Original Article

Aerobic bacteria study, clinical spectrum, and outcome of patients with community-acquired multidrug-resistant pathogens

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Abstract

Context: Infectious diseases are the leading cause of death in developing countries like India. Hence, even small relative increases in the mortality rate for infections due to multidrug-resistant pathogens would lead to substantial increases in the number of deaths as a result of infections worldwide. **Aims:** The aim of the study was to study the microbiological data of community-acquired pathogens and the corresponding outcomes due to antibiotic-resistant versus antibiotic-susceptible bacterial microorganisms. **Settings and Design:** A single-center prospective cohort study for two years undertaken during the study period of March 2022 to 31 October 2023. **Materials and Methods:** All clinical samples of 402 patients diagnosed microbiologically as community-acquired infections were included. Culture samples were collected and processed according to standard operating procedures and clinical details were recorded. **Statistical Analysis Used:** Categorical variables were expressed as counts and percentages. Fisher's exact test was used for testing differences in proportions. Two-sided distribution *P* values of <0.05 were considered significant. **Results:** Among Gram-positive organisms, *Staphylococcus aureus* and *Streptococcus pyogenes* were predominant isolates. *Escherichia coli* and *Klebsiella* species were the majority of the pathogens among Gram-negative isolates. Mortality rates observed in community-acquired respiratory tract infections (CA-RTIs), community-acquired urinary tract infections (CA-UTIs), community-acquired skin and soft tissue infections (CA-SSTIs), and community-acquired bloodstream infections (CA-BSIs) were 13.6%, 6.56%, 4.5%, and 31.5%, respectively. The length of hospital stay of more than three days was found as 56.06%, 36.2%, 40.9%, and 73.6% in CA-RTIs, CA-UTIs, CA-SSTIs, and CA-BSIs, respectively. **Conclusions:** Performing cultures earlier during hospitalization and determining the timing of colonization can allow more targeted choices and reduce morbidity and mortality rates among infected patients.

Keywords: Community-acquired infections, multidrug-resistant bacteria

Introduction

Community-acquired multidrug-resistant (MDR) pathogens typically noted were *Neisseria gonorrhoeae*, non-typhoidal *Salmonella*, *Shigella*, and *Streptococcus pneumoniae*. Classical hospital pathogens that are MDR have been isolated in communities like methicillin-resistant *Staphylococcus aureus* (MRSA), Carbapenem Resistant Acinetobacter baumanii (CRAB), MDR, *Pseudomonas aeruginosa*, and *Enterobacteriaceae*.[1] Viral etiologies account for 20–40% of community-acquired pneumonia cases; a significant proportion of respiratory infections are being observed,[2,3] but the overuse of antibiotics is still a concern. Knowing the exact etiologies is an important step in managing the burden of infectious diseases in our country; it aids in reducing inappropriate prescriptions.

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Worldwide, the surge of antibiotic-resistant pathogens is compromising the results of cancer care, transplantation, and surgical procedures.[4] Acquisition of multidrug resistance genes was driven by risk factors such as antimicrobial exposure, healthcare exposure, chronic illness, indwelling devices, malignancies, and immunosuppression.[5]

It is unfortunate that the emergence of community-acquired MDR organisms is associated with the misuse of antimicrobials in both empirical and definitive therapy. We conducted this study to project the microbiological data of community-acquired pathogens, study the corresponding outcomes, and evaluate the mortality and length of stay due to antibiotic-resistant versus antibiotic-susceptible bacterial microorganisms.

Materials and Methods

Study design and settings

This was a single-center, prospective cohort study for two years undertaken at a tertiary care multispecialty hospital in the southern part of India. The analysis uses data collected in the ongoing cohort from March 2022 until 31 October 2023. Hospitalized patients in this study hail from both urban and rural areas in and around our hospital. Informed consent was obtained from the patient; for patients falling into the category of minors, mentally incapable of decision-making, and unconscious, consent for testing was obtained from parents/guardians/immediate family members.

Study population and inclusion/exclusion criteria

Patients admitted to the KIMS SAVEERA tertiary care hospital with microbiologically confirmed community-acquired infections were eligible for inclusion in this study.

Inclusion Criteria

1. The study subjects were adults of both sexes (≥18 years old) confirmed microbiologically with community-acquired pathogens in their tested specimens.
2. A microbiology culture specimen obtained within 48 hours of admission and showing evidence of existing infections on admission.

