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Multi-drug resistant *Pseudomonas aeruginosa*: a 2019–2020 single center retrospective case control study

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SUMMARY

Multi-drug resistance in the post COVID-19 world is a growing concern. The objective of this study was to describe temporal trends and explore independent risk factors for the isolation of multi-drug resistant (MDR) *P. aeruginosa*.

Methods: This was a retrospective case-control study of patients with *P. aeruginosa* isolates recovered from January 2019 to December 2020. MDR *P. aeruginosa* was defined as non-susceptibility to at least one agent in three or more anti-pseudomonal antimicrobial categories.

Results: In total, 258 unique isolates were identified. Prolonged hospitalization ($P<0.001$), prior antibiotic use ($P<0.001$), and respiratory sources ($P<0.001$) were strongly associated with the presence of MDR *P. aeruginosa*. From 2019 to 2020, there was a decrease in the total number of *P. aeruginosa* isolates but a significant increase in the proportion of MDR *P. aeruginosa* isolates ($P=0.015$).

Conclusions: Over a period that coincided with the COVID-19 pandemic, there was an increased proportion of MDR *P. aeruginosa* isolates from hospitalized patients. Improved identification of patients at risk for MDR *P. aeruginosa* could facilitate appropriate empiric antibiotic decisions like dual anti-pseudomonal therapy. The features of the COVID-19 outbreak that had a severe impact on patient care and that may have affected drug resistance in other respiratory pathogens should be explored.

Background

P. aeruginosa infections account for approximately 8–13.8% of HAIs (hospital acquired infections) and a higher rate of 13.2–22.6% in intensive care units (ICUs) [1]. It is one of the most common pathogens found in ventilator-associated

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pneumonia, catheter-associated urinary tract infections, and surgical site infections leading to bacteremia [1—3]. *P. aeruginosa* is also responsible for a wide range of other infections including burn wound infection, osteomyelitis, bacterial keratitis in contact lens wearers, endophthalmitis, otitis externa, ecthyma gangrenosum, infective endocarditis, and peritonitis [4—11].

Antimicrobial resistance among clinical isolates of *P. aeruginosa* is a growing concern. According to the Center for Disease Control 2019 Antimicrobial Resistance Report, there were an estimated 32,600 cases of MDR *P. aeruginosa* infections and 2,700 deaths in 2017 [12]. The emergence of MDR *P. aeruginosa* contributes not only to higher mortality but also to more than $10,000 net loss per case for hospitals in the United States [13]. In 2020, the National Healthcare Safety Network reported rates of antimicrobial resistance in hospital-acquired *P. aeruginosa* infections: aminoglycosides (5.8%—22.6%), extended-spectrum cephalosporins (10.2%—30.6%), fluoroquinolones (11—53.2%), carbapenems (9.1%—42.6%) and piperacillin/tazobactam (7.7%—23.9%) [3]. *P. aeruginosa* is intrinsically resistant to various antimicrobial agents due to its outer membrane with low permeability, and demonstrates other inducible methods of antibiotic resistance including efflux pumps, porin alterations, beta-lactamases (including AmpC beta lactamase), aminoglycoside modifying enzymes, and target modification via point mutation [14]. Surgical site infections with *P. aeruginosa* have the lowest rates of resistance, whereas device-associated infections including ventilator-associated pneumonias (VAPs), catheter-associated urinary tract infections (CAUTIs), and central line—associated bloodstream infections (CLABSIs) have higher rates of resistance [3,15]. Respiratory isolates of *P. aeruginosa* are more often MDR when compared with *P. aeruginosa* isolates from other sources [16,17]. It has been hypothesized that the capacity for *P. aeruginosa* to form biofilms provides an advantage in establishing infections, particularly VAP and cystic fibrosis lung infections, within susceptible hosts [18].

