



Microbial coinfections and superinfections in critical COVID-19: a Kenyan retrospective cohort analysis

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ABSTRACT

Objectives: The aim of our study was to outline the burden, risk factors, and outcomes for critical COVID-19 patients with coinfections or superinfections.

Methods: This was a retrospective descriptive study of adults who were admitted with critical COVID-19 for ≥ 24 hours. Data collected included demographic profiles and other baseline characteristics, laboratory and radiological investigations, medical interventions, and clinical outcomes. Outcomes of interest included the presence or absence of coinfections or superinfections, and in-hospital mortality. Differences between those with and without coinfections or superinfections were compared for statistical significance.

Results: In total, 321 patient records were reviewed. Baseline characteristics included a median age (IQR) of 61.4 (51.4–72.9) years, and a predominance of male (71.3%) and African/black (66.4%) patients. Death occurred in 132 (44.1%) patients, with a significant difference noted between those with added infections (58.2%) and those with none (36.6%) ($p = 0.002$, odds ratio (OR) = 2.41). One patient was coinfecting with pulmonary tuberculosis. Approximately two-thirds of patients received broad-spectrum antimicrobial therapy.

Conclusion: Added infections in critically ill COVID-19 patients were relatively uncommon but, where present, were associated with higher mortality. Empiric use of broad-spectrum antimicrobials was common, and may have led to the selection of multidrug-resistant organisms. More robust local data on antimicrobial susceptibility patterns may help in appropriate antibiotic selection, in order to improve outcomes without driving up rates of drug-resistant pathogens.

INTRODUCTION

The COVID-19 pandemic has resulted in more than 220 million infections and 4.5 million deaths, posing unique challenges to health-care systems globally (Ouma et al., 2020; Vaillancourt and Jorth, 2020; Moynihan et al., 2021). Determining the optimal therapeutic approach for COVID-19, including the role of antibiotics, continues to be an area of active research. Use of antibiotics, such as azithromycin, as therapy for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, or as empiric treatment for suspected coinfections and superinfections, has been extensive (Cavalcanti et al., 2020; Furtado et al., 2020). However, there are limited data to support this practice (Ginsburg and Klugman, 2020; Hsu, 2020). A recent review of COVID-19 management in 10 African countries, including Kenya, was undertaken by Adebisi et al. They found that empiric or prophylactic use of antibiotics was generally recommended by local guidelines, contrary to World Health Organization (WHO) guidelines (Adebisi et al., 2021). In another review, up

to 75% of patients with COVID-19 had received empiric antimicrobial medication (Langford et al., 2021). This widespread empiric antimicrobial use has raised concerns regarding increased antibiotic resistance and an upsurge in the prevalence of multidrug-resistant organisms.

Antimicrobial use has partly been driven up by the concern that coinfections and superinfections in patients with COVID-19 lead to poor outcomes (Musuuza et al., 2021). A recent study by Lansbury et al. demonstrated that the rate of coinfection in patients hospitalized with COVID-19 pneumonia was low (7%), except for those admitted to the intensive care unit (ICU) (51%). Superinfection was associated with a higher mortality (75%) in comparison with non-infected patients (44%) (Lansbury et al., 2020). This is comparable to the higher mortality rates seen with viral-bacterial coinfections found in community-acquired pneumonia (Voiriot et al., 2016). Other studies also point to the low incidence of coinfections in patients admitted with COVID-19 (Garcia-Vidal et al. 2020; Hughes et al., 2020). This is in contrast with observations made during outbreaks of influenza, where rates of bacte-

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rial coinfection of up to 65% have been reported (Klein et al., 2016). The combined effects of reported higher rates of added microbial infections and increased risk of death in patients with critical COVID-19 warrants local characterization of the rates, risk factors, and likely pathogens among these patients.