Exclusion criteria

1. Duplicate isolates, defined as the same bacteria isolated from the same patient and sample, were excluded from our study.
2. Patients who got an infection after staying at the hospital for longer than 48 hours and there is no evidence of infection during admission.
3. Pathogens are considered colonizers after clinical and laboratory evaluation.

Data collection and clinical outcomes

All clinical samples of 402 patients' diagnosed culture-wise as community-acquired infections were included in the study population. Details in relation to specimens like type, time of collection, time of processing, organism isolated, sensitivity pattern, and patient details such as age, sex, presenting complaints, microbiology data, diagnosis, duration of hospital stay, intensive care unit (ICU) admission, underlying medical problem, O_2 requirement, need for surgery, outcome, and ventilator support were recorded. The severity scoring systems such as CURB 65, APACHE II, SOFA scores, and Charlson severity of illness index were evaluated at the time of admission.

Cultures were processed by standard operating procedures in use by the microbiology laboratory as part of the initial clinical workup. All clinical samples collected from every patient diagnosed with a community-acquired infection were inoculated on media plates immediately after receiving them at the laboratory and processed according to the routine laboratory diagnostic protocol, which included identifications by morphological, biochemical, culture characteristics, and antibiotic susceptibility testing as per Clinical and Laboratory Standards Institute (CLSI) guidelines of 2022.

Statistical methodology

Study characteristics (such as patient details, microbiology details, clinical details, and outcomes) were recorded in the Excel spreadsheet during the study period. Descriptive statistics were employed to summarize and present the demographic and clinical characteristics of the study population. Categorical variables were expressed as counts and percentages. Fisher's exact test was used for testing differences in proportions. Two-sided distribution *P* values of <0.05 were considered significant.

Results

Demographic data

Community-acquired infections in hospitalized patients 402 were assessed; among them, infections were predominantly noted in the elderly age group of >60 years, that is, 55.2% (222/402). The majority of the study population were males; it was 60.6% (244/402) [Table 1].

Microbiological data

After evaluation of microbiological data and the clinical condition of patients, a total of 402 patient specimens that were considered community-acquired infections including respiratory tract infections, urinary tract infections, skin and soft tissue infections, reproductive tract infections, and others were analyzed, among which 435 organisms were isolated. Polymicrobial organisms' isolation was observed in 7.58% (33 out of 435). Moreover, 95 (23.6%) out of 402 patients were infected with MDR superbugs [Table 1]; 102 (23.4%) out of 435 organisms were MDR pathogens, and the remaining 333 (76.5%) were non-MDR pathogens.

By the site of infection, the most common focus of infections among community-acquired infections was urinary tract infections (64.4%), followed by respiratory tract infections (16.4%), skin and soft tissue infections (10.9%), bloodstream infections (4.7%), reproductive tract infections (1.7%), and others (1.7%) [Table 1].

Table 1: MDR and non-MDR patients in relation to age, sex, and clinical syndromes

Parameters	MDR group (*n*=95)	Non-MDR group (*n*=307)	*P*
Age in years			
≤30	12 (12.6%)	31 (10.09%)	0.484
31–60	27 (28.4%)	110 (35.8%)	0.183
>60 years	56 (58.9%)	166 (54.07%)	0.411
Sex			
Female	25 (26.3%)	133 (43.3%)	0.003
Male	70 (73.6%)	174 (56.6%)	
Clinical syndrome	**MDR group (*n*=95)**	**non-MDR group (*n*=307)**	**Total (%)**
Respiratory tract infection	15 (22.7%)	51 (77.2%)	66 (16.4%)
Skin and soft tissue infections	8 (18.1%)	36 (81.8%)	44 (10.9%)
Urinary tract infections	65 (25.09%)	194 (74.9%)	259 (64.4%)
Reproductive tract infections	1 (14.2%)	6 (85.7%)	7 (1.7%)
Bloodstream infections	6 (31.5%)	13 (68.4%)	19 (4.7%)
Others	0	7 (100%)	7 (1.7%)
Total	95 (23.6%)	307 (76.3%)	402 (100%)

Among Gram-positive organisms, *Staphylococcus aureus* and *Streptococcus pyogenes* were the predominant isolates. *Escherichia coli* and *Klebsiella* species were the majority of the pathogens among Gram-negative isolates [Figure 1].