Previous use of antibiotics, particularly cephalosporins, carbapenems, and fluoroquinolones, and prior hospital stay have been risk factors most strongly associated with acquisition of MDR versus susceptible *P. aeruginosa* [19,20]. The 2016, the Infectious Diseases Society of America (IDSA) guidelines also identify the "need for ventilatory support for septic shock" as a major risk factor for MDR *P. aeruginosa* [21]. Admission from chronic care facilities has been associated with an increased risk of MDR *P. aeruginosa* [22]. The use of invasive devices such as Foley catheters, mechanical ventilation and central lines have also been identified as significant risk factors for MDR *P. aeruginosa* [22]. Patients with cystic fibrosis and bronchiectasis are more likely to be chronically colonized with *P. aeruginosa* and are therefore also likely to be at an increased risk for MDR *P. aeruginosa* [19]. Other factors studied but not consistently found to have a significant association with MDR *P. aeruginosa* include diabetes, liver disease, renal disease, chronic obstructive pulmonary disease, and comorbid severity scores [20]. However, at least one study has found an association between diabetes and MDR *P. aeruginosa* [23]. COVID-19, which has substantially impacted hospital care in the United States since March 2020, may also be expected to have affected trends in hospital microbial resistance. Large numbers of patients overwhelmed hospitals and required prolonged stays, often complicated by the need for mechanical ventilation and glucocorticoid treatment. Absent clear management guidelines and effective therapies made strict adherence to antimicrobial stewardship during this period difficult.

Current empiric treatments for MDR *P.aeruginosa* infections include anti-pseudomonal beta-lactams, fluoroquinolones and carbapenems. In addition to antimicrobial use, other preventative measures include hand hygiene, environmental cleaning, proper device disinfection and sterilization, removal of unnecessary invasive devices, utilization of antimicrobial biomaterials in invasive devices, and water system management [24—26]. Delays in starting appropriate therapy may contribute to persistence of infection, increased length of hospital stay, and increased mortality [22,27]. While combination therapy was believed to increase the likelihood of therapeutic success through an extended spectrum of activity and a decreased potential for promoting resistant bacteria, multiple studies have demonstrated no difference in clinical outcomes between monotherapy and dual coverage for MDR *P. aeruginosa* [28,29]. The 2016 IDSA guidelines suggest combination anti-pseudomonal therapy only for patients with hospital-acquired and ventilator-associated pneumonia who remain in septic shock or are at high risk of death [30].

The primary objective of this study was to identify clinical risk factors associated with MDR *P. aeruginosa* infection. The secondary objectives of this study were to evaluate the influence of MDR *P. aeruginosa* on patient outcomes and the trends in time and resistance patterns between 2019 and 2020 among *P. aeruginosa* isolates, trends that occurred against the backdrop of the COVID-19 pandemic.

Methods

Definitions

Multi-drug resistance (MDR) for *P. aeruginosa* is defined as non-susceptibility to at least one agent in three or more important anti-pseudomonal antimicrobial categories [31]. Non-multidrug resistance (NDR) is defined as susceptibility to at least four anti-pseudomonal antimicrobial categories.

Microbiologic data

All cases with positive *P.aeruginosa* clinical cultures from a tertiary care center recovered from Jan 1st, 2019—Dec 31st, 2020 were reviewed. Data collected included the date of culture collection, the date the result was recorded, the specimen source, other organisms isolated from the same culture, and antibiotic susceptibilities. The antibiotics tested included piperacillin-tazobactam, cefepime, ciprofloxacin, levofloxacin, meropenem, tobramycin, amikacin, gentamicin, and aztreonam. Intermediate results were considered resistant. Susceptibility was determined by automated broth micro dilution testing (MicroScan Neg Combo 67 panel; Beckman Coulter, Brea, CA, USA). All tests were performed according to Clinical Laboratory Standards Institute guidelines. If there were multiple isolates from a patient with the same antibiotic susceptibilities from the same source from a single hospitalization, then only the first isolate from each source was subject to review. Isolates from the same patient with different antibiotic susceptibilities across different antimicrobial categories were analyzed separately as were isolates from the same