In Kenya, 246 643 confirmed COVID-19 cases and 4995 deaths have been reported since March 2020 (WHO dashboard, accessed September 22, 2021: <https://covid19.who.int/>). Our experience in managing COVID-19 points to widespread empiric use of antibiotics, often with little evidence of coinfections or superinfections. This has the potential to worsen antibiotic resistance patterns and facilitate the emergence of multidrug-resistant organisms, which is already a major healthcare challenge in our region (Tadesse et al., 2017). To the best of our knowledge, no studies thus far have examined coinfections and superinfections in those hospitalized with critical COVID-19 in Kenya or in the wider sub-Saharan Africa. Our study therefore examined the demographics, incidence, risk factors, and outcomes associated with coinfections and superinfections in critically ill COVID-19 patients in a tertiary health facility in Nairobi, which has been the epicentre of the outbreak in our country.

METHODS

Study design and participants

This was a retrospective cohort study involving patients admitted with critical COVID-19 for a period of at least 24 hours, and who subsequently died or were discharged. The study was carried out at the Aga Khan University Hospital, Nairobi (AKUHN), a 258-bed, private, not-for-profit, tertiary-level teaching and referral hospital. The institution has 15 critical-care beds available for the management of critical COVID-19 patients.

All critical COVID-19 patients aged ≥ 18 years with a confirmed diagnosis of COVID-19 pneumonia were enrolled. Confirmation was based on a positive real-time reverse-transcription polymerase chain reaction (RT-PCR) assay for SARS-CoV-2 in nasopharyngeal swabs or samples from the lower respiratory tract obtained via tracheal aspirate or broncho-alveolar lavage. In addition, radiological evidence of pneumonia based on chest radiographs or chest computed tomography (CT) scans was required. Patients with a clinical presentation that was suggestive of COVID-19, but who had a negative RT-PCR test, and those with any re-admissions for post-COVID-19 complications were excluded.

Definitions

COVID-19 pneumonia: Clinical and radiological features consistent with pneumonia and a positive SARS-CoV-2 PCR test from a respiratory specimen. The extent of lung parenchymal involvement on baseline chest CT scans was determined using the CT severity score (Saeed et al., 2021). Critical COVID-19 was defined according to the WHO COVID-19 disease severity classification (WHO, 2021), to include those with acute respiratory distress syndrome (ARDS), sepsis, or septic shock. ARDS was characterized using the 2012 Berlin definition (Ferguson et al., 2012), whereas sepsis or septic shock was defined according to the third international consensus definitions (Singer et al., 2016).

Bloodstream infection (BSI): Isolation of a pathogenic microbe from at least one blood culture, or isolation of an organism considered to be a skin commensal from at least two sets of blood cultures, in the presence of a compatible syndrome, as ascertained by an infectious disease specialist in the study team (JR or FR).

Bacterial/viral/mycobacterial/fungal pneumonia: Growth of a bacterial or fungal isolate from a respiratory sample (sputum/tracheal aspirate/broncho-alveolar lavage fluid), or a positive PCR result from a respiratory sample with a compatible clinical syndrome, as ascertained by an infectious disease specialist in the study team.

All of these clinically significant added infections were categorized either as coinfections (diagnosis made at the time of, or within the first 48 hours of, COVID-19 hospital admission) or superinfections (diagnosis made after 48 hours of hospitalization). Multidrug-resistant organisms (MDROs), including extended spectrum beta-lactamase producing enterobacterales, carbapenem-resistant enterobacterales, carbapenem-resistant *Acinetobacter baumannii*, multidrug-resistant *Pseudomonas aeruginosa*, and methicillin-resistant *Staphylococcus aureus* were classified using the Centers for Disease Control and Prevention (CDC) definitions for nosocomial infections (Garner et al., 1988, 2019).

Data collection

The manual and electronic health records for all the patients admitted to the critical care units with a diagnosis of critical COVID-19 prior to the study period were reviewed, and data of interest were extracted and entered into a REDCap® database.

