission (OR 3.79; 95% CI 1.86–7.70), antibiotics in prior 90 days (OR 3.05; 1.52–6.12), and immunosuppressive medications in prior 90 days (OR 3.0; 95% CI 1.32–6.82). Supplement Figure S1 shows the results of the bootstrapped LASSO and random forest analyses, which both ranked tracheostomy followed by gastrostomy as the most important predictors of MRSA or *P. aeruginosa*. Tracheostomy and/or gastrostomy were present in 20 of 33 (61%) MRSA and *P. aeruginosa* cases.

TABLE 1 Demographic and clinical characteristics among all patients admitted with clinically defined community acquired pneumonia.

Characteristics ($N = 1133$)	No. (%)
Male	656 (57.9)
Age ≥ 65 years	609 (53.8)
Race or ethnicity	
Black	364 (32.1)
Non-Hispanic white	318 (28.0)
Asian	187 (16.5)
Hispanic	29 (2.6)
Native Hawaiian/Pacific Islander	16 (1.4)
American Indian or Alaska Native	3 (0.3)
Other race	216 (19.1)
Residence in LTCF	314 (27.7)
Hospitalized prior 90 days	259 (22.9)
Admission diagnoses[a]	
ED provider diagnosis of CAP	427 (37.7)
ED provider diagnosis of sepsis	101 (8.9)
Hospitalist diagnosis[b] of CAP	554 (48.9)
Hospitalist diagnosis[b] of sepsis	196 (17.3)
Immediate ICU admission	193 (17.0)
Died during study period	203 (17.9)

Abbreviations: CAP, community acquired pneumonia; ED, emergency department; LTCF, long-term care facility.

[a]Patients with diagnosis of sepsis only were required to have a hospital discharge diagnosis of pneumonia.

[b]Hospitalist diagnosis documented within first 48 hours of admission.

4 | LIMITATIONS

This study has several limitations. That the study period coincided with the height of the COVID pandemic limits generalizability to other time periods in various ways, such as altering the incidence and relative prevalence of both bacterial and viral CAP pathogens and changing physician and respiratory therapist behavior around ordering and obtaining microbiologic specimens. Though studying a single health care system limits generalizability, the aim was to derive results specific to our institution. On the other hand, many of the challenges we encountered carrying out the ATS/IDSA recommendations using available EHR data, and during the COVD pandemic, likely are generalizable. Manual chart review of radiology reports and microbiologically confirmed cases, and judging whether isolates were truly attributable to pneumonia, could have introduced bias. Others have also highlighted the challenge of correctly categorizing chest imaging and pneumonia diagnosis based on computerized EHR query alone.[15] Supplemental manual chart review was also required to ascertain several predictor variables. We did not assess interrater reliability. We made the necessary assumption that Cohort 1 patients with negative or incomplete microbiological testing (eg, missing sputum cultures) were not infected with MRSA or *P. aeruginosa*. Small sample size hampered our risk factor analysis. It may be preferable to separate the prediction (and empiric coverage) of MRSA from that of *P. aeruginosa*; our sample size was not big enough to perform these separate analyses.

TABLE 2 Microbiology results among microbiologically confirmed cases (N = 109).

Organism	No. (%) of patients with pathogen detected	Isolated from blood	Isolated from sputum	Same organism isolated in both
Staphylococcus aureus (all)	35 (32.1)	25	14	4
MRSA	11 (10.1)	6	6	1
Pseudomonas aeruginosa	24 (22.0)	1	24	1
Escherichia coli (all)	23 (21.1)	14	9	0
Escherichia coli MDRO	7 (6.4)	3	4	0
Klebsiella pneumoniae (all)	17(15.6)	8	11	2
Klebsiella pneumoniae MDRO	5 (4.6)	1	4	0
Streptococcus pneumoniae	13 (11.9)	11	2	0
Haemophilus influenzae	1 (0.9)	1	0	0
Klebsiella aerogenes	1 (0.9)	0	1	0
Enterobacter cloacae	1 (0.9)	1	0	0
Group G Streptococcus sp.	1 (0.9)	1	0	0
Legionella pneumophila (urine antigen)	1 (0.9)	–	–	–
Mycoplasma pneumoniae (IgG)	1 (0.9)	–	–	–

Abbreviations: MRSA, methicillin-resistant *Staphylococcus aureus*; MDRO, multidrug-resistant organism, (in gram-negative bacteria, this signifies resistance to third-generation cephalosporins).