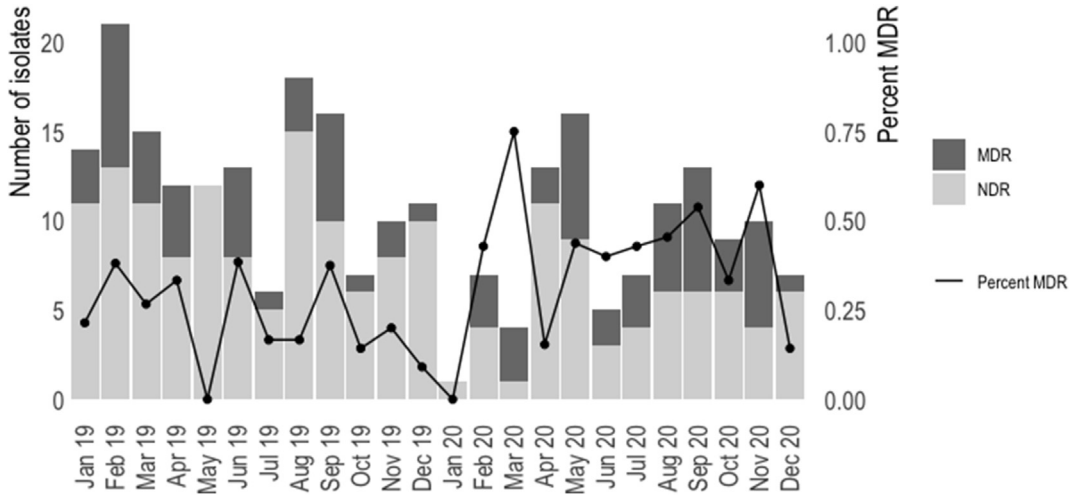

Figure 1. Proportion of MDR/NDR Pseudomonas isolates over time. In the x-axis labels: 19 = 2019, 20 = 2020. MDR = Multi-drug resistant. NDR = non-drug resistant. Percent MDR = percent of isolates that are multi-drug resistant.

patient from different hospitalizations. Isolates without antibiotic susceptibilities were excluded.

Clinical data

Data were collected from computerized patient records and applied to a pre-prepared electronic questionnaire. The data retrieved for each patient included age, sex, underlying disorders (congestive heart failure, chronic obstructive pulmonary disease, COVID-19, malignancy, diabetes mellitus, HIV, renal disease, liver disease, use of immunosuppressants), Charlson Comorbidity Index, cause of hospitalization, use of invasive devices (mechanical ventilation, foley, central line), prior hospitalization in the past 30 days, prior antibiotic use in the past 30 days, ward of hospitalization, length of intensive care unit (ICU) stay, and location prior to hospitalization. The recorded outcomes were mortality and length of hospital stay.

Data analysis

In the univariate analysis, categorical variables were compared using the Pearson $\chi 2$ or Fisher exact test, and continuous variables were compared using the Student t or Mann-Whitney U test. Bonferroni correction was applied to $\chi 2$ post hoc analysis. Univariate analysis was performed using a two-sided *P*-value of 0.05. For correlation analysis between continuous and categorical variables, linear regression models were used to compute R-squared values. For the multivariate logistic regression model, variable selection was performed via the Morgan and Tatar exhaustive search algorithm [32]. Akaike's information criterion (AIC) was used to determine measure of fit. All statistical analyses were performed in R statistical software (v3.6.1 (2019-07-05), available at http://www.r-project.org).

Ethical compliance

This study was performed in accordance within the ethical standards of the institutional research board and with the 1964 Helsinki Declaration and its later amendments.

Results

Epidemiology

Three hundred and ten isolates of *P. aeruginosa* were identified: 258 unique isolates from 181 patients. There were 155 total isolates and 37 MDR isolates from 2019 and 103 total isolates and 40 MDR isolates from 2020 (Figure 1). The mean age of the patients was 56.2 + 22.8 years. The average length of hospital stay was 30.0+36.5 days, and the average length of ICU stay was 12.2+21.9 days. The average number of hospitalization days until the recovery of a *P. aeruginosa* isolate was 13+25 days. There was an increased median length of hospitalization in 2020 (22 days) compared to 2019 (13 days) (Figure 2). 130 (50.3%) isolates were obtained within two days