Data obtained included: clinical demographic profiles (age, sex, race); comorbid conditions (hypertension, diabetes, cancer, rheumatological diseases, HIV, chronic heart/lung/kidney disease); days since onset of symptoms; source of admission to critical care (direct, medical ward, interhospital transfer); baseline inflammatory markers on admission to critical care ward (c-reactive protein, lymphocyte counts, procalcitonin, ferritin, d-dimer); microbiological data on record (blood, urine, respiratory tract cultures; viral multiplex PCRs from respiratory specimens; mycobacterial nucleic acid amplification tests; mycobacterial cultures); radiological tests (CT scans of the chest, chest radiographs); specific therapies offered to the patients for COVID-19 (remdesivir, dexamethasone, tocilizumab); antimicrobial therapy given before/during hospitalization; presence and duration of indwelling catheters (central venous catheters, urethral catheters); duration of hospitalisation; duration of critical care stay; duration of mechanical ventilation; and discharge status (alive at discharge/transfer to another hospital or dead). After data collection and coding, the data collected were exported to SPSS for analysis (IBM Statistical Package for the Social Sciences, version 22.00).

Statistical analysis

Continuous variables, such as baseline inflammatory markers, duration of hospital stay, and duration of mechanical ventilation, were expressed as medians with interquartile ranges (IQRs). Categorical variables, such as the outcome variable, sex, and comorbidities, as well as the interventions used, were expressed as frequencies and percentages. Normality of the data was analyzed using the Shapiro–Wilk test for continuous data. Differences between groups with no infections and those with added infections were compared using Student's *t*-test or the Wilcoxon–Mann–Whitney test (depending on the normality of the data) for continuous variables, and using chi square (χ^2) or Fisher's exact test for categorical variables. A *p*-value < 0.05 was considered significant.

RESULTS

Clinical demographics

Data collected between March 2020 and May 2021 were reviewed. During this period, 321 patients were admitted to the AKUHN critical care units with respiratory failure secondary to critical COVID-19 pneumonia. Of these, 229 (71.3%) were male, 213 (66.4%) were African/black, and 257 (80.1%) had at least one comorbid condition. The median (IQR) age of this cohort was 61.4 (51.4–72.9) years. Systemic arterial hypertension, diabetes mellitus, and pre-existing renal disease were the most frequently reported comorbidities, at 184/321 (57.3%), 154/321 (48%), and 41/321 (12.8%), respectively. 13 (4%) of the patients had a coexisting malignancy, while eight (2.5%) had HIV

Table 1
Baseline clinical characteristics of patients with critical COVID-19

Variables	Total (N = 321)*	No infections (N = 254)	Infections (N = 67)	p-value
Age, years	61.4 (51.4–72.9)	61.6 (52.3–73.7)	59.1 (48.7–72.5)	0.451
Male sex	229, 71.3%	180, 70.9%	49, 73.1%	0.763
African/Black	213, 66.4%	164, 64.6%	49, 73.1%	0.669
Comorbid conditions				
Diabetes mellitus	154, 48.0%	128, 50.4%	26, 38.8%	1.000
Hypertension	184, 57.3%	149, 58.7%	35, 52.2%	0.405
CKD	41, 12.8%	32, 12.6%	9, 13.4%	1.000
Cancer	13, 4.0%	8, 3.1%	5, 7.5%	0.155
Baseline inflammatory markers on admission to critical care				
Lymphocytes, 10 ⁹ /L	1.0 (0.7–1.3)	1.0 (0.7–1.3)	0.9 (0.7–1.4)	0.908
CRP, mg/L	108.0 (56.5–181.5)	106.0 (53.0–180.0)	124.0 (78.5–220.0)	0.046
Ferritin, ng/ml (n = 253)	932.0 (353.7–1531.0)	910.0 (349.0–1483.0)	1019.5 (386.0–1663.0)	0.585
Lactate, mmol/L (n = 88)	1.6 (1.2–2.1)	1.6 (1.2–2.1)	1.7 (1.5, 2.1)	0.527
PCT, ng/ml	0.2 (0.1–0.4)	0.2 (0.1–0.4)	0.2 (0.1–0.5)	0.806