5 | DISCUSSION

To our knowledge, this is the first published study that specifically sought to carry out the charge set forth in the 2019 ATS/IDSA guidelines, to determine, at a local medical system level, the current prevalence of MRSA and *P. aeruginosa*, and risk factors for these pathogens, among adult patients hospitalized for CAP– as now more broadly defined. In our overall clinically defined cohort, isolation of MRSA or *P. aeruginosa* was uncommon. However, we isolated a bacterial pathogen of any kind in only a minority of CAP cases, and among this small microbiologically confirmed cohort, MRSA and *P. aeruginosa* were quite common. The surprisingly high prevalence of MRSA and *P. aeruginosa* in our patients meeting the new CAP definition in whom a bacterial pathogen was actually isolated mandates that our EPs focus carefully on proper empiric antibiotic selection. Results of our local risk factor analysis indicate that presence of a tracheostomy or gastrostomy tube are the most important predictors of resistance in our study cohort. Such results should prove increasingly valuable in informing our empiric therapy guidelines as we add data from more CAP patients and refine the risk factor analysis.

We isolated a bacterial pathogen in just 9.6% of CAP cases, which is somewhat lower than contemporary studies of adult CAP etiology where sophisticated microbiology techniques were used consistently.[16,17] Our low yield is likely due to obtaining sputum cultures less commonly during the study period, no routine use of *S. pneumoniae* urinary antigen testing and very selective use of *Mycoplasma* and *Legionella* testing in our system. The low prevalence of *S. pneumoniae* parallels a trend evident in other studies of CAP etiology, thought to be related to widespread use of pneumococcal vaccines and less cigarette smoking.[18,19]

Among our microbiologically confirmed bacterial CAP cases, MRSA was isolated in 10% and *P. aeruginosa* in 22%, which, although much higher than in studies of CAP etiology that excluded patients meeting HCAP criteria,[16,20,21] is on par with rates found in studies of HCAP.[10,22] Indeed, approximately 80% of patients in our microbiologically confirmed cohort met HCAP criteria. *P. aeruginosa* is known to be particularly common in CAP patients with a tracheostomy, and 29% of our microbiologically confirmed cohort had a tracheostomy.[23]. Additionally, many MDR gram-negative bacteria besides *Pseudomonas* were isolated in our microbiologically confirmed cohort. Excluding the 2 atypical organisms, 49 of 109 (45%) isolates were predicted to be resistant or harbor inducible resistance to ceftriaxone. Still, the patients with these resistant isolates accounted for just 4.1% of the overall clinically defined CAP cohort.

Despite its limitations, the results of our risk factor analysis are mostly consistent with those of similar, larger studies conducted in a variety of patient populations before the new ATS/IDSA guidelines.[12,24–26] These studies used the outcome of infection with either MRSA or *P. aeruginosa* or with any drug-resistant pathogen. Most included a measure of comorbidity or functional status as a candidate predictor variable (which our study did not), but not presence of a tracheostomy. Multiple studies found—as we did—that tube feeding and residence in a LTCF were strongly correlated with resistant pathogens. Our study appears to be the first to report a strong correlation with presence of a tracheostomy. Other studies also found that infection severity (requiring ICU care) correlated with having a resistant pathogen, though that correlation was relatively weak in our study. Ultimately, as the ATS/IDSA guidelines recognize, predictors as well as prevalence of MRSA and *P. aeruginosa* will vary significantly according to a hospital's geographic location and patient mix. In small hospital

TABLE 3 Results of univariate regression analysis showing associations between candidate predictor variables and isolation of MRSA or *Pseudomonas aeruginosa* among all clinically defined cases.

Predictor variable[a]	Total No.	Not MRSA or Pseudomonas No. (%) ($n = 1100$)	MRSA or Pseudomonas No. (%) ($n = 33$)	OR (95% CI)
Age ≥65	609	582 (52.91%)	27 (81.82%)	4.01 (1.64–9.78)
Age <65[b]	524	518 (47.09%)	6 (18.18%)	
Race – White	317	311 (28.27%)	6 (18.18%)	0.68 (0.29–1.60)
Race – Non-White[b]	816	789(71.73%)	27 (81.82%)	
Initial ICU Admission	193	179 (16.27%)	14 (42.42%)	3.79 (1.86–7.70)
Initial inpatient floor[b]	940	921 (83.73%)	19 (57.58%)	
ICU admission within 48 hours of arrival	789	767 (69.73%)	22 (66.67%)	4.61 (2.21–9.61)
Inpatient floor only[b]	344	333 (30.27%)	11 (33.33%)	
Hospital admission in prior 90 days	259	247 (22.45%)	12 (36.36%)	1.97 (0.96–4.07)
No recent admission[b]	874	853 (77.55%)	21 (63.64%)	
History of MRSA positive culture	26	25 (2.27%)	1 (3.03%)	1.34 (0.18–10.23)
No history of MRSA[b]	1107	1075 (97.73%)	32 (96.97%)	
History of Pseudomonas in respiratory cultures	6	5 (0.45%)	1 (3.03%)	6.84 (0.78–60.28)
No prior pseudomonas in respiratory cultures[b]	1127	1095 (99.55%)	32 (96.97%)	
History of chronic lung disease	302	291 (26.45%)	11 (33.33%)	1.39 (0.67–2.90)
No history of chronic lung disease[b]	831	809 (73.55%)	22 (66.67%)	
Gastrostomy tube present	112	93 (8.45%)	19 (57.58%)	14.70 (7.14–30.26)
No gastrostomy tube present[b]	1021	1007 (91.55%)	14 (42.42%)	
Tracheostomy present	58	40 (3.64%)	18 (54.56%)	22.08 (10.39–46.96)
No tracheostomy present[b]	1075	1060 (96.36%)	15 (45.45.%)	
Central line catheter present	45	39 (3.55%)	6 (18.18%)	6.05 (2.36–15.49)
No central line catheter present[b]	1088	1061 (96.45%)	27 (81.82%)	
Patient on hemodialysis	71	71 (6.45%)	0 (0%)	Not estimated
No hemodialysis	1029	1029 (93.55%)	33 (100%)	
Antibiotic use in prior 90 days	301	284 (25.82%)	17 (51.52%)	3.05 (1.52–6.12)
No antibiotic use in prior 90 days[b]	832	816 (72.18%)	16 (48.48%)	
Immunosuppressive medication use in prior 90 days	114	106 (9.64%)	8 (24.24%)	3.00 (1.32–6.82)
No immunosuppressive medication use in prior 90 days[b]	1019	994 (90.36%)	25 (75.76%)	
Residence in LTCF	314	287 (26.09%)	27 (81.82%)	12.75 (5.21–31.19)
No LTCF residence[b]	819	813 (73.91%)	6 (18.18%)	