Among respiratory tract infections (n = 66), the most common pathogens isolated were *Klebsiella pneumoniae* (42.02%), *Streptococcus pyogenes* (20.2%), and *Staphylococcus aureus* (17.3%). *Escherichia coli* (49.2%) and *Klebsiella pneumoniae* (13.4%) were the predominant pathogens in urinary tract infections (n = 259). *Escherichia coli* (31.3%), *Staphylococcus aureus* (25.4%), and coagulase-negative *Staphylococci* (17.6%) were the most common organisms isolated from skin and soft tissue infections (n = 44). Bloodstream infections (n = 19) predominant pathogens were *Escherichia coli* (26.3%), *Klebsiella oxytoca* (21.05%), and *Klebsiella pneumoniae* (15.7%) [Table 2].

Clinical assessment

During the clinical assessment of both antibiotic-resistant and antibiotic-susceptible organisms infected patients, mortality, hospital stay, and other clinical data were analyzed. The mortality rate observed in community-acquired respiratory tract infections (CA-RTIs), community-acquired urinary tract infections (CA-UTIs), community-acquired skin and soft tissue infections (CA-SSTIs), and community-acquired bloodstream infections (CA-BSIs) was 13.6%, 6.56%, 4.5%, and 31.5%, respectively. The length of hospital stay lasting more than three days was found to be 56.06%, 36.2%, 40.9%, and 73.6% in CA-RTIs, CA-UTIs, CA-SSTIs, and CA-BSIs, respectively [Table 3].

Discussion

Community spread of pathogens is more dangerous as it leads to a large increase in the population-at-risk and, subsequently, an increase in the number of MDR bacteria. The most critical danger is that if the community-acquired MDR infections cross the specific threshold, then the empiric therapy would be broad-spectrum antibacterial and/or combination antibacterial therapy.

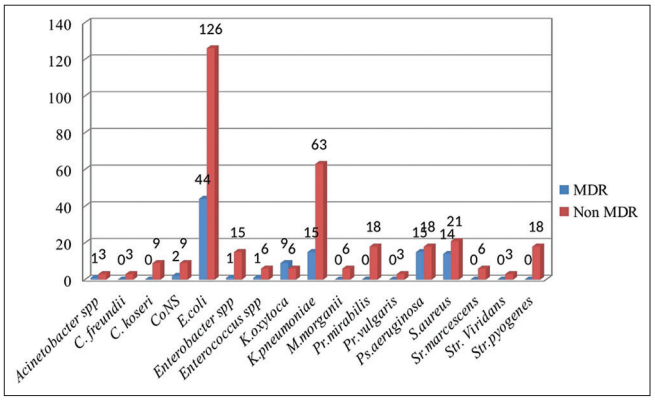

Figure 1: Distribution of MDR and non MDR pathogens in community acquired infections

Community-acquired MDR infection is considered a major public health concern because of increased length of hospital stay, worse outcomes, microbial resistance, drug-related adverse events, ICU admission and care, an increase in hospitalization costs, and the fact that drugs that are active against MDR infections tend to be less effective and more toxic than conventional agents.[6]

MDR bacteria are well recognized to be one of the most important current public health problems. Hospital-acquired MDR pathogens and their serious consequences have been published worldwide; infections due to these have been frequent. Whereas community-acquired MDR pathogens are emerging nowadays, this is because, first and most importantly, there is misuse of antibiotics in veterinary medicine and animal husbandry, and secondly, no usage restrictions for antibiotics.

Community-acquired infections

A community-acquired infection was defined as an infection contracted outside of a healthcare facility or an infection present at the time of admission. Very few research works were published on all community-acquired infections among hospitalized patients.[7] Most of the studies projected either more severe forms of infections, like

Table 2: Distribution of various pathogens among various community-acquired infections