* Continuous variables are expressed as median (interquartile range); categorical variables are expressed as n, %. Abbreviations: CKD, chronic kidney disease; CRP, C-reactive protein; PCT, procalcitonin

coinfection. Oral antibiotic use prior to admission was reported in 40 patients (12.5%). These were predominantly penicillins, cephalosporins, and macrolides, at 16/40 (40%), 14/40 (35%), and 14/40 (35%), respectively. The median (IQR) time to presentation to hospital from onset of symptoms was 6 (3–7) days, and 287 (90%) of the patients had crepitations on chest examination at arrival. Baseline chest radiographs showed severe (~50%) lung parenchymal involvement in 199/293 (67.9%) patients. Table 1 provides a summary of these clinical demographics by different categories.

Interventions and outcomes

The patients were admitted to critical care units from the medical isolation wards (51.4%), directly through the accidents and emergency (A&E) department (44.2%), or as transfers from other facilities (4.4%). 143 patients (44.5%) eventually required invasive mechanical ventilation. Other interventions offered included dexamethasone (87.5%), tocilizumab (62%), and methylprednisone (14%). Antimicrobial drugs were prescribed to 224 (69.8%) patients, including 57.1% who had no microbiologically confirmed concomitant infections. The antibiotics prescribed in the 224 patients included: penicillins (52.2%), carbapenems (46.8%), cephalosporins (31.7%), macrolides (31.2%), vancomycin (21.5%), echinocandins (10.2%), voriconazole (3.9%), polymyxins (2.9%), and trimethoprim/sulfamethoxazole (2.9%). 99 patients received more than one antimicrobial agent.

The overall mortality in our study population was 41.1% (132/321). All except five were intubated and mechanically ventilated. The five patients were on non-invasive ventilation with advance directives or change-of-goals-of-care orders in place, prohibiting intubation and mechanical ventilation. The mortality rate for mechanically ventilated patients was 88% (127 of 143 patients). The presence of added microbial infections was significantly associated with higher mortality (unadjusted OR = 2.41, translating into 141% higher odds for infections leading to death compared with no infections), as well as prolonged time to discharge from critical care or discharge from hospital for survivors. Factors that significantly increased the risk for added infections included duration of hospital stay, the need for and duration of invasive mechanical ventilation, the presence and duration of indwelling urethral or central venous catheters, and receipt of tocilizumab (Table 2). Prior use of outpatient antibiotics did not significantly reduce the rates of added infections in this study population.

Microbiological profiles

In total, 1033 clinical samples submitted for culture by attending physicians from 231 of the 321 patients as part of their regular care

were reviewed. These comprised 594 blood cultures, 242 urine cultures, and 169 tracheal aspirate or pleural fluid cultures, as well as 28 mycobacterium tuberculosis cultures. Pathogenic microbes were found in 67 patients, representing 29% of those who had a microbiological sample submitted. Of these, five patients had documented coinfections, with the rest being superinfections. Blood cultures yielded 84 isolates from 78 of the samples. Pathogens isolated included: *Klebsiella pneumoniae* — 17 (20%), *Pseudomonas aeruginosa* (16; 19%), *Acinetobacter baumannii* (seven; 8%), and *Enterococcus faecalis* (seven; 8%). Candidemia was documented from seven (8%) samples. There were 23 uropathogens isolated from 23 of the cultured samples. *Escherichia coli* accounted for the majority, comprising 10 (43%) of the 23 isolates. Respiratory fluid cultures yielded 104 pathogens from 87 of the cultured samples, with *Klebsiella pneumoniae* (26; 25%), *Pseudomonas aeruginosa* (17; 16%), and *Escherichia coli* (17; 16%) being the most common isolates. Only two patients had *Aspergillus* isolated from respiratory samples, with possible invasive fungal pneumonia. Table 3 provides a summary of the pathogenic isolates identified. The isolated multidrug-resistant organisms included 27 of the 32 *E. coli* isolates, 25 of the 46 *K. pneumoniae* isolates, 21 of the 22 *A. baumannii* isolates, five of the 36 *P. aeruginosa* isolates, and six of the eight *S. aureus* isolates (Table 4).