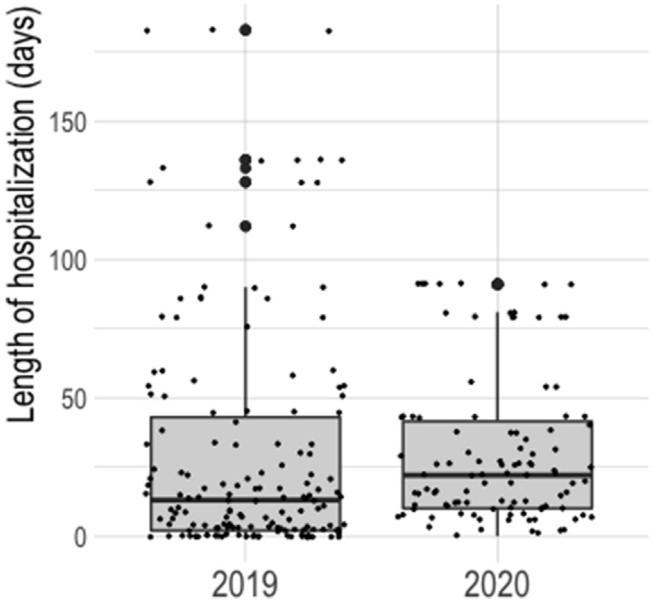

Figure 2. Length of hospitalization between 2019 and 2020. For all patients with positive *Pseudomonas aeruginosa* cultures.

of hospitalization, of those isolates 57 patients had documented history of hospitalization or antibiotic use in the past 30 days. 132 (50.7%) isolates were obtained while a patient was on mechanical ventilation, 99 (38.3%) isolates were obtained while a patient had a Foley catheter. 93 (36.1%) isolates were recovered along with other organisms. The most common bacteria isolated with *P. aeruginosa* were *Staphylococcus aureus* (n=25), *Klebsiella pneumoniae* (n=19), and *Enterococcus faecalis* (n=14). Respiratory isolates were the most common [n=104 (40.3%)], followed by urinary [n=64 (24.8%)], skin/soft tissue/bone [n=48 (18.6%)], blood [n=26 (12.1%)], and other sources including peritoneal fluid (n=7), conjunctiva (n=4), placenta (n=1), and bile (n=1).

Antimicrobial susceptibility

There were 77 (29.8%) MDR *P. aeruginosa* isolates and 181 (70.1%) NDR *P. aeruginosa* isolates, 99 (38.3%) of which were completely sensitive to all antibiotics tested. Resistance was most common to aztreonam [n=103 (39.9%)], followed by cefepime [n=67 (26%)], gentamicin [n=66 (25.6%)], piperacillin/tazobactam [n=63 (24.4%)], levofloxacin [n=56 (21.7%)], ciprofloxacin [n=49 (19%)], meropenem [n=39 (15.1%)], amikacin [n=21 (8.1%)], and tobramycin [n=6 (2.3%)].

The cross resistance between antibiotics is shown in Table I. Aztreonam, piperacillin/tazobactam, and cefepime resistance were strongly correlated ($\chi 2 = 18.78$, $P<0.001$). For example, if an isolate was resistant to cefepime, 90% of those isolates would also be resistant to aztreonam, and 79% of those isolates would also be resistant to piperacillin/tazobactam. Isolates resistant to meropenem were most likely to be susceptible to aminoglycosides (10% also resistant to tobramycin, 21% also resistant to amikacin) and ciprofloxacin (41% also resistant to ciprofloxacin, but 59% also resistant to levofloxacin).

Risk factors for MDR P. aeruginosa

In the univariate analysis (Table II), MDR *P. aeruginosa* isolates were more associated with increased length of hospitalization ($P < 0.001$), any antibiotic use in the past 30 days ($P < 0.001$), respiratory sources ($P < 0.001$), isolates from the year 2020 (P=0.015), length of ICU stay ($P < 0.020$), and male sex ($P = 0.035$). MDR *P. aeruginosa* cases were less frequently associated with skin and wound sources ($P = 0.028$), when isolated with other organisms ($P = 0.001$), and when in the emergency room at time of isolation (P=0.008). Prior hospitalization, length of ICU stay, location prior to admission, and comorbidities including congestive heart failure, chronic obstructive pulmonary disease, COVID-19, malignancy, diabetes mellitus, HIV, renal disease, liver disease, use of immunosuppressants, and the Charlson Comorbidity Index were not statistically significant factors for MDR *P. aeruginosa*.