Pathogens	MDR pathogens	%	Non-MDR pathogens	%	Total	%
CA-RTIs						
Klebsiella pneumoniae	7	24.1	22	75.8	29	42.02
Streptococcus pyogenes	0	0	14	100	14	20.2
Staphylococcus aureus	3	25	9	75	12	17.3
Acinetobacter	1	25	3	75	4	5.7
Pseudomonas aeruginosa	3	60	2	40	5	7.2
Streptococci viridans	0	0	3	100	3	4.3
Klebsiella oxytoca	2	100	0	0	2	2.8
Total	16	23.1	53	76.8	69	100
CA-UTIs						
Escherichia coli	40	28.7	99	71.2	139	49.2
Klebsiella pneumoniae	7	18.4	31	81.5	38	13.4
Staphylococcus aureus	5	71.4	2	28.5	7	2.4
CoNS	0	0	2	100	2	0.7
Enterobacter	1	6.25	15	93.7	16	5.6
Pseudomonas aeruginosa	11	42.3	15	57.6	26	9.2
Klebsiella oxytoca	6	66.6	3	33.3	9	3.1
Citrobacter freundii	0	0	3	100	3	1.06
Citrobacter koseri	0	0	9	100	9	3.1
Morganella morganii	0	0	6	100	6	2.1
Proteus mirabilis	0	0	18	100	18	6.3
Proteus vulgaris	0	0	3	100	3	1.06
Serratia	0	0	6	100	6	2.1
CA-BSIs						
Escherichia coli	2	40	3	60	5	26.3
Klebsiella pneumoniae	1	33.3	2	66.6	3	15.7
Klebsiella oxytoca	1	25	3	75	4	21.05
Streptococcus pyogenes	0	0	2	100	2	10.5
Staphylococcus aureus	1	33.3	2	66.6	3	15.7
Pseudomonas. aeruginosa	1	50	1	50	2	10.5
Total	6	31.5	13	68.4	19	100
CA-SSTIs						
Streptococcus pyogenes	0	0	2	100	2	3.92
Staphylococcus aureus	5	38.4	8	61.5	13	25.4
CoNS	2	22.2	7	77.7	9	17.6
Enterococcus	1	14.2	6	85.7	7	13.7
Escherichia coli	2	12.5	14	87.5	16	31.3
Klebsiella pneumoniae	0	0	4	100	4	7.8
Total	10	19.6	41	80.3	51	100

CoNS: Coagulase Negative Staphylococci

pneumonia,[8] urinary tract infections,[9] bacteremia,[10] or a specific pathogen or antibiotic resistance. This is the reason we chose this research work on all hospitalized patients with community-acquired infections with a special focus on MDR pathogens.

Todorovic Markovic M *et al.*[7] found the most common focus of infection to be the lower respiratory tract (39%), and urinary tract (19%), followed by the skin, soft tissues, and bones (9%). The site of infection was not found in 26% of all infections.

Todorovic Markovic M *et al.*[7] observed that among Gram-positive microorganisms *Staphylococcus aureus* (16%) and *Streptococcus pneumoniae* (7%) were predominant pathogens. *Escherichia coli* (30%) was a major bacteria isolated among Gram-negative pathogens. Two percent of all positive tests were anaerobes and 1.6% were *Candida* species. The predominance of Gram-negative infections among community-acquired sepsis was documented by Henriksen *et al.*[11]

Community-acquired respiratory tract infections

CA-RTIs are among the most common infections causing major morbidities and mortalities.[12] The World Health Organization recorded 1.6–2.2 million deaths caused by acute respiratory illness in children aged <5 years.[13] A study on MDR pathogens in Community acquired pneumonia (CAP) patients stated that 30% of patients with pneumonia caused by MDR organisms were categorized as CAP.[14]

In this study, the most common pathogens isolated from respiratory samples were *Klebsiella pneumoniae* (26.6%), *Streptococcus pyogenes* (21.3%), *Staphylococcus aureus* (18.6%). In Asia, CAP causative agents observed were 29% *Streptococcus pneumoniae*,

Table 3: Clinical outcome of community-acquired infections

	MDR group	Non-MDR group	*P*	Statistical significance
CA-RTIs				
Mortality	5 (33.3%)	4 (7.8%)	0.0233	SS
LOS >3 days	12 (80%)	25 (49.01%)	0.0415	SS
RR >64	13 (86.6%)	28 (54.9%)	0.0342	SS
CURB 65 score ≥4	11 (73.3%)	18 (35.2%)	0.0163	SS
MV	12 (80%)	7 (13.7%)	<0.00001	SS
CA-UTIs				
Mortality	2 (3.07)	15 (7.7)	0.254	NS
LOS >3 days	38 (58.4)	56 (28.8)	0	SS
Temp >36	57 (87.6)	158 (81.4)	0.339	NS
Pus cells in urine >10 cells/HPF	54 (83.07)	142 (73.1)	0.133	NS
Progressed to bacteremia	7 (10.7)	25 (12.8)	0.828	NS
CA-SSTIs				
Mortality	0	2 (5.5)	-	-
LOS >3 days	6 (75)	12 (33.3)	0.0478	SS
Debridement/surgery required	5 (62.5)	25 (69.4)	0.6951	NS
Progressed to bacteremia	6 (75)	9 (25)	0.0126	SS
CA-BSIs				
Mortality	4 (66.6)	2 (15.3)	0.046	SS
LOS >3 days	5 (83.3)	9 (69.2)	1	NS
Charlson index	4 (66.6)	8 (61.5)	1	NS