Twelve patients had samples submitted for a polymerase chain reaction (PCR) BIOFIRE® Respiratory 2.1 panel, from which one coinfection with respiratory syncytial virus (RSV) was detected. Pulmonary tuberculosis (PTB) coinfection was documented in only one patient, based on Gene-Xpert® nucleic-acid amplification test analysis.

DISCUSSION

Presence of coinfections and superinfections in COVID-19 have been a source of concern and uncertainty in the management of COVID-19 infection. This led us our aim of investigating their frequency and impact in critically ill patients in our institution. Low rates of coinfections and superinfections in COVID-19 patients have been reported in previous studies (Hughes et al., 2020). However, rates are disproportionately higher (up to 56%) in critically ill COVID-19 patients (Fattorini et al., 2020; Kim et al., 2020; Lv et al., 2020), and have been associated with increased mortality (Shafran et al., 2021; Silva et al., 2021).

Most guidelines currently discourage empiric use of antibiotics in COVID-19, except for those with clinical suspicion of coinfections or those requiring direct ICU admission due to critical illness (Adebisi et al., 2021). In our study of critically ill COVID-19 patients, coinfections and superinfections were documented in 29% of the patients with microbiological samples, which was substantially lower than the rates reported in other studies. Previous authors have suggested that use of prophylactic antibiotics may be a factor in the low rates of added infections

Table 2
Interventions received and outcomes for the study population

Variables	Total(N = 321)*	No infections(N = 254)	Infections(N = 67)	p-value
Invasive mechanical ventilation	143, 44.5%	86, 33.9%	57, 85.1%	< 0.001
Days on IMV (n = 140)	6.0 (2.0–13.0)	4.0 (1.0–7.0)	13.0 (7.0–22.5)	< 0.001
Died	132, 41.1%	93, 36.6%	39, 58.2%	0.002
TTO from ICU admission, days	8.0 (4.0–14.0)	6.0 (3.0–11.0)	18.0 (11.0–33.0)	< 0.001
Therapeutics administered				
Remdesivir	38, 11.8%	33, 13.0%	5, 7.5%	0.288
Tocilizumab	199, 62.0%	147, 57.9%	52, 77.6%	0.003
Dexamethasone	281, 87.5%	220, 86.6%	61, 91.0%	0.409
Indwelling catheters				
UC	152, 47.4%	92, 36.2%	60, 89.6%	< 0.001
CVC	151, 47.0%	92, 36.2%	59, 88.1%	< 0.001
Duration of UC, days (n = 152)	6.0 (3.0–13.0)	4.0 (2.0–9.0)	14.0 (7.0–20.5)	< 0.001
Duration of CVC, days (n = 151)	7.0 (3.0–13.0)	4.0 (2.0–9.0)	14.0 (7.0–21.0)	< 0.001

* Continuous variables are expressed as median (interquartile range); categorical variables are expressed as n, %.IMV = invasive mechanical ventilator; TTO = time to outcome (i.e. discharge/transfer out or death); ICU = intensive care unit; UC = urethral catheter; CVC = central venous catheter

Table 3
Summary of clinically significant microbial isolates obtained from cultured samples