Abbreviations: CI, confidence interval; LTCF, long-term care facility; MRSA, methicillin -resistant *Staphylococcuscus aureus* OR, odds ratio.
[a]Predictor variables are defined in detail in supplement Table S1.
[b]Indicates reference (unexposed) group for odds ratio estimation.

systems such as ours, several years of data collection and refinement of the risk prediction model will be needed to determine which predictors should be used clinically to guide empiric treatment.

We hope that other medical systems can benefit from seeing the challenges we faced in carrying out the ATS/IDSA guidelines. Lessons learned include the following: infectious disease and antibiotic stewardship leaders need robust partnerships with EHR data analytics experts; EHRs should capture accurate and granular data about patients' home setting, for example, whether they are unhoused or come from an LTCF, and their functional or ambulatory status and presence of indwelling lines and tubes; sophisticated software is likely required to identify language in radiology reports that actually implies pneumonia is present[27]; it can be difficult to divine from the EHR whether CAP was the working diagnosis in the ED, and strategies to encourage better documentation of infection type are needed. Increasing emphasis on sepsis as a critical diagnosis, requiring immediate treatment and hospital admission, seems to have reduced a focus on, and documentation of, the specific type of infection responsible. Finally, correctly attributing respiratory culture results to pneumonia versus colonization is a well-recognized challenge that has an impact on

apparent prevalence of resistant pathogens and on predictive models of resistance. Manual review of the EHR and microbiology results by ID experts was required to address this issue. Because the emergency medicine imperative is to cover resistant organisms whenever they *could* be causative, we felt it was acceptable to set a low threshold for considering MRSA or *P. aeruginosa* isolates causative.

We hope to see more research in the future along several lines. Additional studies are needed of contemporary CAP bacteriology in other geographic regions. Studies should explore how EPs might better identify and document the likeliest source of sepsis. We need to understand how results of rapid respiratory virus panels, serum markers of bacterial infection and molecular tests for bacteria might all be incorporated into models that specifically predict drug resistant CAP.[20] Informatics studies should demonstrate how EHR systems can be leveraged to help identify infections likely (and unlikely) caused by resistant pathogens. Systems should be built that better capture all relevant clinical and microbiology data, automatically amass a locally valid database (similar to the one built in this study), refine predictive models using artificial intelligence and provide real-time clinical decision support for empiric antibiotic selection. Finally, research is needed that evaluates clinical outcomes associated with the latest ATS/IDSA CAP definition and empiric therapy guidelines.

AUTHOR CONTRIBUTIONS

Bradley W. Frazee conceived the study. Amarinder Singh, Bradley W. Frazee, and Matt Labreche designed the study. Amarinder Singh performed the electronic query and managed the data. Bradley W. Frazee, Amarinder Singh, Matt Labreche, Robert McCabe, and Kevin Ha performed chart review. Partow Imani performed the statistical analysis, with assistance from Jon Furszyfer del Rio and Eugene Kreys. Bradley W. Frazee drafted the manuscript and all authors contributed to its revision. Amarinder Singh and Bradley W. Frazee take responsibility for the paper as a whole.

CONFLICT OF INTEREST STATEMENT

Bradley W. Frazee is a clinical advisor for, and has equity in, BioAmp Diagnostics, a startup developing a point of care biochemical test for MDR urinary tract infections.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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