SS: statistically significant; NS: not significant. ++++. HPF: High Power Field

15% *Haemophilus influenzae*, 13% *Chlamydia pneumoniae*, and 11% *Mycoplasma pneumoniae*.[15] A study on 84 CA-RTIs at the emergency department revealed 22% human rhinovirus, 17% *Streptococcus pneumoniae*, 10% metapneumovirus, and 10% influenza A virus.[16] *Mycobacterium tuberculosis* was the predominant pathogen (20%) in a study done in Zambia.[17] There is a wide variation in the etiologies in different countries like viruses, bacteria, tuberculosis, and fungi; knowing the pathogen and its antibiotic susceptibility pattern is most important to formulate guidelines on empirical therapy.

A study in Italy on New Delhi metallo-β-lactamase (NDM)-producing *Enterobacteriaceae* bloodstream stream infections observed that a significant proportion of patients infected with NDM-producing pathogens were of community origin.[18] MDR pathogen gene exchange and their diffusion in the community are posing a public health threat.

Historically, *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Legionella* species have accounted for the most common causes of community-acquired pneumonia.[19] Among MDR organisms, PES pathogens like *Pseudomonas aeruginosa*, extended-spectrum β-lactamase-producing *Enterobacterales*, and MRSA are emerging in hospital-based settings.[20] In recent years, carbapenem-resistant *Enterobacteriaceae* (CRE), MDR *Pseudomonas aeruginosa*, and *Acinetobacter* have emerged in communities or long-term facilities. It is quite challenging for clinicians, pharmacists, researchers, and public health authorities eliminate these pathogens and to treat infections.[21]

In review outcome studies among CAP patients, mortality rates varied depending on the site of care; it was about 5.1% for outpatients plus inpatients and 13.6% for inpatients alone.[22] Administration of antibiotics within eight hours of admission at the emergency room (ER) department was associated with a 15% decrease in the odds of death among hospitalized patients with CAP.[23] Few studies have identified a significant risk of complications, length of hospital stay, and mortality rate among patients with MDR pathogens compared to non-MDR-infected patients.[24,25] In one study, they observed that in patients with antimicrobial-resistant pneumococcal infections, the length of stay and rate of complications were not significantly worse.[26]

Despite improvements in management, severe CAP is associated with significant mortality. Many organizations and researchers validated a few scores for the estimation of community-acquired pneumonia severity, which helps in the estimation of mortality and determining inpatient versus outpatient treatment. Few validated or proposed scores such as the CURB-65 score,[27] ARUC score,[14] PES score,[28] Drug Resistant in Pneumonia (DRIP) score[29] aid in identifying patients at high risk of pneumonia and at risk of acquiring MDR pathogens.

Community-acquired urinary tract infections

Enterobacteriaceae are most commonly responsible for community-acquired infections. MDR *Enterobacteriaceae* are considered when they are mediated by extended-spectrum beta-lactamases (ESBL).

As per the current study observations, *Escherichia coli* (57.2%) and *Klebsiella pneumoniae* (23.9%) dominate as predominant pathogens of CA-UTIs, which accounting for 81.1% of total urine samples. Our study is supported by many other studies listed here.

Bahadin J *et al.*[30] *Escherichia coli* and *Klebsiella* species are the most prevalent organisms responsible for CA-UTIs. Other bacteria isolated from UTI include *Enterococcus* species, *Proteus* species, *Pseudomonas aeruginosa*, and *Staphylococci* among others. Many research studies from different countries also observed *Escherichia coli* as the most frequent uropathogen isolated in CA-UTIs.[31–34] It was about 50% of isolates. *Staphylococcus aureus* is a predominant pathogen in a few countries. A study in Uganda[35] reported *Staphylococcus aureus* as the predominant pathogen, which was 46.3%, and another study from the same region identified *Staphylococcus aureus* as the second most common pathogen with an isolation rate of 15.4%.[36] The microbiota differs in each region, which is why antibiotic treatment guidelines are different for each country.