Pathogens isolated [†]	Source		
	Bloodstream N = 77	Respiratory tract N = 102	Urine N = 18
<i>Bacteria</i>			
<i>Acinetobacter baumannii</i>	7	13	2
<i>Burkholderia cepacia</i>	2		
<i>Citrobacter koseri</i>	1		
<i>Citrobacter freundii</i>		2	
<i>Coagulase negative staphylococcus</i>	8		
<i>Enterobacter aerogenes</i>		2	
<i>Enterobacter asburiae</i>		1	
<i>Enterobacter cloacae</i>	1	5	
<i>Enterococcus faecalis</i>	7		
<i>Enterococcus faecium</i>	6		
<i>Escherichia coli</i>	5	17	10
<i>Granulicatella adiacens</i>	1		
<i>Klebsiella pneumoniae</i>	17	26	3
<i>Leuconostoc pseudomesenteroides</i>	1		
<i>Pseudomonas aeruginosa</i>	16	17	3
<i>Salmonella group D</i>	1		
<i>Serratia marcescens</i>	1		
<i>Staphylococcus aureus</i>		8	
<i>Stenotrophomonas maltophilia</i>		10	
<i>Streptococcus parasanguinis</i>	1		
<i>Streptococcus pneumoniae</i>		1	
<i>Fungi</i>	N = 7	N = 2	N = 5
<i>Aspergillus flavus</i>		2	
<i>Candida albicans</i>	1		5
<i>Candida auris</i>	5		
<i>Candida parapsilosis</i>	1		

[†] Eight patients had pathogens isolated from bloodstream, respiratory tract, and urine; 24 patients had blood and tracheal aspirate isolates; 11 patients had blood and urine isolates; 11 patients had urine and tracheal aspirate isolates. 10 patients had similar pathogens isolated from blood and tracheal aspirate cultures, two patients had similar pathogens isolated from blood and urine cultures, and five patients had similar pathogens isolated from urine and tracheal aspirate cultures.

Table 4
Commonly identified pathogens and their resistance profiles

Pathogens isolated (N)	Multidrug-resistant organisms [§]	
	ESBL-E	CRE
<i>Escherichia coli</i> (32)	25/32 (78.1%)	2/32 (6.3%)
<i>Klebsiella pneumoniae</i> (46)	15/46 (32.6%)	10/46 (22.7%)
<i>Acinetobacter baumannii</i> (22)	21/22 (95.5%)	CRAB
		MDR
<i>Pseudomonas aeruginosa</i> (36)	5/36 (13.9%)	MRSA
<i>Staphylococcus aureus</i> (8)	6/8 (75.0%)*	

[§] Number of isolates expressed as n/N (%).

* Five of the six MRSA isolates were from one patient. Abbreviations: ESBL-E, extended-spectrum beta-lactamase-producing Enterobacterales; CRE, carbapenem-resistant Enterobacterales; CRAB, carbapenem-resistant *Acinetobacter baumannii*; MDR, multidrug resistant; MRSA, methicillin-resistant *Staphylococcus aureus*

Broad-spectrum antibiotics were administered in a large proportion of our study population, with 46.8% of those given antibiotics receiving carbapenems. Use of broad-spectrum antibiotics is a documented risk for driving up antimicrobial resistance rates (Sonmez et al., 2016), and discretion is necessary in ensuring that their utilization is appropriate. Our study found a high percentage of MDROs among the commonly isolated pathogens: 21 of 22 (95.5%) *A. baumannii*, 10 of 46 (22.7%) *K. pneumoniae*, two of 32 (6.3%) *E. coli*, and five of 36 (13.9%) *P. aeruginosa* isolates were carbapenem resistant. This was a higher percentage of MDROs compared with our institution’s 2020 antibiotic susceptibility report, in which carbapenem resistance was documented in 65% of *A. baumannii*, 7% of *K. pneumoniae*, 1% of *E. coli*, and 15% of *P. aeruginosa* bloodstream isolates (report in the supplementary appendix). A recent study on *Acinetobacter* infections in our institution also revealed that 86% of the isolates were multidrug-resistant (Patel et al., 2019), which is still a lower frequency than that noted in our study. This aberration in the rates of MDROs between our study findings and the institutional antibiotic susceptibility report may be in part related to increased empiric use of broad-spectrum antimicrobial agents.