In the multivariate analysis (Table III), the significant risk factors identified for MDR *P. aeruginosa* were antibiotic use in the past 30 days (odds ratio: 2.26; 95% CI: 1.16−4.52), respiratory isolates (odds ratio: 3.3; 95% CI: 1.15−11.11) and the year 2020 (odds ratio 2.29; 95% CI: 1.26 4.20).

Community vs healthcare associated vs hospital acquired

Of the isolates obtained within two days of admission, 64 did not have a history of hospitalization or antibiotic use within the past 30 days. Urine isolates were the most common [19], followed by skin/soft tissue/bone [17], respiratory [16], conjunctiva [4], blood [3], and other sources [4]. Of the urine isolates, nine (56.2%) isolates were from patients with chronic indwelling urinary devices, and two isolates were from patients with renal transplants. Of the skin/soft tissue/bone samples, thirteen (81.3%) isolates contained other bacteria present at the same culture sample site. Of all respiratory samples, seven (43.8%) isolates were from patients with chronic tracheostomies, four isolates were from patients with airway obstructions secondary to either foreign objects, nasopharyngeal masses, or asphyxiation and one isolate from aspiration. True community acquired *P. aeruginosa* pneumonia was seen in three patients, each with complex medical histories including interstitial lung disease secondary to systemic lupus erythematosus and metastatic lymphoma.

Clinical outcomes

Thirty one patients died during hospitalization with a *P. aeruginosa* isolate out of 207 patient encounters. MDR or NDR status at the time of death was determined by the most recent isolate prior to death. MDR *P. aeruginosa* was significantly associated with increased mortality ($P = 0.0466$).

Table I
Associated antibiotic resistances in *Pseudomonas aeruginosa* isolates

If resistant to →	AMK	AZT	CEF	CIP	GEN	LVX	MEN	TZP	TOB
Then also resistant to ↓	n=21	n=103	n=67	n=49	n=66	n=56	n=39	n=63	n=6
Amikacin	1.00	0.13	0.16	0.22	0.52	0.20	0.21	0.13	0.50
Aztreonam	0.67	1.00	0.90	0.61	0.32	0.68	0.77	0.95	0.67
Cefepime	0.52	0.58	1.00	0.49	0.35	0.54	0.54	0.84	0.33
Ciprofloxacin	0.52	0.29	0.36	1.00	0.24	0.77	0.41	0.29	0.33
Gentamicin	1.00	0.33	0.34	0.33	1.00	0.32	0.36	0.33	0.67
Levofloxacin	0.52	0.37	0.45	0.88	0.27	1.00	0.59	0.37	0.17
Meropenem	0.38	0.29	0.31	0.33	0.21	0.41	1.00	0.32	0.67
Pip/Tazo	0.38	0.58	0.79	0.37	0.32	0.41	0.51	1.00	0.33
Tobramycin	0.14	0.04	0.03	0.04	0.06	0.02	0.10	0.03	1.00

The values in the table represent percentages in decimal form. The first line indicates the number of isolates resistant to that antibiotic. The value represents the percentage of those isolates also resistant to the antibiotic listed in the column. AMK = amikacin, AZT = aztreonam, CEF = cefepime, CIP = ciprofloxacin, GEN = gentamicin, LVX = levofloxacin, MEN = meropenem, TZP = piperacillin/tazobactam, TOB = tobramycin.

Table II
Clinical characteristics of patients with *Pseudomonas aeruginosa* infections via univariate analysis