A study on community-acquired MDR pathogens causing urinary tract infection among patients ≥65 years revealed length of hospital stay ($P = 0.029$) and inadequate empirical antimicrobial therapy (IEAT) ($P < 0.001$) were statistically high in the MDR group when compared to the non-MDR group. There was no significant difference in mortality rate between MDR and non-MDR groups.[37]

Community-acquired skin and soft tissue infections

SSTIs are one of the most common diseases presented to the emergency department. The most common CA-SSTIs presented in this study were abscesses, infected ulcers, and cellulitis. In the United States (US), an estimated 29.7 SSTI-related ER visits per 1000 population in 2014.[38]

In the present study, *Staphylococcus aureus* is the most common cause of SSTIs, which is supported by other studies.[39,40] Ray GT *et al.*[41] found that 80% of culture-positive SSTIs were *Staphylococcus aureus*, and half of those were MRSA. Other important pathogens identified were beta-hemolytic *streptococci* (9%), *Escherichia coli* (4%), and *Pseudomonas aeruginosa* (3%). In a case-control study in Spain on community-onset MDR infections, the most frequently isolated microorganisms were *Escherichia coli* (102/194), *Klebsiella* species (25/194), and *Staphylococcus. aureus* (25/194).[42] A one-year multicentric prospective study of the US noted that 4% of *Escherichia coli* community-onset isolates were ESBL producers.[43]

Community-acquired bloodstream infections

Community-onset bloodstream infections are those that occur in outpatients or are first identified <48 h after admission to the hospital, and they may be sub-classified further as healthcare-associated, when they occur in patients with significant prior healthcare-associated exposure, or community-associated, in other cases. Antimicrobial-resistant organisms, most notably MRSA and ESBL/ Metallobeta lactamase (MBL)-producing *Enterobacteriaceae*, have emerged as important etiologies of community-onset BSI.[44]

Similar to the study, many other overall population-based studies noted that *Escherichia coli* is the most common cause of BSIs.[45,46] A prospective study on South and Southeast Asia published in databases between 1990 and 2010 revealed that 9% of the studied population was confirmed to have community-acquired bacteremia. *Salmonella enterica serotype Typhi* was the most common bacterial pathogen (30%), followed by *Staphylococcus aureus, Escherichia Coli,* and other Gram-negative organisms. *Salmonella Typhi* (25%), *Streptococcus pneumoniae*, and *H. influenzae* infections were observed in children.[47] A study in Chennai observed 14.3% MRSA, 60% ESBL *Escherichia coli*, 20% MDR *Acinetobacter baumannii*, and 20% MDR *Pseudomonas aeruginosa* isolates among community-acquired BSIs.[48]

Strengths

To the best of our knowledge, this is the first study on bacteriology, focusing on the infection and clinical profile of hospitalized patients with community-acquired infections. Our study might be helpful to clinicians, public health experts, and epidemiologists in tackling the public health challenge of emerging community-acquired antibiotic-resistant infections.

Limitations

The limitations of this study are that the identification of fastidious pathogens, which are a common cause of community-acquired infections like *Legionella, Mycoplasma, Chlamydia*, and *Neisseria* is quite challenging in our country despite the medical advancements in infection management; could not test these organisms routinely due to the high test price. Assessment by conventional culture methods for the detection of pathogens, knowing that it has low sensitivity, is a time-consuming procedure, and cannot rapidly provide a result during the early acute phase of presentation.

Future researchers on community-acquired MDR pathogen burden in different geographies help to know whether the epidemiology is shifting and if so whether the shift holds across other states and regions.

Conclusion

Patients who have a community-onset infection and who don't meet any of the criteria related to a healthcare-associated infection are considered to be community-acquired. MDR bacteria could be a colonizer acquired from the community or a pathogen, so it is important to know the timing of colonization, rather than the timing of the diagnosis of infection to determine the origin of MDR bacteria.

The most common pathogens of community-acquired infections such as respiratory tract infections, urinary tract infections, and bacteremia are the *Enterobacteriaceae* family. MDR pathogens spreading in communities cause devastation as they can diffuse in elderly populations in long-term care facilities or those who stay at home for a longer time with multiple comorbidities. Patients affected by community-acquired MDR pathogens pose a more critical danger and are quite challenging for clinicians due to the limited availability of antibiotics when compared to non-MDR

pathogen-infected patients. Active surveillance of MDR cases and pathogens associated with the emergency department will definitely aid us in avoiding the transmission of infections through early identification. Performing cultures earlier during hospitalization and determining the timing of colonization can allow more targeted choices and reduce morbidity and mortality rates among infected patients.

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Conflicts of interest

There are no conflicts of interest.

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