Factors significantly associated with high rates of added infections were: need for and duration of mechanical ventilation; presence and duration of invasive urethral or central venous catheters; tocilizumab administration, and duration of ICU stay; these findings were consistent with those of other authors (Garcia-Vidal et al., 2020; Zhang et al., 2020). The necessity for these interventions should be carefully considered daily, and discontinued whenever indicated in order to mitigate

(Garcia-Vidal et al., 2020). However, our study did not demonstrate a statistically significant difference in the rates of added infections between those with or without prior exposure to outpatient antibiotics.

Almost two-thirds of the patients in this study received in-patient antimicrobials (antibiotics and/or antifungals), which was consistent with rates reported in a review by Rawson et al. (Rawson et al., 2020). The discrepancy between the frequency of antimicrobial use and actual confirmed infections, as demonstrated by our study and others (Chedid et al., 2021) is concerning in terms of the potential to select for multidrug-resistant organisms (MDROs) (Clancy and Nguyen, 2020).

against the risk of infection that they pose. The presence of added bacterial or fungal infections was associated with higher mortality in our study population (58% compared with 36% for those with no added infections). Due to the association of added microbial infections with increased mortality, especially in critically ill patients, we would advocate for characterization of the local patterns of susceptibility for these concomitant infections. This would facilitate appropriate utilization of antimicrobial agents, thus improving outcomes without unnecessarily driving up the rates of drug-resistant pathogens.

PTB-COVID-19 coinfection was only demonstrated in one of our patients, who was HIV negative. This patient had an excellent response to concurrent therapy for both infections, did not require invasive mechanical ventilation, and was discharged after a brief stay in the ICU. Given that our country is in a TB-endemic zone, this was a reassuringly low rate of coinfection given the risk of increased COVID-19 mortality in the presence of TB coinfection (Sarkar et al., 2021). Despite the low incidence in our study, vigilance is still required because therapies like steroids and tocilizumab may exacerbate or unmask undiagnosed TB infection (Bandyopadhyay et al., 2020; Tadolini et al., 2020). HIV in COVID-19 pneumonia has also been cited as a risk factor for increased mortality. Though our numbers were limited, this pattern was not demonstrated in our study. Out of eight HIV-positive patients, six survived to discharge. All eight patients had been on antiretroviral drugs, with documented viral suppression at admission.

There were some important limitations to our study. As this was a single-centre study, our findings may not be generalizable given that there may exist variation among the different institutions in our region in terms of frequently isolated nosocomial pathogens, availability of adjunctive laboratory tests, or interventions such as invasive mechanical ventilation and vasopressors. Second, the absence of a microbiological isolate does not rule out the possibility of an intercurrent infection, while the reliability of microbiology test results can vary between laboratories. In addition, antibiotics may have been prescribed to some of the patients before microbiological samples were obtained. Lastly, as this was a retrospective cohort analysis, it is conceivable that the attending physicians might not have requested microbiological samples in patients who could have had coinfections and superinfections.

CONCLUSION

Our study reported relatively low rates of microbial infections in our cohort of critically ill COVID-19 patients. However, where present, these were associated with higher death rates, greater need for mechanical ventilation, and prolonged hospitalization. Multidrug-resistant pathogens were frequent among the commonly isolated bacteria, such as *K. pneumoniae*, *P. aeruginosa*, *E. coli*, and *A. baumannii*. Given the high rates of empiric broad-spectrum antimicrobial use in our study cohort, broader regional epidemiology, microbiology, and susceptibility patterns of likely additional infections in critical COVID-19 patients is becoming necessary in order to develop local guidance on approaches to rational empiric antimicrobial usage.

Disclosures

The authors of this paper report no conflicts of interest with regards to this study.

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Ethical approval

Ethical approval for this study was obtained from the Institutional Ethics Review Committee (IERC) of the Aga Khan University, East Africa

Medical College (reference number: 2021/IERC-16 (v1)). A waiver of consent was granted by the IERC, since this was a retrospective analysis of data obtained as part of routine care, with no collection of patient identifiers such as name or hospital number. A research license was also secured from the National Commission for Science, Technology and Innovation (NACOSTI) (license number: NACOSTI/P/21/9035).

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ljregi.2021.09.008.

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