	MDR (n=77)	NDR (n=181)	*P*-value
Age (mean + SD)	58.3 + 21	55.9 + 23	0.434
Sex			0.035
Male	55 (71%)	104 (57%)	
Female	22 (29%)	77 (43%)	
Year			0.015
2019	37 (48%)	118 (65%)	
2020	40 (52%)	63 (35%)	
History			
Hospitalization in the past 30 days	35 (45%)	60 (33%)	0.061
Antibiotics in the past 30 days	60 (78%)	92 (51%)	5.18E-05
Hospitalization			
Length of hospitalization (mean + SD)	43.8 + 40	24.1 + 33	2.47E-04
Length of ICU stay (mean + SD)	17.2 + 23	10.1 + 21	0.020
Days of hospitalization till isolate [median (IQR)]	15 (33)	1 (8)	2.56E-09
Isolate obtained within 2 days of admission	19 (25%)	111 (61%)	7.14E-08
Isolated with other organisms (mean + SD)	1.3 + 0.6	1.6 + 0.9	0.001
Died in hospital[1]	12	19	0.047
Location prior to admission			0.067
Home	52 (68%)	146 (81%)	0.134
Nursing home	13 (17%)	20 (11%)	1.000
Other	12 (16%)	15 (8%)	0.479
Isolation site			4.42E-04
Respiratory (all)	46 (60%)	58 (32%)	3.33E-04
Respiratory with Mechanical ventilation	43 (56%)	52 (29%)	1.000
Urine (all)	15 (19%)	49 (27%)	1.000
Urine with Foley/nephrostomy/suprapubic catheter	5 (33%)	21 (43%)	1.000
Wound	6 (8%)	43 (24%)	0.028
Blood	5 (6%)	21 (12%)	1.000
Other	7 (9%)	12 (6%)	1.000
Ward			0.002
ICU	27 (35%)	45 (25%)	0.946
ED	6 (8%)	51 (28%)	0.003
Outpatient	3 (4%)	15 (8%)	1.000
Pediatric	2 (3%)	6 (3%)	1.000
General Med-Surg	39 (51%)	64 (35%)	0.218
Comorbidities			
Charlson Comorbidity Index	5.79 + 3	4.9+ 3	0.062
Cancer	14 (18%)	22 (12%)	0.201
Chronic kidney disease	30 (39%)	64 (35%)	0.582
Chronic obstructive pulmonary disease	5 (7%)	14 (8%)	0.920
Congestive heart failure	11 (14%)	25 (14%)	0.920
COVID-19	8 (10%)	15 (8%)	0.588
Diabetes	37 (48%)	81 (45%)	0.626
HIV/AIDS	5 (6%)	8 (4%)	0.700
Immunosuppressive therapy	22 (29%)	50 (28%)	0.801

IQR = interquartile range, SD = standard deviation, ICU = intensive care unit, ED = emergency department. MDR = multi-drug resistant, NDR = non-multi drug resistant.
[1] MDR/NDR status of deceased patients based on most recent isolate prior to death for each hospitalization.

Discussion

Multi-drug resistant *P. aeruginosa* presents an increasing burden on healthcare systems. The results of our study agree with previous data implicating recent antibiotic use [19,20], prolonged hospital stay [22], and respiratory samples [16,17] as risk factors for MDR *P. aeruginosa* infection. Prolonged hospital stay only mildly increased the odds of MDR *P. aeruginosa*, possibly due to its associations with other variables including prior antibiotic use ($r2 = 0.17$, $P<0.001$) and respiratory isolates ($r2 = 0.10$, $P<0.001$). In our study, mechanical ventilation with respiratory sampling was not identified as a risk factor for MDR *P. aeruginosa* when compared to NDR *P. aeruginosa,* as the majority of patients with respiratory isolates from both groups were on mechanical ventilation. Similarly, samples from foley catheters or other urinary indwelling devices were not

Table III
Multivariate analysis for MDR Pseudomonas aeruginosa risk factors

	Odds ratio	CI (2.5)	CI (97.5)	*P*-value
Days of hospitalization till isolate	1.01	1.00	1.03	0.039*
Isolation site: other	2.60	0.52	12.98	0.236
Isolation site: respiratory	3.14	1.11	10.41	0.041*
Isolation site: urine	1.64	0.53	5.74	0.410
Isolation site: wound	0.71	0.18	2.83	0.616
Antibiotics in the past 30 days	2.27	1.17	4.55	0.009*
Year: 2020	2.25	1.23	4.15	0.017*

* = *P*-value < 0.05.

associated with MDR isolates. Although ICU stay is usually found to be a significant risk factor for MDR *P. aeruginosa* [20], our data showed no statistically significant association between MDR isolates and patients in the ICU at the time of isolation. The strong association with NDR isolates from the emergency department is consistent with prolonged hospital stay as a risk factor for MDR *P. aeruginosa*.

MDR *P. aeruginosa*was less frequently associated with skin and wound sources and is less likely to be isolated with other organisms, supporting previous data on how intact communities of commensals can prevent colonization of multi-drug resistant organisms [33,34]. This is consistent with the theory that a healthy microbiome is protective against pathogenic colonization, and antibiotic use is associated with disruptions in the microbiome that may reduce colonization resistance and select for antibiotic resistance [34]. Our data adds to the evidence that diabetes, COPD, and immunosuppression are not significant risk factors for MDR P. aeruginosa.

Despite a reported decrease in the rate of MDR *P. aeruginosa* infections over the past twenty years per the SENTRY Antimicrobial Surveillance Program [17], there is increasing evidence pointing towards increased rates of multi-drug resistant organism outbreaks due to the COVID-19 pandemic [35–38]. At least one study found a decrease in the proportion of hospital acquired multi-drug resistant organisms from Q1-2020 to Q2-2020 [39]. Our study identified fewer total *P. aeruginosa* isolates from the year 2020 (n=103) compared to the 2019 (n=155), but an increasing proportion of multi-drug resistance from 2020 (38.8%) compared to 2019 (23.8%, *P*=0.015). The COVID-19 pandemic may have contributed to both the decrease in isolates and the increased proportion of resistance from 2019 to 2020. Reasons for a decrease in total number of isolates potentially include: a decreased hospital census following the initial wave of the COVID-19 pandemic, changes in hand hygiene practices, enhanced environmental cleaning, and implementation of new isolation and personal protection procedures. The increased proportion of resistant isolates may be related to increased mechanical ventilation and ventilator-associated pneumonia, increased use of empiric antibiotics [40], increased severity of disease and longer hospitalizations for patients that were admitted to the hospital, increased proportion of patients in the ICU, and decreased outpatient and emergency department isolates. Our data did not suggest an increased proportion of respiratory isolates in 2020 (n=43, 41%) compared to 2019 (n=61, 39%); however, there was an increased median length of hospitalization in 2020 (22 days) compared to 2019 (13 days) (Figure 2), increased patients in the ICU in 2020 (n=40, 39%) compared to 2019 (n=32, 21%), and decreased patients in the ED/outpatient setting in 2020 (n=12, 11%) compared to 2019 (n=63, 41%). Our study did not identify a positive COVID-19 polymerase chain reaction (PCR) test during hospitalization as a significant risk factor for MDR *P. aeruginosa*.

Limitations of our study include single-center data collection and lack of adjustment for unmeasured confounders including infection control, antimicrobial stewardship practices, and hospital census. There are also limitations in chart review as the patient may have had undocumented prior hospitalizations, antibiotics, comorbidities, and other medical history. Our dataset included multiple isolates from the same patient during hospitalization if the antibiogram of the isolates were different, however determination of MDR status via disk diffusion may be imprecise and multiple isolates may be reflective of colonization rather than infection. Even so, multiple isolates from patients within the same hospitalization made up less than 15% of the total dataset. Additionally, while our data suggests that hospital mortality is associated with MDR *P. aeruginosa*, it is unclear if the relationship is due to improper empiric therapy, virulence of the microorganisms, or patients with increased burden of disease at baseline.

Conclusion

Prior use of antibiotics, prolonged hospital stay, and respiratory isolates were significant risk factors for acquisition of MDR *P. aeruginosa*. There was a decrease in the number of *P. aeruginosa* isolates from 2019 to 2020, but a significant increase in the proportion of MDR *P. aeruginosa* isolates, possibly secondary to the increased length of hospitalizations and use of antibiotics in the COVID-19 era. These findings emphasize the need for antimicrobial stewardship in the post COVID-19 world. Changes to empiric therapy may be required with the increasing prevalence of antimicrobial resistance among hospitalized patients, and improved identification of patients at risk for MDR *P. aeruginosa* could facilitate appropriate empiric antibiotic decisions and improve hospital mortality.

Credit Author Statement

Ann Fan Yang: Conceptualization, methodology, data curation, writing, visualization. **Vivian Huang**: Conceptualization, data curation. **Jevon Samaroo-Campbell:** Conceptualization, data curation, writing reviewing and editing. **Michael Augenbraun:** Conceptualization, methodology, writing reviewing and editing.

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Conflict of interest

No conflicts of interest.

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